

FILED

**IN THE UNITED STATES DISTRICT COURT
FOR THE EASTERN DISTRICT OF VIRGINIA
ALEXANDRIA DIVISION**

2012 JUN -1 P 1:09
CLERK US DISTRICT COURT
ALEXANDRIA, VIRGINIA

HUMAN GENOME SCIENCES, INC.)

Plaintiff,)

v.)

Case No.: 1:12cv607
GBL/TCB

DAVID J. KAPPOS, in his official capacity as)
Under Secretary of Commerce for Intellectual)
Property and Director of the United States Patent)
and Trademark Office)

Defendant.)

COMPLAINT

Plaintiff Human Genome Sciences, Inc. ("HGS"), for its complaint against the Honorable David J. Kappos ("Defendant"), states as follows:

NATURE OF THE ACTION

1. This is an action by the assignee of United States Patent No. 8,071,092 ("the '092 patent") seeking judgment, pursuant to 35 U.S.C. § 154(b)(4)(A), that the patent term adjustment for the '092 patent be changed from 1,597 days to 2,654 days.

JURISDICTION AND VENUE

2. This action arises under 35 U.S.C. § 154 and the Administrative Procedure Act, 5 U.S.C. §§ 701-706.

3. This Court has jurisdiction to hear this action and is authorized to issue the relief sought pursuant to 28 U.S.C. §§ 1331, 1338(a), and 1361, 35 U.S.C. § 154(b)(4)(A), and 5 U.S.C. §§ 701-706.

4. Venue is proper in this district by virtue of 35 U.S.C. § 154(b)(4)(A).

5. This Complaint is being timely filed in accordance with 35 U.S.C. § 154(b)(4)(A) and Fed. R. Civ. P. 6(a)(3).

THE PARTIES

6. Plaintiff HGS is a corporation, organized, existing, and doing business under and by virtue of the laws of the State of Delaware, with its principal place of business located at 14200 Shady Grove Road, Rockville, MD 20850.

7. Defendant David J. Kappos is sued in his official capacity as Under Secretary of Commerce for Intellectual Property and Director of the United States Patent and Trademark Office (“PTO”). The Director of the PTO is designated by statute as the official responsible for determining the period of patent term adjustments and, therefore, is the proper defendant in a suit seeking review of such determinations. See 35 U.S.C. §§ 154(b)(3) and 154(b)(4)(A).

BACKGROUND

Patent Term Adjustments

8. Section 154 of title 35 of the United States Code requires that the Director of the PTO grant a patent term adjustment (“PTA”) in accordance with the provisions of section 154(b).

9. In determining PTA, the Director of the PTO must take into account “PTO Delay” under 35 U.S.C. § 154(b)(1), any overlap in “PTO Delay” under 35 U.S.C. § 154(b)(2)(A), and any “Applicant Delay” under 35 U.S.C. § 154(b)(2)(C).

10. “PTO Delay” under 35 U.S.C. § 154(b)(1) breaks down into three categories known as “A Delay,” “B Delay,” and “C Delay.” Only “A Delay” and “B Delay” are at issue in this case.

11. “A Delay” occurs when the PTO fails to act within a particular time period, for example, if the PTO does not “issue a patent within 4 months after the date on which the issue fee was paid . . . and all outstanding requirements were satisfied.” See 35 U.S.C. § 154(b)(1)(A). The statute provides that “the term of the patent shall be extended 1 day for each day after the end of the period specified . . . until the action described . . . is taken.” *Id.*

12. “B Delay” occurs when the PTO fails to issue a patent within three years of the actual filing date of the patent application, excluding certain periods of delay attributable to the applicant. See 35 U.S.C. § 154(b)(1)(B). Similar to “A delays,” the statute provides that “the term of the patent shall be extended 1 day for each day after the end of that 3-year period until the patent is issued.” *Id.*

13. 35 U.S.C. § 154(b)(3)(B) states that “the Director shall- (i) make a determination of the period of any patent term adjustment under this subsection, and shall transmit a notice of that determination with the written notice of allowance of the application”

14. The PTO had taken the position that whenever an application is subject to both “A Delay” and “B Delay,” those periods always “overlap” within the meaning of 35 U.S.C. § 154(b)(2)(A) even if they occur on different calendar days. Thus, for the purposes of PTA, the PTO counted the greater of the “A Delay” or the “B Delay,” but never both periods of delay.

15. In *Wyeth v. Dudas*, 580 F. Supp. 2d 138 (D.D.C. 2008), the District Court for the District of Columbia rejected the PTO’s interpretation of 35 U.S.C. § 154(b)(2)(A), and this holding was affirmed by the Federal Circuit in *Wyeth v. Kappos*, 591 F.3d 1364 (Fed. Cir. 2010). The Court held that “[t]he only way that periods of time can ‘overlap’ is if they occur on the same day” under 35 U.S.C. § 154(b)(2). *Id.* at 141. Thus, “[i]f an ‘A delay’ occurs on one

calendar day and a 'B delay' occurs on another, they do not overlap, and § 154(b)(2)(A) does not limit the extension to one day." *Id* at 141-42.

16. "Applicant Delay" under 35 U.S.C. § 154(b)(2)(C) arises where an applicant "failed to engage in reasonable efforts to conclude prosecution of the application," and results in a reduction of any accumulated PTA. See 37 C.F.R. § 1.704(a). The Director has prescribed regulations setting out the specific circumstances deemed to be "Applicant Delay." See 37 C.F.R. § 1.704.

17. Under 35 U.S.C. § 154(b)(4)(A), "[a]n applicant dissatisfied with a determination made by the Director under paragraph (3) shall have remedy by a civil action against the Director filed in the United States District Court for the Eastern District of Virginia within 180 days after the grant of the patent. Chapter 7 of title 5 shall apply to such action."

The '092 Patent

18. Guo-Liang Yu, Reinhard Ebner, and Jian Ni are the inventors (also referred to as "Applicants") of the '092 patent, entitled "Methods of Inhibiting B Lymphocytes Using Antibodies to Neutrokin-alpha," which issued from U.S. Patent Application No. 09/589,288 ("the '288 application") on December 6, 2011. The '092 patent is attached hereto as Exhibit A.

19. HGS is the assignee of the '092 patent, as evidenced by the assignment document recorded at the PTO for the parent application, U.S. Patent Application No. 09/507,968.

20. The '288 application that issued as the '092 patent was filed on June 8, 2000, and, therefore, the '092 patent is eligible for patent term adjustment under 35 U.S.C. § 154.

21. The '092 patent is subject to a terminal disclaimer based on the expiration date of the full statutory term of U.S. Patent No. 7,879,328. The 20-year patent term for U.S. Patent No. 7,879,328 expires on June 15, 2021. The face of U.S. Patent No. 7,879,328 indicates that it is entitled to 762 days of patent term adjustment.

PTO PTA Calculation Errors

22. Both the PTO's calculation of "PTO Delay" arising under 35 U.S.C. § 154(b)(1)(A)(iv) (also referred to as "A Delay") and the PTO's calculation of "PTO Delay" arising under 35 U.S.C. § 154(b)(1)(B) (also referred to as "B Delay") are in error.

23. An "Application for Patent Term Adjustment Pursuant to 37 C.F.R. § 1.705(b)" (hereinafter "First Petition to Correct PTA") was filed by Applicants with the PTO on October 25, 2011, in an effort to have the PTO correct PTA calculation errors identified herein. The PTO "dismissed as premature" the First Petition to Correct PTA by way of a "Decision on Request for Reconsideration of Patent Term Adjustment" dated November 4, 2011.

24. An "Application for Patent Term Adjustment (37 C.F.R. § 1.705(d)) and Statement of the Correct Patent Term Adjustment and Basis Therefor Under 37 C.F.R. § 1.702" (hereinafter "Second Petition to Correct PTA") was filed by Applicants with the PTO on February 6, 2012, in an effort to have the PTO correct PTA calculation errors identified herein. The PTO "dismissed" (i.e., denied) the Second Petition to Correct PTA by way of a "Decision on Request for Reconsideration of Patent Term Adjustment" dated February 28, 2012.

Improper Calculation of "A Delay"

25. Under 35 U.S.C. § 154(b)(1)(A)(iv), the failure of the PTO to "issue a patent within 4 months after the date on which the issue fee was paid under section 151 and all outstanding requirements were satisfied" results in an extension of the patent term by "1 day for each day after the end of the period." Such a delay by the PTO is one of several types of delay by the PTO referred to as "A Delay."

26. Under 37 C.F.R. § 1.703(a)(6), "[t]he period of adjustment . . . is . . . [t]he number of days, if any, in the period beginning on the day after the date that is four months after the date

the issue fee was paid and all outstanding requirements were satisfied and ending on the date a patent was issued.”

27. A Notice of Allowance was mailed by the PTO with respect to the ‘288 application on July 27, 2009.

28. An issue fee transmittal, together with the payment of the appropriate issue fee, was timely filed by Applicants with respect to the ‘288 application on October 22, 2009, which is within the required three months of the July 27, 2009, mailing date of the Notice of Allowance, thereby satisfying the requirements under 37 C.F.R. § 1.703(a)(6) on October 22, 2009.

29. The day after the date that is four months after the date the issue fee was paid and all outstanding requirements were satisfied is February 23, 2010.

30. An Issue Notification was mailed by the PTO with respect to the ‘288 application on September 15, 2010, indicating a projected patent issue date of October 5, 2010.

31. A petition to withdraw the ‘288 application from issue, together with a Request for Continued Examination (“RCE”), was filed by Applicants on September 23, 2010. As such, Applicants ended the period of adjustment under 37 C.F.R. § 1.703(a)(6) on September 23, 2010, prior to issuance of the ‘092 patent.

32. The PTO failed to issue the ‘092 patent within 4 months after the date the issue fee was paid by Applicants and all outstanding requirements were satisfied.

33. The PTO’s PTA calculation indicates that the total “A Delay” is 1,677 days. The PTO’s PTA calculation does not reflect any delay by the PTO to issue the ‘092 patent within 4 months after the issue fee was paid by Applicants and all outstanding requirements were satisfied.

34. The “A Delay” properly includes the time period from the day after the date four months after the issue fee was paid by Applicants and all outstanding requirements were satisfied (i.e., February 23, 2010) to the date Applicants filed a petition to withdraw the patent from issue (i.e., September 23, 2010), which is a time period of 213 days. See 35 U.S.C. § 154(b)(1)(A) and 37 C.F.R. § 1.703(a)(6).

35. In calculating only 1,677 days for the period of “A Delay,” the PTO failed to correctly calculate the period of “A Delay” by failing to include the period of 213 days of PTO delay from the day after the date four months after the issue fee was paid by Applicants and all outstanding requirements were satisfied (i.e., February 23, 2010) to the date Applicants filed a petition to withdraw the patent from issue (i.e., September 23, 2010), as required by 35 U.S.C. § 154(b)(1)(A) and 37 C.F.R. §§ 1.702(a) and 1.703(a). Therefore, the correct period of A delay is 1,890 days (i.e., 1,677 days + 213 days).

Improper Calculation of “B Delay”

36. Under 35 U.S.C. § 154(b)(1)(B), the failure of the PTO to “issue a patent within 3 years after the actual filing date of the application” results in an extension of the patent term by “1 day for each day after the end of that 3-year period until the patent is issued.” Such a delay by the PTO is referred to as “B Delay.”

37. Under 37 C.F.R. § 1.703(b), “[t]he period of adjustment . . . is the number of days, if any, in the period beginning on the day after the date that is three years after the date on which the application was filed . . . and ending on the date a patent was issued, but not including the sum of [recited] periods.”

38. The day after the date that is three years after the date on which the ‘288 application was filed is June 9, 2003.

39. The ‘092 patent issued on December 6, 2011.

40. The number of days in the period beginning on the day after the date that is three years after the date on which the '288 application was filed (i.e., June 9, 2003) and ending on the date the '092 patent was issued (i.e., December 6, 2011) is 3,103 days.

41. 35 U.S.C. § 154(b)(1)(B) also states that the period of delay due to the failure of the PTO to issue a patent within 3 years after the actual filing date does not include, *inter alia*, (a) "any time consumed by continued examination of the application requested by the applicant under section 132(b)," (b) "any time consumed by a proceeding under section 135(a)," i.e., an interference proceeding, and (c) "any time consumed by appellate review by the Board of Patent Appeals and Interferences [("BPAI")]."

42. A Notice of Appeal was filed by Applicants with respect to the '288 application on February 12, 2003.

43. In response to the Notice of Appeal, an Office Action under 35 U.S.C. § 132 was mailed by the PTO on June 3, 2003.

44. Jurisdiction over the '288 application did not pass to the BPAI between the time of the filing of the Notice of Appeal by Applicants on February 12, 2003, and the mailing of an Office Action by the PTO on June 3, 2003.

45. The number of days beginning on the date on which the Notice of Appeal was filed by Applicants on February 12, 2003, and ending on the date of mailing of an action by the PTO under 35 U.S.C. § 132 on June 3, 2003, is 112 days (hereinafter referred to as "Time Period 1").

46. A first RCE was filed by Applicants with respect to the '288 application on December 2, 2004.

47. The PTO declared an interference involving the '288 application on August 15, 2006.

48. The PTO has treated the interference involving the '288 application as terminated on September 15, 2008.

49. The number of days beginning on the date the interference involving the '288 application was declared by the PTO on August 15, 2006, and ending on the date on which the interference involving the '288 application has been treated as terminated by the PTO on September 15, 2008, is 763 days (hereinafter referred to as "Time Period 2").

50. The PTO mailed a first Notice of Allowance to Applicants on July 27, 2009.

51. The number of days beginning on the date of the filing of the first RCE by Applicants on December 2, 2004, until the date on which the PTO mailed the first Notice of Allowance to Applicants on July 27, 2009, is 1,698 days (hereinafter referred to as "Time Period 3").

52. Time Period 3 wholly encompasses Time Period 2, and Time Period 3 exclusive of Time Period 2 consists of 935 days.

53. A second RCE was filed by Applicants with respect to the '288 application on September 23, 2010.

54. The number of days beginning on the date on which the PTO mailed the first Notice of Allowance to Applicants on July 27, 2009, until the date of the filing of the second RCE by Applicants on September 23, 2010, is 423 days (hereinafter referred to as "Time Period 4").

55. The PTO mailed a second Notice of Allowance to Applicants on July 25, 2011.

56. The number of days beginning on the date of the filing of the second RCE by Applicants on September 23, 2010, until the date on which the PTO mailed the second Notice of Allowance to Applicants on July 25, 2011, is 305 days (hereinafter referred to as "Time Period 5").

57. The number of days beginning on the date on which the PTO mailed the second Notice of Allowance to Applicants on July 25, 2011, and ending on the date on which the PTO issued the '092 patent on December 6, 2011, is 135 days (hereinafter referred to as "Time Period 6").

58. The period of "B Delay" calculated by the PTO is 430 days.

Time Period 1 – "B Delay" Calculation Relating to Notice of Appeal

59. 35 U.S.C. § 154(b)(1)(B) states that the period of delay due to the failure of the PTO to issue a patent within 3 years after the actual filing date does not include "any time consumed by appellate review by the Board of Patent Appeals and Interferences."

60. 37 C.F.R. § 1.703(b)(4) states that the period of adjustment under § 1.702(b) does not include "[t]he number of days, if any, in the period beginning on the date on which a notice of appeal to the Board of Patent Appeals and Interferences was filed under 35 U.S.C. 134 and § 41.31 of this title and ending on the date of the last decision by the Board of Patent Appeals and Interferences or by a Federal court in an appeal under 35 U.S.C. 141 or a civil action under 35 U.S.C. 145, or on the date of mailing of either an action under 35 U.S.C. 132, or a notice of allowance under 35 U.S.C. 151, whichever occurs first, if the appeal did not result in a decision by the Board of Patent Appeals and Interferences."

61. In calculating the period of "B Delay," the PTO erroneously included a reduction in the period of "B Delay" of 112 days for Time Period 1, i.e., the time period beginning on February 12, 2003, the date on which a Notice of Appeal was filed by Applicants, and ending on June 3, 2003, the date of mailing of an action by the PTO under 35 U.S.C. § 132.

62. The PTO issued a Notice of Proposed Rule Making on December 28, 2011, in which the PTO proposes to clarify the rules of practice to indicate that the period of appellate

review under the PTA provisions of 35 U.S.C. § 154(b)(1)(B) begins when jurisdiction over the application passes to the BPAI, rather than the date on which a Notice of Appeal to the BPAI is filed by the applicants. Proposed Rules, 76 Fed. Reg. 81432, 81437 (Dec. 28, 2011).

63. The Notice of Proposed Rule Making states, *inter alia*, that the PTO is proposing to amend 37 C.F.R. § 1.703(b)(4) to define the period of delay “as the sum of the number of days, if any, in the period beginning on the date on which jurisdiction over the application passes to the BPAI under § 41.35 of this title and ending on the date of a final decision in favor of the applicant by the BPAI or by a Federal court in an appeal under 35 U.S.C. 141 or a civil action under 35 U.S.C. 145.” Proposed Rules, 76 Fed. Reg. at 81435.

64. The period of delay calculated under 37 C.F.R. § 1.703(b)(4) for the ‘092 patent should be 0 days, i.e., Time Period 1 should not be excluded from the period of “B Delay,” because the filing of the Notice of Appeal did not result in jurisdiction over the ‘288 application passing to the BPAI.

65. Accordingly, the PTA calculation for the ‘092 patent should *not* include a reduction in the period of “B Delay” of 112 days, i.e., the period of “B Delay” should include Time Period 1, such that the period of “B Delay” as calculated by the PTO should be increased by 112 days.

Time Period 2 – “B Delay” Calculation Relating to Interference

66. 35 U.S.C. § 154(b)(1)(B) states that the period of delay due to the failure of the PTO to issue a patent within 3 years after the actual filing date does not include “any time consumed by a proceeding under section 135(a).” An interference is a proceeding under 35 U.S.C. § 135(a).

67. 37 C.F.R. § 1.703(b)(2) states that the period of adjustment under § 1.702(b) does not include “[t]he number of days, if any, in the period beginning on the date an interference was

declared or redeclared to involve the application in the interference and ending on the date that the interference was terminated with respect to the application.”

68. Accordingly, if the period of “B Delay” includes Time Period 2, i.e., the period beginning on August 15, 2006, the date on which an interference involving ‘288 application was declared by the PTO, and ending on September 15, 2008, the date the PTO has determined to be the termination date of the interference involving the ‘288 application, then the PTA calculation for the ‘092 patent should include a reduction in the period of “B Delay” of 763 days for Time Period 2.

Time Periods 3-6 – “B Delay” Calculation Relating to Filing of RCE

69. 35 U.S.C. § 154(b)(1)(B) states that the period of delay due to the failure of the PTO to issue a patent within 3 years after the actual filing date does not include “any time consumed by continued examination of the application requested by the applicant under section 132(b).”

70. In contrast to 35 U.S.C. § 154(b)(1)(B), 37 C.F.R. § 1.703(b) states that the period of time after the filing of an RCE is not to be considered in calculating the patent term adjustment under 37 C.F.R. § 1.702(b). Specifically, 37 C.F.R. § 1.703(b)(1) states that the period of adjustment does not include “the sum of . . . [t]he number of days, if any, in the period beginning on the date on which a request for continued examination of the application under 35 U.S.C. 132(b) was filed and ending on the date the patent was issued.”

71. In calculating the period of “B Delay,” the PTO erroneously subtracted Time Period 3, Time Period 4, Time Period 5, and Time Period 6. In effect, the PTO excluded from the period of “B Delay” all of the time after the filing of the first RCE by Applicants until the issuance of the ‘092 patent.

72. However, 37 C.F.R. § 1.703(b) is in conflict with 35 U.S.C. § 154(b)(1)(B). In particular, unlike 35 U.S.C. § 154(b)(1)(B), 37 C.F.R. § 1.703(b) indicates that the period of time after the filing of a RCE is not to be considered in calculating the patent term adjustment under 37 C.F.R. § 1.702(b). Thus, while the determination of patent term adjustment is controlled by 35 U.S.C. § 154, which contains no such exclusion of the time period from the filing of an RCE until the issue of the patent for purposes of calculating the PTA, 37 C.F.R. § 1.703(b) cuts off the PTA period under 35 U.S.C. § 154(b)(1)(B) with the filing of an RCE.

73. 37 C.F.R. § 1.703(b) should not control the determination of the PTA under 35 U.S.C. § 154(b)(1)(B) to the extent that the provisions of 37 C.F.R. § 1.703(b) conflict with the provisions of 35 U.S.C. § 154(b)(1)(B).

74. The period of “B Delay” should include Time Period 3, i.e., the period of time from the filing of the first RCE (i.e., December 2, 2004) until the mailing of the first Notice of Allowance (i.e., July 27, 2009), excluding the overlap with Time Period 2, i.e., the period of time for the interference.

75. The period of “B Delay” should include Time Period 4, i.e., the period of time from the mailing of the first Notice of Allowance (i.e., July 27, 2009) until the filing of the second RCE (i.e., September 23, 2010).

76. The period of “B Delay” should include Time Period 5, i.e., the period of time from the filing of the second RCE (i.e., September 23, 2010) until the mailing of the second Notice of Allowance (i.e., July 25, 2011).

77. The period of “B Delay” should include Time Period 6, i.e., the period of time from the mailing of the second Notice of Allowance (i.e., July 25, 2011) until the date of issuance of the ‘092 patent (i.e., December 6, 2011).

78. 37 C.F.R. § 1.702(b) indicates that “[a]ny delay in the processing of the application by the Office that was requested by the applicant” is not to be included in the consideration of the 3-year pendency guarantee.

79. Even assuming that the filing of an RCE is a delay in the processing of the application requested by the applicant, the subsequent indication by the PTO that the application is allowable ends such a delay and causes the application to be “back on track” with respect to typical prosecution in the absence of an RCE.

80. Under such an interpretation, the time period from an indication of allowability by the PTO and ending on the date the patent issued does not constitute “[a]ny delay in the processing of the application by the Office that was requested by the applicant,” such that the time period from an indication of allowability by the PTO and ending on date the patent issued should not be excluded from calculation of the period of “B Delay.”

81. Under such an interpretation, the filing of an RCE would cause the period of “B Delay” to include the period of time from one day after the 3-year pendency anniversary and ending on the date the patent issued minus the period of time from the filing of the RCE until the indication of allowability by the PTO (as opposed to ending on the patent issuance date). In other words, under such an interpretation, the period of “B Delay” would stop with the filing of an RCE by an applicant but would start again with the indication of allowability by the PTO because the application is “back on track.”

Correct Calculation of “B Delay”

82. The correct “B Delay” calculation should be 2,340 days when the period of B delay currently calculated by the PTO (i.e., 430 days) is adjusted to include (a) Time Period 1, i.e., the 112 days for the period beginning on February 12, 2003, the date on which a Notice of Appeal was filed, and ending on June 3, 2003, the date of mailing of an action under 35 U.S.C. § 132,

(b) Time Period 3, i.e., the 1,698 days for the period beginning on December 2, 2004, the date on which a first RCE was filed, until July 27, 2009, the date of mailing of a first Notice of Allowance, excluding overlapping Time Period 2, i.e., the 763 days for the period beginning on August 15, 2006, the date on which an interference involving '288 application was declared by the PTO, and ending on September 15, 2008, the date the PTO has determined to be the termination date of the interference involving the '288 application, (c) Time Period 4, i.e., the 423 days for the period beginning on July 27, 2009, the date of mailing of a first Notice of Allowance, until September 23, 2010, the date on which a second RCE was filed, (d) Time Period 5, i.e., the 305 days for the period beginning on September 23, 2010, the date on which a second RCE was filed, until July 25, 2011, the date of mailing of a second Notice of Allowance, and (e) Time Period 6, i.e., the 135 days for the period beginning on July 25, 2011, the date of mailing of a second Notice of Allowance, and ending on December 6, 2011, the date the '092 patent issued (i.e., 430 days + 112 days + 1698 days – 763 days + 423 days + 305 days + 135 days = 2,340 days).

Calculation of Overlap in PTO Delay

83. The PTO's patent term adjustment calculation indicates that the total "C Delay" is 763 days.

84. When the period of "B Delay" is corrected to include the period from the day after the date that is three years after the date on which the '288 application was filed (i.e., June 9, 2003) through the date the '092 patent issued (i.e., December 6, 2011), the entire period of "A Delay" (i.e., 1,890 days) overlaps with either "B Delay" or "C Delay," such that the total number of overlapping days between the "A Delay" and "B Delay" and between the "A Delay" and "C Delay" is 1,890 days.

85. When the period of “B Delay” includes a reduction for the period of time from the filing of the first RCE (i.e., from December 2, 2004) until the mailing of the first Notice of Allowance (i.e., until July 27, 2009), and the period of time from the filing of the second RCE (i.e., from September 23, 2010) until the mailing of the second Notice of Allowance (i.e., until July 25, 2011), 62 days of “A Delay” overlap with “B Delay,” and 763 days of “A Delay” overlap with “C Delay,” such that the total number of overlapping days between the “A Delay” and “B Delay” and between the “A Delay” and “C Delay” is 825 days.

86. When the period of “B Delay” includes a reduction for the period of time from the filing of the first RCE (i.e., from December 2, 2004) until the mailing of the second Notice of Allowance (i.e., until July 25, 2011), 62 days of “A Delay” overlap with “B Delay,” and 763 days of “A Delay” overlap with “C Delay,” such that the total number of overlapping days between the “A Delay” and “B Delay” and between the “A Delay” and “C Delay” is 825 days.

87. When the period of “B Delay” includes a reduction for the period from December 2, 2004, the date on which a first RCE was filed, through December 6, 2011, the date the ‘092 patent issued, 62 days of “A Delay” overlap with “B Delay,” and 763 days of “A Delay” overlap with “C Delay,” such that the total number of overlapping days between the “A Delay” and “B Delay” and between the “A Delay” and “C Delay” is 825 days.

Calculation of “Applicant Delay”

88. The PTO’s PTA calculation indicates that the total “Applicant Delay” under 37 C.F.R. § 1.704 is 449 days.

89. The PTO’s PTA calculation indicates an “Applicant Delay” of 92 days from May 21, 2001, the day after the date that is three months after the date of mailing of a Restriction Requirement, through August 20, 2001, on which date a Reply to Restriction Requirement was filed by Applicants.

90. The PTO's PTA calculation indicates an "Applicant Delay" of 86 days from February 7, 2002, the day after the date that is three months after the date of mailing of an Office Action, through May 3, 2002, on which date a Reply to Office Action was filed by Applicants.

91. The PTO's PTA calculation indicates an "Applicant Delay" of 91 days from November 14, 2002, the day after the date that is three months after the date of mailing of an Office Action, through February 12, 2003, on which date a Notice of Appeal was filed by Applicants.

92. The PTO's PTA calculation indicates an "Applicant Delay" of 90 days from September 4, 2003, the day after the date that is three months after the date of mailing of an Office Action, through December 2, 2003, on which date a Reply to Office Action was filed by Applicants.

93. The PTO's PTA calculation indicates an "Applicant Delay" of 90 days from September 4, 2004, the day after the date that is three months after the date of mailing of an Office Action, through December 2, 2004, on which date a Request for Continued Examination was filed by Applicants.

94. Other than the circumstances described above, there have been no circumstances that could reasonably be construed as a failure of Applicants to engage in reasonable efforts to conclude processing or examination of this application.

Correct PTA Calculation

95. When the period of "B Delay" is corrected to include the period from the day after the date that is three years after the date on which the '288 application was filed (i.e., June 9, 2003) until the date the '092 patent issued (i.e., December 6, 2011), the correct PTA is 2,654 days. The correct PTA represents the combination of (1) the examination delay of 1,890 days by the PTO under 37 C.F.R. §§ 1.702(a) and 1.703(a), (2) the examination delay of 2,340 days by

the PTO under 37 C.F.R. §§ 1.702(b) and 1.703(b), and (3) the examination delay of 763 days by the PTO under 37 C.F.R. §§ 1.702(c)-(e) and 1.703(c)-(e), *minus* 1890 overlapping days between the “A Delay” and “B Delay,” and the “A Delay” and “C Delay,” *minus* 449 days of “Applicant Delay” under 37 C.F.R. § 1.704 (i.e., $(1,890 + 2,340 + 763) - 1890 - 449 = 2,654$).

96. If the period of “B Delay” is corrected to include the period from the day after the date that is three years after the date on which the ‘288 application was filed (i.e., June 9, 2003) through the date the ‘092 patent issued (i.e., December 6, 2011), minus the period of time from the filing of the first RCE (i.e., from December 2, 2004) until the mailing of the first Notice of Allowance (i.e., until July 27, 2009), and minus the period of time from the filing of the second RCE (i.e., from September 23, 2010) until the mailing of the second Notice of Allowance (i.e., until July 25, 2011), then the PTA would be 2,479 days. This PTA represents the combination of (1) the examination delay of 1,890 days by the PTO under 37 C.F.R. §§ 1.702(a) and 1.703(a), (2) the examination delay of 1,100 days by the PTO under 37 C.F.R. §§ 1.702(b) and 1.703(b), and (3) the examination delay of 763 days by the PTO under 37 C.F.R. §§ 1.702(c)-(e) and 1.703(c)-(e), *minus* 825 overlapping days between the “A Delay” and “B Delay,” and the “A Delay” and “C Delay,” *minus* 449 days of “Applicant Delay” under 37 C.F.R. § 1.704 (i.e., $(1,890 + 1,100 + 763) - 825 - 449 = 2,479$).

97. If the period of “B Delay” is corrected to include the period from the day after the date that is three years after the date on which the ‘288 application was filed (i.e., June 9, 2003) through the date the ‘092 patent issued (i.e., December 6, 2011), minus the period of time from the filing of the first RCE (i.e., from December 2, 2004) until the mailing of the second Notice of Allowance (i.e., until July 25, 2011), then the PTA would be 2,056 days. This PTA represents the combination of (1) the examination delay of 1,890 days by the PTO under 37 C.F.R. §§

1.702(a) and 1.703(a), (2) the examination delay of 677 days by the PTO under 37 C.F.R. §§ 1.702(b) and 1.703(b), and (3) the examination delay of 763 days by the PTO under 37 C.F.R. §§ 1.702(c)-(e) and 1.703(c)-(e), *minus* 825 overlapping days between the “A Delay” and “B Delay,” and the “A Delay” and “C Delay,” *minus* 449 days of “Applicant Delay” under 37 C.F.R. § 1.704 (i.e., $(1,890 + 677 + 763) - 825 - 449 = 2,056$).

98. If the period of “B Delay” includes a reduction for the period from the date on which a first RCE was filed (i.e., December 2, 2004) through the date the ‘092 patent issued (i.e., December 6, 2011), then the PTA would be 1,921 days. This PTA represents the combination of (1) the examination delay of 1,890 days by the PTO under 37 C.F.R. §§ 1.702(a) and 1.703(a), (2) the examination delay of 542 days by the PTO under 37 C.F.R. §§ 1.702(b) and 1.703(b), (3) the examination delay of 763 days by the PTO under 37 C.F.R. §§ 1.702(c)-(e) and 1.703(c)-(e), *minus* 825 overlapping days between the “A Delay” and “B Delay,” and the “A Delay” and “C Delay,” *minus* 449 days of “Applicant Delay” under 37 C.F.R. § 1.704 (i.e., $(1,890 + 542 + 763) - 825 - 449 = 1,921$).

99. The PTO’s determination of the PTA for the ‘092 patent was arbitrary, capricious, an abuse of discretion, or otherwise not in accordance with law under 5 U.S.C. § 706(2)(A).

CLAIM FOR RELIEF

100. The allegations of paragraphs 1-99 are incorporated in this claim for relief as if fully set forth herein.

101. The PTA for the ‘092 patent, as determined by the Defendant under 35 U.S.C. § 154(b) and listed on the face of the ‘092 patent, is 1,597 days. See Exhibit A at 1.

102. Under 35 U.S.C. § 154(b)(1)(A), Plaintiff is entitled to an adjustment of the term of the '092 patent of 1,890 days, the number of days attributable to PTO examination delay ("A Delay").

103. Under 35 U.S.C. § 154(b)(1)(B), Plaintiff is entitled to an adjustment of the term of the '092 patent of 112 days, which is the number of days for the period beginning on February 12, 2003, the date on which a Notice of Appeal was filed, and ending on June 3, 2003, the date of mailing of an action under 35 U.S.C. § 132 ("B Delay").

104. Under 35 U.S.C. § 154(b)(1)(B), Plaintiff is entitled to an adjustment of the term of the '092 patent of 1,698 days, which is the number of days for the period beginning on December 2, 2004, the date on which a first RCE was filed, until July 27, 2009, the date of mailing of a first Notice of Allowance, excluding 763 days for the period beginning on August 15, 2006, the date on which an interference involving '288 application was declared by the PTO, and ending on September 15, 2008, the date the PTO has determined to be the termination date of the interference involving the '288 application ("B Delay").

105. Under 35 U.S.C. § 154(b)(1)(B), Plaintiff is entitled to an adjustment of the term of the '092 patent of 423 days, which is the number of days for the period beginning on July 27, 2009, the date of mailing of a first Notice of Allowance, until September 23, 2010, the date on which a second RCE was filed ("B Delay").

106. Under 35 U.S.C. § 154(b)(1)(B), Plaintiff is entitled to an adjustment of the term of the '092 patent of 305 days, which is the number of days for the period beginning on September 23, 2010, the date on which a second RCE was filed, until July 25, 2011, the date of mailing of a second Notice of Allowance ("B Delay").

107. Under 35 U.S.C. § 154(b)(1)(B), Plaintiff is entitled to an adjustment of the term of the '092 patent of 135 days, which is the number of days for the period beginning on July 25, 2011, the date of mailing of a second Notice of Allowance, and ending on December 6, 2011, the date the '092 patent issued ("B Delay").

108. 35 U.S.C. § 154(b)(2)(A) provides that "to the extent that periods of delay attributable to grounds specified in paragraph [b](1) overlap, the period of any adjustment . . . shall not exceed the actual number of days the issuance of the patent was delayed." In *Wyeth v. Dudas*, 580 F. Supp. 2d 138 (D.D.C. 2008), the Court explained that for purposes of identifying "overlap" between "A Delay" and "B Delay" under 35 U.S.C. § 154(b)(2)(A), the "period of delay" for "B Delay" begins when the PTO has failed to issue a patent within three years, not before.

109. In accordance with *Wyeth*, the correct patent term adjustment under 35 U.S.C. § 154(b)(1) and (2) is the sum of the "A Delay" and "B Delay" and "C Delay" ($1,890 + 2,340 + 763 = 4,993$ days) reduced by the number of days of "A Delay" that overlaps with "B Delay," and the number of days of "A Delay" that overlaps with "C Delay," (1,890 days) and reduced by the number of days of applicant delay (449 days) for a net adjustment of 2,654 days.

110. If the period of "B Delay" is corrected to include the period from the day after the date that is three years after the date on which the '288 application was filed (i.e., June 9, 2003) through the date the '092 patent issued (i.e., December 6, 2011), minus the period of time from the filing of the first RCE (i.e., from December 2, 2004) until the mailing of the first Notice of Allowance (i.e., until July 27, 2009), and minus the period of time from the filing of the second RCE (i.e., from September 23, 2010) until the mailing of the second Notice of Allowance (i.e., until July 25, 2011), then the correct patent term adjustment under 35 U.S.C. § 154(b)(1) and (2),

in accordance with *Wyeth*, is the sum of the “A Delay” and “B Delay” and “C Delay” ($1,890 + 1,100 + 763 = 3,753$ days) reduced by the number of days of “A Delay” that overlaps with “B Delay,” and the number of days of “A Delay” that overlaps with “C Delay,” (825 days) and reduced by the number of days of applicant delay (449 days) for a net adjustment of 2,479 days.

111. If the period of “B Delay” is corrected to include the period from the day after the date that is three years after the date on which the ‘288 application was filed (i.e., June 9, 2003) through the date the ‘092 patent issued (i.e., December 6, 2011), minus the period of time from the filing of the first RCE (i.e., from December 2, 2004) until the mailing of the second Notice of Allowance (i.e., until July 25, 2011), then the correct patent term adjustment under 35 U.S.C. § 154(b)(1) and (2), in accordance with *Wyeth*, is the sum of the “A Delay” and “B Delay” and “C Delay” ($1,890 + 677 + 763 = 3,330$ days) reduced by the number of days of “A Delay” that overlaps with “B Delay,” and the number of days of “A Delay” that overlaps with “C Delay,” (825 days) and reduced by the number of days of applicant delay (449 days) for a net adjustment of 2,056 days.

112. If the period of “B Delay” includes a reduction for the period from the date on which a first RCE was filed (i.e., December 2, 2004) through the date the ‘092 patent issued (i.e., December 6, 2011), then the correct patent term adjustment under 35 U.S.C. § 154(b)(1) and (2), in accordance with *Wyeth*, is the sum of the “A Delay” and “B Delay” and “C Delay” ($1,890 + 542 + 763 = 3,195$ days) reduced by the number of days of “A Delay” that overlaps with “B Delay,” and the number of days of “A Delay” that overlaps with “C Delay,” (825 days) and reduced by the number of days of applicant delay (449 days) for a net adjustment of 1,921 days.

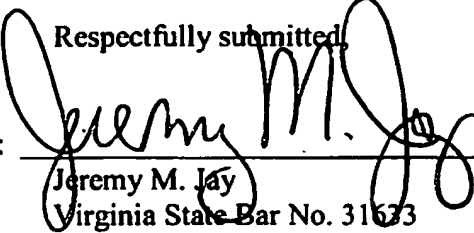
113. The Director's determination that the '092 patent is entitled to only 1,597 days of patent term adjustment is arbitrary, capricious, an abuse of discretion, or otherwise not in accordance with the law and in excess of statutory jurisdiction, authority, or limitation.

PRAYER FOR RELIEF

WHEREFORE, Plaintiff demands judgment against Defendant and respectfully requests that this Court enter Orders:

- A. Changing the period of PTA for the '092 patent from 1,597 days to 2,654 days, and requiring Defendant to extend the term of the '092 patent to reflect the 2,654-day PTA;
- B. Granting such other and further relief as the nature of the case may admit or require and as may be just and equitable.

Dated: June 1, 2012

Respectfully submitted,
By: 
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Washington, D.C. 20005-3960
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*Attorney for Plaintiff
Human Genome Sciences, Inc.*

JS 44 (Rev. 12/07)

CIVIL COVER SHEET

The JS 44 civil cover sheet and the information contained herein neither replace nor supplement the filing and service of pleadings or other papers as required by law, except as provided by local rules of court. This form, approved by the Judicial Conference of the United States in September 1974, is required for the use of the Clerk of Court for the purpose of initiating the civil docket sheet. (SEE INSTRUCTIONS ON THE REVERSE OF THE FORM.)

I. (a) PLAINTIFFS
HUMAN GENOME SCIENCES, INC.

(b) County of Residence of First Listed Plaintiff _____
(EXCEPT IN U.S. PLAINTIFF CASES)

(c) Attorney's (Firm Name, Address, and Telephone Number)
Jeremy M. Jay, LEYDIG, VOIT & MAYER, PC
700 Thirteenth Street N.W., Suite 300, Washington, D.C. 20005-3960
202-737-6770

DEFENDANTS
DAVID J. KAPPOS, in his official capacity as Under Secretary of
Commerce for Intellectual Property and Director of the United States
Patent and Trademark Office

County of Residence of First Listed Defendant _____
(IN U.S. PLAINTIFF CASES ONLY)

NOTE: IN LAND CONDEMNATION CASES, USE THE LOCATION OF THE
LAND INVOLVED.

Attorneys (If Known)

II. BASIS OF JURISDICTION (Place an "X" in One Box Only)

- ☐ 1 U.S. Government Plaintiff
☐ 3 Federal Question (U.S. Government Not a Party)
☒ 2 U.S. Government Defendant
☐ 4 Diversity (Indicate Citizenship of Parties in Item III)

III. CITIZENSHIP OF PRINCIPAL PARTIES (Place an "X" in One Box for Plaintiff and One Box for Defendant)

- | | PTF | DEF | | PTF | DEF |
|---|----------------------------|----------------------------|---|----------------------------|----------------------------|
| Citizen of This State | <input type="checkbox"/> 1 | <input type="checkbox"/> 1 | Incorporated or Principal Place of Business in This State | <input type="checkbox"/> 4 | <input type="checkbox"/> 4 |
| Citizen of Another State | <input type="checkbox"/> 2 | <input type="checkbox"/> 2 | Incorporated and Principal Place of Business in Another State | <input type="checkbox"/> 5 | <input type="checkbox"/> 5 |
| Citizen or Subject of a Foreign Country | <input type="checkbox"/> 3 | <input type="checkbox"/> 3 | Foreign Nation | <input type="checkbox"/> 6 | <input type="checkbox"/> 6 |

IV. NATURE OF SUIT (Place an "X" in One Box Only)

CONTRACT	TORTS	FORFEITURE/PENALTY	BANKRUPTCY	OTHER STATUTES
<input type="checkbox"/> 110 Insurance <input type="checkbox"/> 120 Marine <input type="checkbox"/> 130 Miller Act <input type="checkbox"/> 140 Negotiable Instrument <input type="checkbox"/> 150 Recovery of Overpayment & Enforcement of Judgment <input type="checkbox"/> 151 Medicare Act <input type="checkbox"/> 152 Recovery of Defaulted Student Loans (Excl. Veterans) <input type="checkbox"/> 153 Recovery of Overpayment of Veteran's Benefits <input type="checkbox"/> 160 Stockholders' Suits <input type="checkbox"/> 190 Other Contract <input type="checkbox"/> 195 Contract Product Liability <input type="checkbox"/> 196 Franchise	PERSONAL INJURY <input type="checkbox"/> 310 Airplane <input type="checkbox"/> 315 Airplane Product Liability <input type="checkbox"/> 320 Assault, Libel & Slander <input type="checkbox"/> 330 Federal Employers' Liability <input type="checkbox"/> 340 Marine <input type="checkbox"/> 345 Marine Product Liability <input type="checkbox"/> 350 Motor Vehicle <input type="checkbox"/> 355 Motor Vehicle Product Liability <input type="checkbox"/> 360 Other Personal Injury	<input type="checkbox"/> 610 Agriculture <input type="checkbox"/> 620 Other Food & Drug <input type="checkbox"/> 625 Drug Related Seizure of Property 21 USC 881 <input type="checkbox"/> 630 Liquor Laws <input type="checkbox"/> 640 R.R. & Truck <input type="checkbox"/> 650 Airline Regs. <input type="checkbox"/> 660 Occupational Safety/Health <input type="checkbox"/> 690 Other	<input type="checkbox"/> 422 Appeal 28 USC 158 <input type="checkbox"/> 423 Withdrawal 28 USC 157 PROPERTY RIGHTS <input type="checkbox"/> 820 Copyrights <input checked="" type="checkbox"/> 830 Patent <input type="checkbox"/> 840 Trademark	<input type="checkbox"/> 400 State Reapportionment <input type="checkbox"/> 410 Antitrust <input type="checkbox"/> 430 Banks and Banking <input type="checkbox"/> 450 Commerce <input type="checkbox"/> 460 Deportation <input type="checkbox"/> 470 Racketeer Influenced and Corrupt Organizations <input type="checkbox"/> 480 Consumer Credit <input type="checkbox"/> 490 Cable/Sat TV <input type="checkbox"/> 810 Selective Service <input type="checkbox"/> 850 Securities/Commodities/Exchange <input type="checkbox"/> 875 Customer Challenge 12 USC 3410 <input type="checkbox"/> 890 Other Statutory Actions <input type="checkbox"/> 891 Agricultural Acts <input type="checkbox"/> 892 Economic Stabilization Act <input type="checkbox"/> 893 Environmental Matters <input type="checkbox"/> 894 Energy Allocation Act <input type="checkbox"/> 895 Freedom of Information Act <input type="checkbox"/> 900 Appeal of Fee Determination Under Equal Access to Justice <input type="checkbox"/> 950 Constitutionality of State Statutes
REAL PROPERTY <input type="checkbox"/> 210 Land Condemnation <input type="checkbox"/> 220 Foreclosure <input type="checkbox"/> 230 Rent Lease & Ejectment <input type="checkbox"/> 240 Torts to Land <input type="checkbox"/> 245 Tort Product Liability <input type="checkbox"/> 290 All Other Real Property	CIVIL RIGHTS <input type="checkbox"/> 441 Voting <input type="checkbox"/> 442 Employment <input type="checkbox"/> 443 Housing/Accommodations <input type="checkbox"/> 444 Welfare <input type="checkbox"/> 445 Amer. w/Disabilities - Employment <input type="checkbox"/> 446 Amer. w/Disabilities - Other <input type="checkbox"/> 440 Other Civil Rights	PRISONER PETITIONS <input type="checkbox"/> 510 Motions to Vacate Sentence <input type="checkbox"/> Habeas Corpus: <input type="checkbox"/> 530 General <input type="checkbox"/> 535 Death Penalty <input type="checkbox"/> 540 Mandamus & Other <input type="checkbox"/> 550 Civil Rights <input type="checkbox"/> 555 Prison Condition	LABOR <input type="checkbox"/> 710 Fair Labor Standards Act <input type="checkbox"/> 720 Labor/Mgmt. Relations <input type="checkbox"/> 730 Labor/Mgmt. Reporting & Disclosure Act <input type="checkbox"/> 740 Railway Labor Act <input type="checkbox"/> 790 Other Labor Litigation <input type="checkbox"/> 791 Empl. Ret. Inc. Security Act IMMIGRATION <input type="checkbox"/> 462 Naturalization Application <input type="checkbox"/> 463 Habeas Corpus - Alien Detainee <input type="checkbox"/> 465 Other Immigration Actions	SOCIAL SECURITY <input type="checkbox"/> 861 HIA (1395ff) <input type="checkbox"/> 862 Black Lung (923) <input type="checkbox"/> 863 DIWC/DIWW (405(g)) <input type="checkbox"/> 864 SSD Title XVI <input type="checkbox"/> 865 RSI (405(g)) FEDERAL TAX SUITS <input type="checkbox"/> 870 Taxes (U.S. Plaintiff or Defendant) <input type="checkbox"/> 871 IRS - Third Party 26 USC 7609

V. ORIGIN (Place an "X" in One Box Only)

- ☒ 1 Original Proceeding
☐ 2 Removed from State Court
☐ 3 Remanded from Appellate Court
☐ 4 Reinstated or Reopened
☐ 5 Transferred from another district (specify) _____
☐ 6 Multidistrict Litigation
☐ 7 Appeal to District Judge from Magistrate Judgment

VI. CAUSE OF ACTION

Cite the U.S. Civil Statute under which you are filing (Do not cite jurisdictional statutes unless diversity):

35 U.S.C. § 154(b)(4)(A)

Brief description of cause:

Patent Term Adjustment

VII. REQUESTED IN COMPLAINT:

☐ CHECK IF THIS IS A CLASS ACTION UNDER F.R.C.P. 23

DEMAND \$

CHECK YES only if demanded in complaint:

JURY DEMAND: ☐ Yes ☒ No

VIII. RELATED CASE(S) IF ANY

(See instructions).

JUDGE

DOCKET NUMBER

DATE

1 June 2012

SIGNATURE OF ATTORNEY OF RECORD

Jeremy M. Jay

VA Bar # 31633

FOR OFFICE USE ONLY

RECEIPT # _____ AMOUNT _____ APPLYING IFP _____ JUDGE _____ MAG. JUDGE _____

Court Name: United States District Court

Division: 1

Receipt Number: 14683029199

Cashier ID: sbrown

Transaction Date: 06/01/2012

Payer Name: LEYDIG VOIT AND HAYER

CIVIL FILING FEE

For: LEYDIG VOIT AND HAYER

Amount: \$350.00

CHECK

Rebitter: LEYDIG VOIT AND HAYER

Check/Money Order Num: 9780

Amnt Tendered: \$350.00

Total Due: \$350.00

Total Tendered: \$350.00

Change Amnt: \$0.00

FILING FEE

112CV607

EXHIBIT A



US008071092B1

(12) **United States Patent**
Yu et al.

(10) Patent No.: **US 8,071,092 B1**(45) Date of Patent: ***Dec. 6, 2011**

(54) **METHODS OF INHIBITING B LYMPHOCYTES USING ANTIBODIES TO NEUTROKINE-ALPHA**

(75) Inventors: Guo-Liang Yu, Berkeley, CA (US); Reinhard Ebner, Gaithersburg, MD (US); Jian Ni, Rockville, MD (US)

(73) Assignee: **Human Genome Sciences, Inc.**, Rockville, MD (US)

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 1597 days.

This patent is subject to a terminal disclaimer.

(21) Appl. No.: **09/589,288**

(22) Filed: **Jun. 8, 2000**

Related U.S. Application Data

(63) Continuation of application No. 09/507,968, filed on Feb. 22, 2000, now Pat. No. 6,812,327, and a continuation-in-part of application No. 09/255,794, filed on Feb. 23, 1999, now Pat. No. 6,716,576, which is a continuation-in-part of application No. 09/005,874, filed on Jan. 12, 1998, now Pat. No. 6,689,579, and a continuation-in-part of application No. PCT/US96/17957, filed on Oct. 25, 1996.

(60) Provisional application No. 60/122,388, filed on Mar. 2, 1999, provisional application No. 60/124,097, filed on Mar. 12, 1999, provisional application No. 60/126,599, filed on Mar. 26, 1999, provisional application No. 60/127,598, filed on Apr. 2, 1999, provisional application No. 60/130,412, filed on Apr. 16, 1999, provisional application No. 60/130,696, filed on Apr. 23, 1999, provisional application No. 60/131,278, filed on Apr. 27, 1999, provisional application No. 60/131,673, filed on Apr. 29, 1999, provisional application No. 60/136,784, filed on May 28, 1999, provisional application No. 60/142,659, filed on Jul. 6, 1999, provisional application No. 60/145,824, filed on Jul. 27, 1999, provisional application No. 60/167,239, filed on Nov. 24, 1999, provisional application No. 60/168,624, filed on Dec. 3, 1999, provisional application No. 60/171,108, filed on Dec. 16, 1999, provisional application No. 60/171,626, filed on Dec. 23, 1999, provisional application No. 60/176,015, filed on Jan. 14, 2000, provisional application No. 60/036,100, filed on Jan. 14, 1997.

(51) Int. Cl.
A61K 39/395 (2006.01)
C07K 16/22 (2006.01)
C07K 14/475 (2006.01)

(52) U.S. Cl. 424/130.1; 424/133.1; 424/139.1; 424/141.1; 424/158.1; 424/178.1; 530/387.1; 530/387.3; 530/388.1; 530/389.1; 530/387.9; 530/399

(58) Field of Classification Search 514/2, 4, 514/8, 12; 530/300, 350, 387.1; 424/85.1, 424/130.1, 139.1, 13; 435/69.1, 69.5, 325, 435/328, 331, 335

See application file for complete search history.

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Primary Examiner — Bridget E Bunner

(74) Attorney, Agent, or Firm — Leydig, Voit & Mayer, Ltd.

(57) **ABSTRACT**

The present invention relates to a novel Neutrokin- α , and a splice variant thereof designated Neutrokin- α SV, polynucleotides and polypeptides which are members of the TNF family. In particular, isolated nucleic acid molecules are provided encoding the human Neutrokin- α and/or Neutrokin- α SV polypeptides, including soluble forms of the extracellular domain. Neutrokin- α and/or Neutrokin- α SV polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of Neutrokin- α and/or Neutrokin- α SV activity. Also provided are diagnostic methods for detecting immune system-related disorders and therapeutic methods for treating immune system-related disorders.

102 Claims, 22 Drawing Sheets

US 8,071,092 B1

Page 2

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Neutrokin- α

1 AAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCCCTGCCATGTAGTGCACGCAGGAC 60
 61 ATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATTCTAAAGGCC 120
 121 CCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGGAGCAGTCACGCC 180
 1 M D D S T E R E Q S R L 12
 181 TTACTTCTTGCCCTTAAGAAAAGAGAAGAAATGAACTGAAGGAGTGTGTTCCATCCTCC 240
 13 T S C L K K R E E N K L K E C V S I L P 32
 CD-I
 241 CACGGAAGGAAAGCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCT 300
 33 R K E S P S V R S S K D G K L L A A T L 52
 CD-I
 301 TGCTGCTGGCACTGCTGTCTTGCTGCCTCAGGTGGTGTCTTTCTACCAGGTGGCCGCC 360
 53 L L A L L S C C L T V V S F Y Q V A A L 72
 361 TGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGC 420
 73 Q G D L A S L R A E L Q G H H A E K L P 92
 CD-II
 421 CAGCAGGAGCAGGAGCCCAAGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGGGGAC 480
 93 A G A G A P K A G L E E A P A V T A G L 112
 CD-III
 481 TGAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATA 540
 113 K I F E P P A P G E G N S S Q N S R N K 132
 541 AGCGTGCCGTTCAAGGTCCAGAAGAAACAGTCAAGACTGCTTGCAACTGATTGCAG 600
 133 R A V Q G P E E T V T Q D C L Q L I A D 152
 CD-IV

FIG. 1A

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Neutrokin- α

601	ACAGTGAAACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCT	660
153	S E T P T I Q K G S Y T F <u>V P W L L S F</u>	172
	CD-V	
661	TTAAAAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAACTGGTT	720
173	<u>K R G S A L E E K E N K I L V K E T G Y</u>	192
	CD-V	CD-VI
721	ACTTTTTTATATATGGTCAGGTTTATATACTGATAAGACCTACGCCATGGGACATCTAA	780
193	<u>F F I Y G Q V L Y T D K T Y A M G H L I</u>	212
	CD-VI	CD-VII
781	TTCAGAGGAAGAAGGTCCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGAT	840
213	<u>Q R K K V H V F G D E L S L V T L F R C</u>	232
	CD-VII	CD-VIII
	#	
841	GTATTCAAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTCAGCTGGCATTGCAA	900
233	<u>I Q N M P E T L P N N S C Y S A G I A K</u>	252
	CD-VIII	CD-IX
901	AACTGGAAGAAGGAGATGAACCTCCAACCTGCAATACCAAGAGAAAATGCACAAATATCAC	960
253	<u>L E E G D E L Q L A I P R E N A Q I S L</u>	272
	CD-X	
961	TGGATGGAGATGTCACATTTTTTGGTGCAATTGAACTGCTGTGACCTACTTACACCATGT	1020
273	<u>D G D V T F F G A L K L L</u>	285
	CD-XI	
1021	CTGTAGCTATTTTCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATA	1080
1081	CCAAAAAAAAAAAAAAAAAAAA	1100

FIG.1B

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	10	20	30	
1	WSTESMIR	VE		TNFalpha
1	W		- - - - -	TNFbeta
1	W		- - - - -	LTbeta
1	W	GA		FasLigand
1	W	QQPFNYPPIYW	VDSSASSPWAPPGTV	Neutrokine alpha
1	W	DDSTEREQSRL	TSCCLKREEMKLLKECVSI	Neutrokine alphaSV
1	W	DDSTEREQSRL	TSCCLKREEMKLLKECVSI	
	40	50	60	
17	LPKKTGGPQ	- - - - -	- - - - -	TNFalpha
8	F	- - - - -	- - - - -	TNFbeta
4	- - - - -	LGLEGRGG	- - - - -	LTbeta
30	LPCPTSVPRRPG	QRRPPPPPPPPPP	PPPPPP	FasLigand
31	LPRKESPSVRSS	KKD - - - - -	GKLLAATLLALL	Neutrokine alpha
31	LPRKESPSVRSS	KKD - - - - -	GKLLAATLLALL	Neutrokine alphaSV
	70	80	90	
30	- - - - -	- - - - -	- - - - -	TNFalpha
9	- - - - -	- - - - -	- - - - -	TNFbeta
12	- - - - -	- - - - -	- - - - -	LTbeta
60	PPP	PLPLPL	PLKRRG	FasLigand
58	SCCL	TVVSFF	YQVAAL	Neutrokine alpha
58	SCCL	TVVSFF	YQVAAL	Neutrokine alphaSV

FIG. 2A

	100	110	120	
38	F L	I V A G A T T L F C	L H F G V I G P Q R E E F P R	TNFalpha
31	G A Q G L P G V G L	- - - - -	- - - - -	TNFbeta
32	L L A V P I T V L	A V L A L V P Q D Q G G	L V T E T A D P	LTbeta
90	V L V A L V G L G L	G M F Q L F H L Q K E L	A E L R E S T S	FasLigand
88	A E K L P A G A G A	P K A G L E E A P A V	T A G L K I F E P	Neutrokine alpha
88	A E K L P A G A G A	P K A G L E E A P A V	T A G L K I F E P	Neutrokine alphaSV

	130	140	150	
66	D L S L I S	- P L A - Q A V R S S S R T P S D	- - - K P V A	TNFalpha
41	- - - T P S	- A A Q - T A R Q H P K M H L A H S	T T L K P A A	TNFbeta
62	G A Q A Q Q - G L G F Q K L P E E E P E T D L S	P P E K K E L R K V A	- - -	LTbeta
120	Q M H T A S - S L E - K Q I G H P S P P P E K K E L R K V A	- - -	- - -	FasLigand
118	P A P G E G N S S Q N S R N K R A V Q G P E E T V T T Q D C L	- - -	- - -	Neutrokine alpha
118	P A P G E G N S S Q N S R N K R A V Q G P E E T	- - -	- - -	Neutrokine alphaSV

	160	170	180	
91	H V V A N P Q A E G - Q	- - - - -	Q V L N R R A N A L	TNFalpha
66	H L I G D P S K Q N - S	- - - - -	L L M R A N T D R A F L	TNFbeta
91	H L I G A P L K - G Q G - - - -	- - - - -	L L G W E T T K E Q A F L	LTbeta
148	H L T G K S N S R S M P - - - - -	- - - - -	L L E N E D T Y G I V L L	FasLigand
148	Q L I A D S E T P T I Q K G S Y T F V P V L - - - - -	- - - - -	L L S F K	Neutrokine alpha
142	- - - - -	- - - - -	L L S F K	Neutrokine alphaSV

FIG. 2B

	190	200	210	TNFalpha TNFbeta LTbeta FasLigand Neutrokine alpha Neutrokine alphaSV
1114	A N G V E L R D N - Q L V V P S E G L Y L I Y S Q V L F K G			
89	Q D G F S L S N N - S L E V P T S G I Y F V Y S Q V F S G			
1114	T S G T Q F S D A E G L A L P Q D G L Y Y L Y C L W G Y R G			
1172	- S G V K Y K K G - G L V I N E T G L Y F V Y S K V Y F R G			
1174	R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L Y T D			
1155	R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L Y T D			
	220	230	240	TNFalpha TNFbeta LTbeta FasLigand Neutrokine alpha Neutrokine alphaSV
1413	Q G C P - - - - S T H V L L T H T I S R I A V S V Q T K			
1118	K A Y S P - - K A T S S P L Y L A H E V Q L E S S Q Y P F H			
144	R A P P G G G D P Q G R S V T L R S S L Y R A G G A Y G P G			
200	Q S C N - - - - - N L P L S H K V Y M R N S K V P Q D			
204	K T Y A N G - - - - - H I I Q R K K V H V F G D E L S - -			
185	K T Y A N G - - - - - H I I Q R K K V H V F G D E L S - -			
	250	260	270	TNFalpha TNFbeta LTbeta FasLigand Neutrokine alpha Neutrokine alphaSV
167	V N - - L L S A I K S P C Q R E T P E - - G A E A K P W Y E			
146	V P - - L L S Q K K V Y P - - - - - G L Q E P W L H			
1174	T P E L L L E G A E T V T P V L D P A R R Q G Y G P L W Y T			
222	L V - - M M E G K M N S Y C - - - - - T T G Q M W A R			
226	L V T L F R C I Q N M P E T L P N - - - - - N - - - - -			
207	L V T L F R C I Q N M P E T L P N - - - - - N - - - - -			

FIG. 2C

FIG. 2D

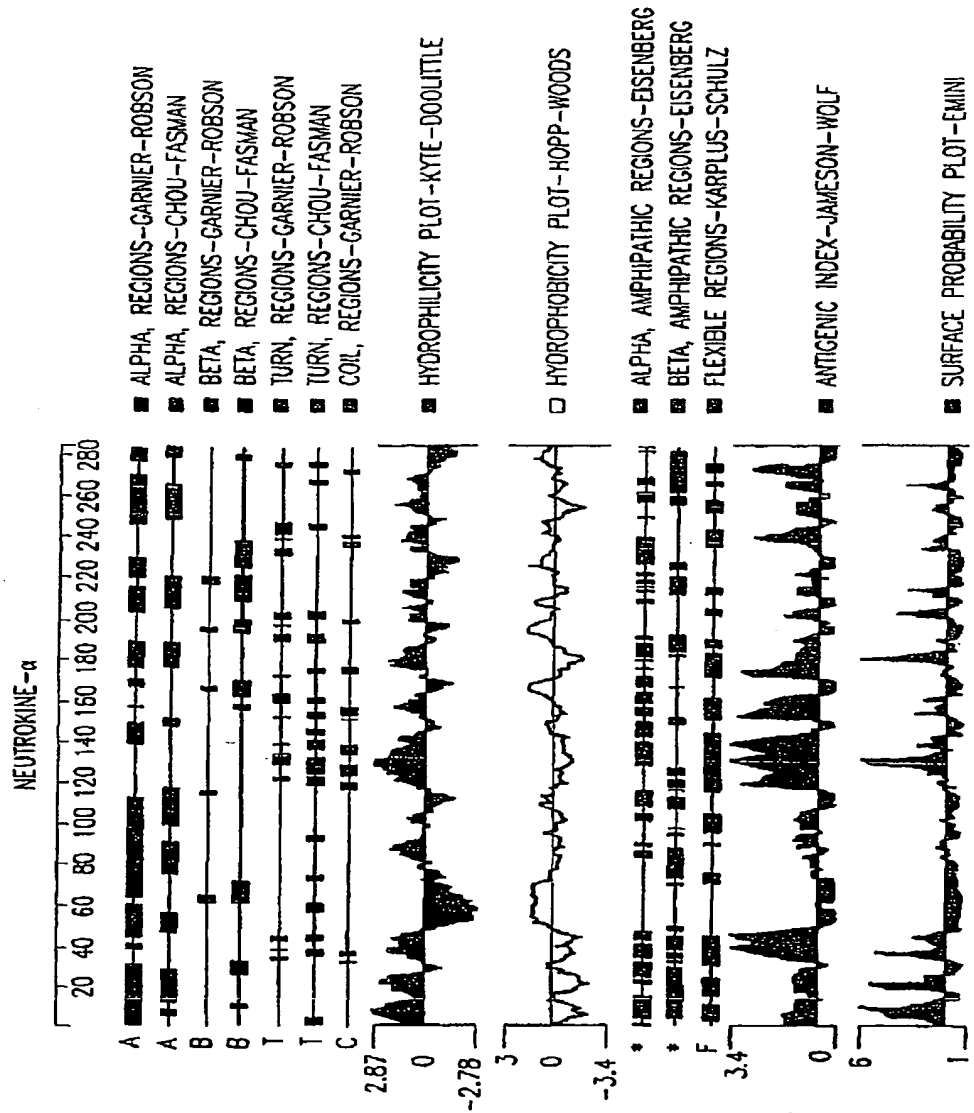


FIG.3

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1
HSOAD55R .....A GGNTAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA
HNEDU15X ...AAATTCA GGATAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA
HSLAH84R .AATTCGGCA NAGNAACTG GTTACTTTT TATATATGGT CAGGTTTTAT
HLTBM08R AATTCGGCAC GAGCAAGGCC GGCCTGGAGG AAGCTCCAGC TGTCACCGCG

51
HSOAD55R GTGCACGCAG GACATCANCA A..ACACANN NNNCAGGAAA TAATCCATTCT
HNEDU15X GTGCACGCAG GACATCAACA A..ACACAGA TAACAGGAAA TGATCCATTCT
HSLAH84R ATACTGATAA GACCTACGCC ATGGGACATC TAGTTCAGAG GAAGAAGGTC
HLTBM08R GGACTGAAAA TCTTTGAACC ACCAGCTCCA GGAGAAGGCA ACTCCAGTCA

101
HSOAD55R CCTGTGGTCA CTTATTCTAA AGGCCCAAC CTTCAAAGTT CAAGTAGTGA
HNEDU15X CCTGTGGTCA CTTATTCTAA AGGCCCAAC CTTCAAAGTT CAAGTAGTGA
HSLAH84R CATGTCTTTG GGGATGAATT GAGTCTGGTG ACTTTGTTT C GATGTATTCA
HLTBM08R GAACAGCAGA AATAAGCGTG CCGTTCAGGG TCCAGAAGAA ACAGTCACTC

151
HSOAD55R TATGGATGAC TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA
HNEDU15X TATGGATGAC TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA
HSLAH84R AAATATGCCT GAAACACTAC CCAATAATTC CTGCTATTCA GCTGGCATTG
HLTBM08R AAGACTGCTT GCAACTGNNT GCAGACAGTG AAACACCAAC TATACAAAAA

201
HSOAD55R AGAAAAGAGA AGAAATGAAA CTGNAAGGAG TGTGTTTCCA TCCTCCCACG
HNEDU15X AGAAAAGAGA AGAAATGAAA CT.GAAGGAG TGTGTTTCCA TCCTCCCACG
HSLAH84R CAAAAC TGGN AGGAAGGA.. ...GATGAAC TCCAAC TTGC AATACCAGGG
HLTBM08R GGCTCCCTTC TGNTGCCACA TTTGGGCCAA GGAATGGAGA GATTTCTTCG

251
HSOAD55R GAAGGAAAGC CCCTCTNTCC GATCCTCCAA AGACGGAAAG CTGCTGGCTG
HNEDU15X GAAGGAAAGC CCCTCTGTCC GATCCTCCAA AGACGGAAAG CTGCTGGCTG
HSLAH84R GAAAATGCAC AATTATCACT GGGATGGAGA TGTTACATT TTTTGGGTGC
HLTBM08R TCTGGAAACA TTTTGCCAAA CTCTTCAGAT ACTCTTTNCT CTCTGGGAAT

301
HSOAD55R CAACCTTGNT GNTGGCATTG TGTCTTGCT GNCTCAAGGT GGTGTTNTT.
HNEDU15X CAACCTTGCT GCTGGCACTG CTGTCTTGCT GCCTCACGGT GGTGCTTTTCT
HSLAH84R CATTGAAACT GCTGTGACCT NCTTACANCA NGTGTGTTN GCTATTTTNC
HLTBM08R CAAAGGAAAA TCTCTACTTA GATTNACACA TTTGTTCCCA TGGGTNTCTT

351
HSOAD55R .....
HNEDU15X TACCAGGTGG CCGCCCTGCA AGGGGACCTG GCCAGCCTCC GGGCAGAGCT
HSLAH84R CTNCCTNTTC TGTGTAACC TCTTAGGAAG GAAGGATTCT TAACTGGGAA
HLTBM08R AAGTTTTAAA AGGGGAGTGC CTTAGGAGG AAAAGGGGAT AAATATTGCG

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FIG.4A

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[illegible]

FIG. 4B

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	801		850
HSOAD55R
HNEDU15X	GTCCATGTCT	TTGGGGATGA	ATTGAGTCTG GTGACTTTGT TTCGATGTAT
HSLAH84R
HLTBM08R
	851		900
HSOAD55R
HNEDU15X	TCAAAATATG	CCTGAAACAC	TACCCAATAA TTCCTGCTAT TCAGCTGGCA
HSLAH84R
HLTBM08R
	901		950
HSOAD55R
HNEDU15X	TTGCAAACT	GGAAGAAGGA	GATGAACTCC AACTTGCAAT ACCAAGAGAA
HSLAH84R
HLTBM08R
	951		1000
HSOAD55R
HNEDU15X	AATGCACAAA	TATCACTGGA	TGGAGATGTC ACATTTTTTG GTGCATTGAA
HSLAH84R
HLTBM08R
	1001		1050
HSOAD55R
HNEDU15X	ACTGCTGTGA	CCTACTTACA	CCATGTCTGT AGCTATTTTC CTCCCTTTCT
HSLAH84R
HLTBM08R
	1051		1100
HSOAD55R
HNEDU15X	CTGTACCTCT	AAGAAGAAAG	AATCTAACTG AAAATACCAA AAAAAAAAAA
HSLAH84R
HLTBM08R
	1101		
HSOAD55R		
HNEDU15X	AAAAAA		
HSLAH84R		
HLTBM08R		

FIG.4C

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Neutrokine- α SV

1 ATGSATGACTCCACAGAAAGGGAGCAGTCACGCCTTACTTCTTGCCTTAAGAAAAGAGAA 60
 1 M D D S T E R E Q S R L T S C L K K R E 20

61 GAAATGAAACTGAAGGAGTGTGTTTCCATCCTCCACGGAAGGAAAGCCCTCTGTCCGA 120
 21 E M K L K E C V S I L P R K E S P S V R 40
 CD-I

121 TCCTCCAAAGACGGAAGCTGCTGGCTGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGC 180
 41 S S K D G K L L A A T L L L A L L S C C 60
 CD-I

181 CTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCCTGCAAGGGGACCTGGCCAGCCTCCGG 240
 61 L T V V S F Y Q V A A L Q G D L A S L R 80
 CD-II

241 GCAGAGCTGCAGGGCCACCACGGGAGAAGCTGCCAGCAGGAGCAGGAGCCCCAAGGCC 300
 81 A E L Q G H H A E K L P A G A G A P K A 100
 CD-II CD-III

301 GGCCTGGAGGAAGCTCCAGCTGTACCGCGGGACTGAAAATCTTTGAACCACCAGCTCCA 360
 101 G L E E A P A V T A G L K I F E P P A P 120
 CD-III

 361 GGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCGTGCCGTTTCAGGGTCCAGAAGAA 420
 121 G E G N S S Q N S R N K R A V Q G P E E 140

421 ACAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGGAAGTGCCCTAGAA 480
 141 T G S Y T F V P W L L S F K R G S A L E 160
 CD-IV

481 GAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTTACTTTTTATATATGGTCAGGTT 540
 161 E K E N K I L V K E T G Y F F I Y G Q V 180
 CD-IV CD-V

541 TTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGGTCCATGTC 600
 181 L Y T D K T Y A M G H L I Q R K K V H V 200
 CD-VI CD-VII

FIG.5A

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Neutrokin- α SV

```
601 TTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTATTCAAAATATGCCTGAAACA 660
201 F G D E L S L V T L F R C I Q N M P E T 220
    CD-VIII                               CD-VIII

661 CTACCCAATAATTCCTGCTATTCAGCTGGCATTGCAAACTGGAAGAAGGAGATGAACTC 720
221 L P N N S C Y S A G I A K L E E G D E L 240
    CD-IX                               CD-X

721 CAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTT 780
241 Q L A I P R E N A Q I S L D G D V T F F 260
    CD-X                               CD-XI

781 GGTGCATTGAAACTGCTGTGACCTACTTACACCATGTCTGTAGCTATTTTCTCCCTTTC 840
261 G A L K L L 266
    CD-XI

841 TCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAAAAAAAAAAAAAAAAAAAAA 900
901 AAA 903
```

FIG.5B

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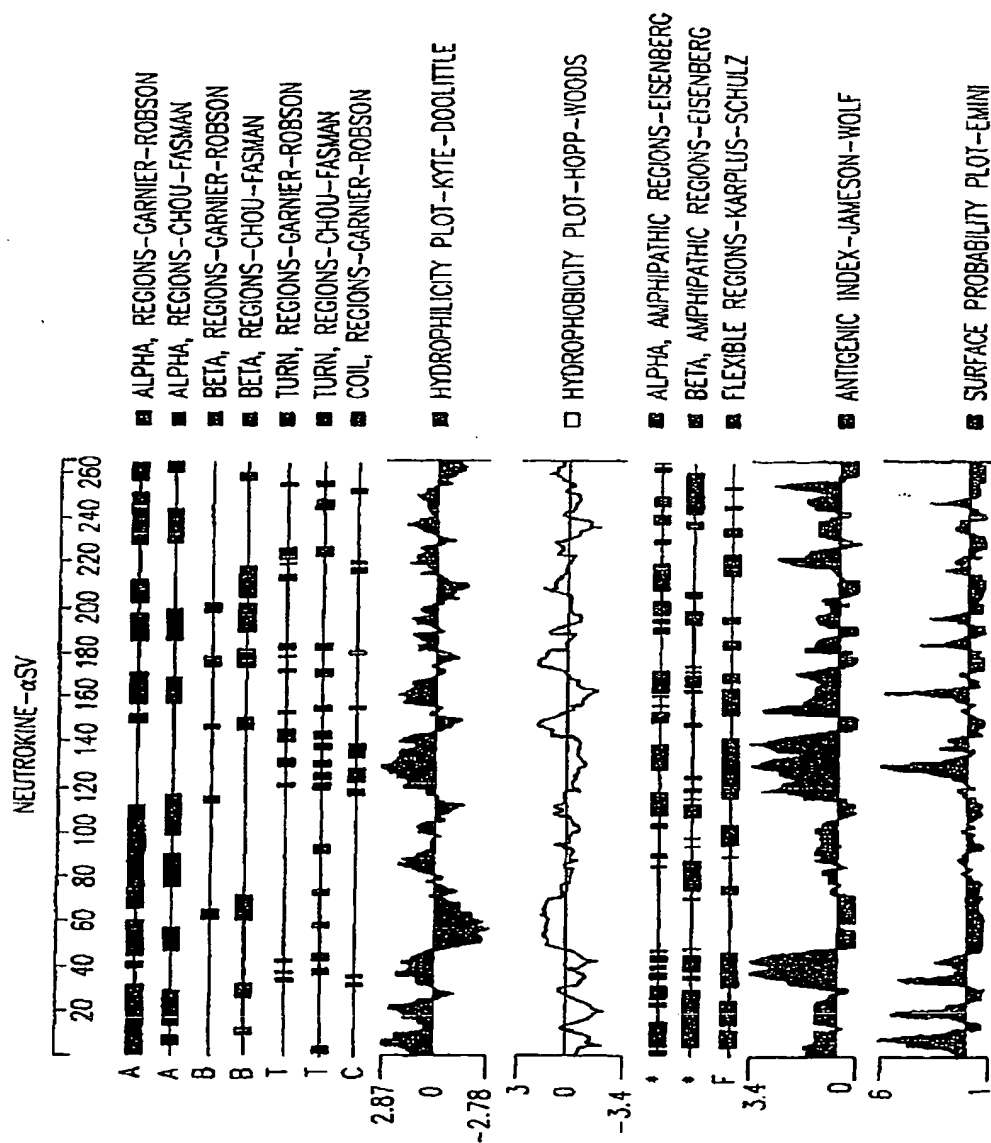


FIG. 6

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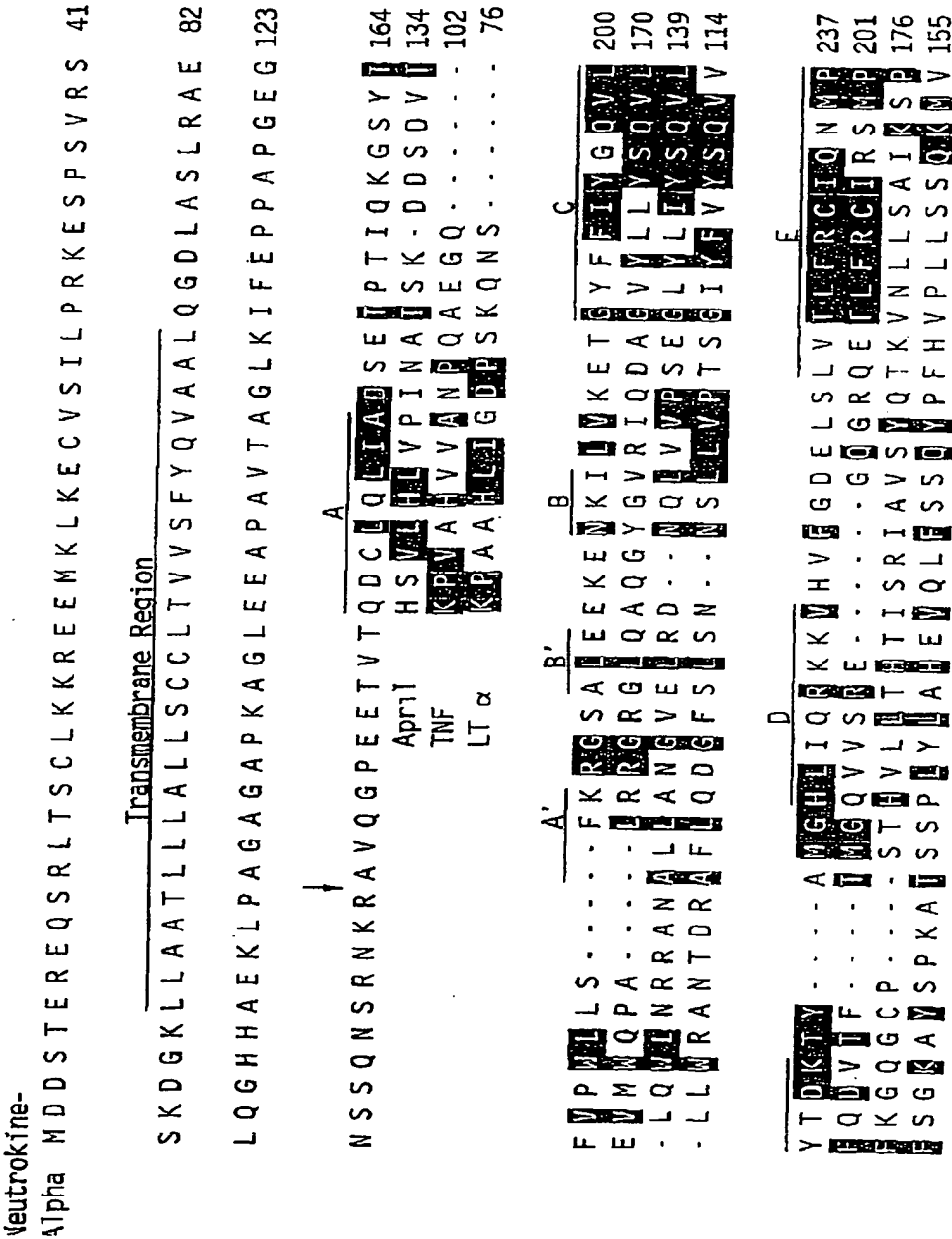


FIG. 7A-2

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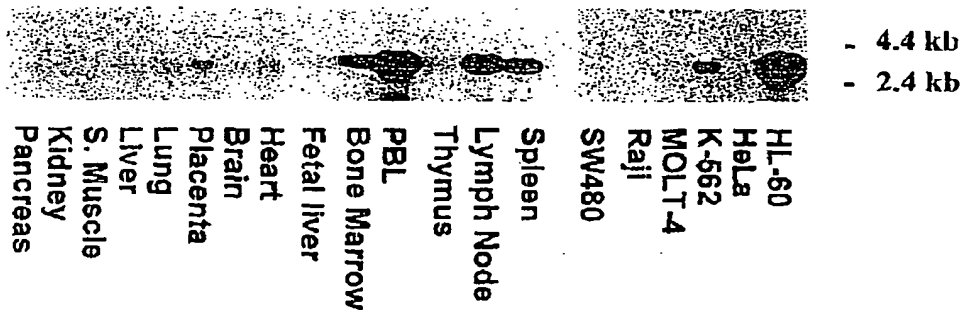


FIG.7B

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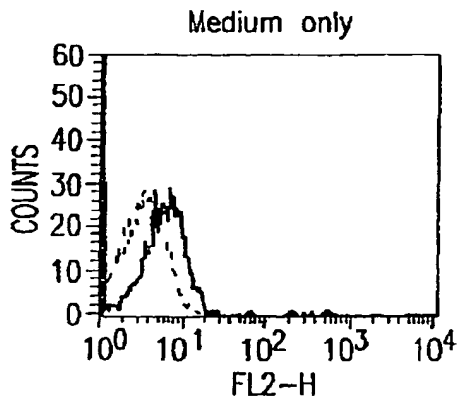


FIG.8A

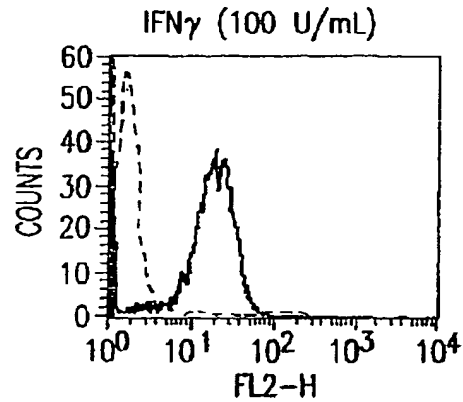


FIG.8B

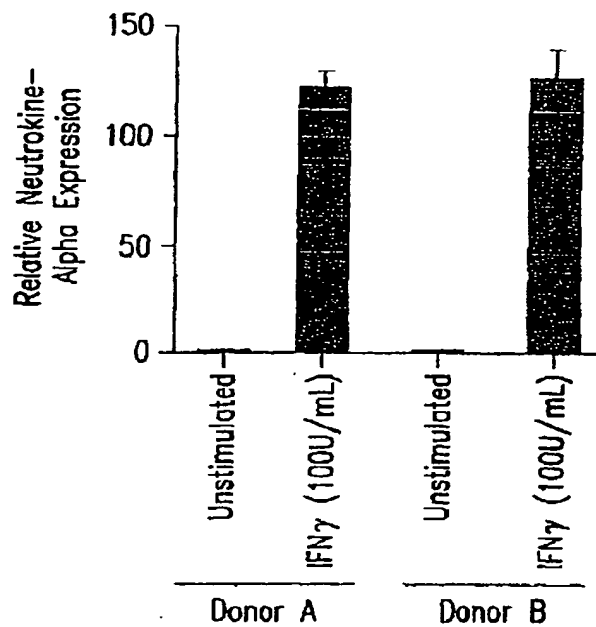


FIG.8C

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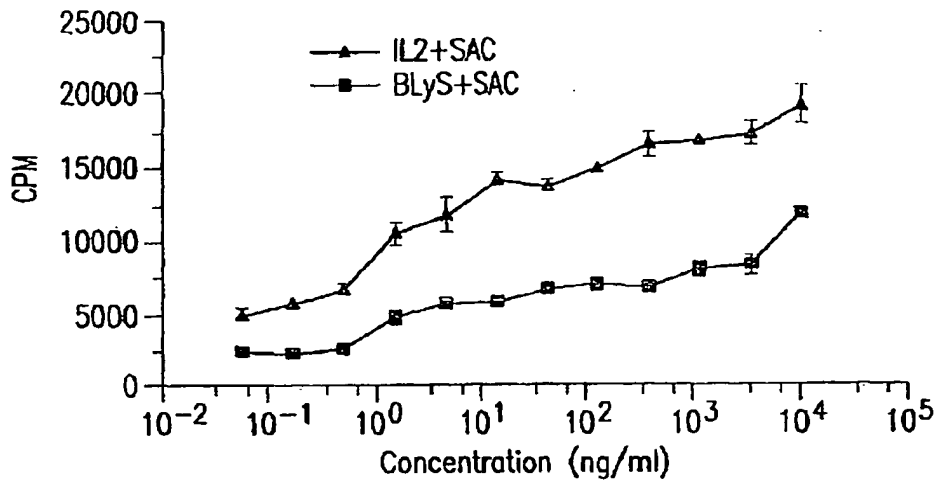


FIG. 9A

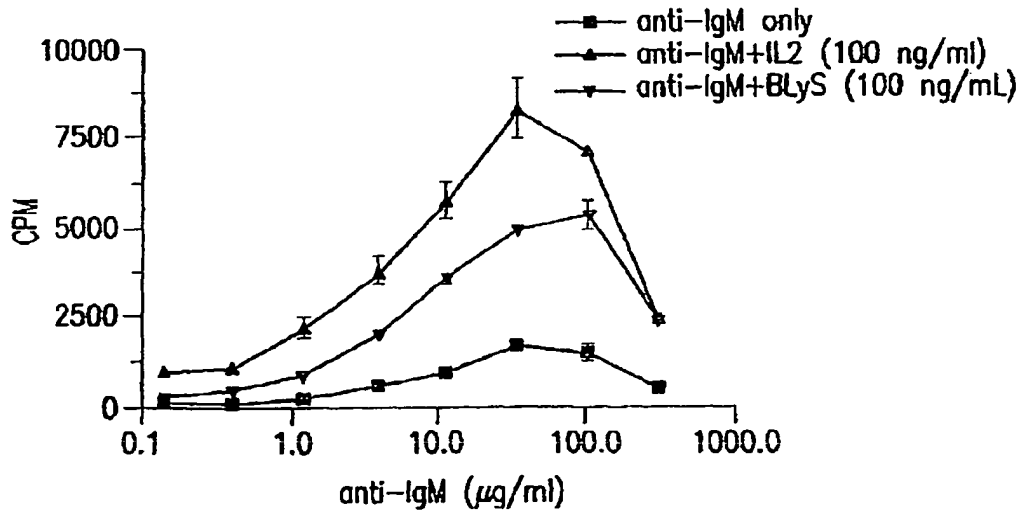


FIG. 9B

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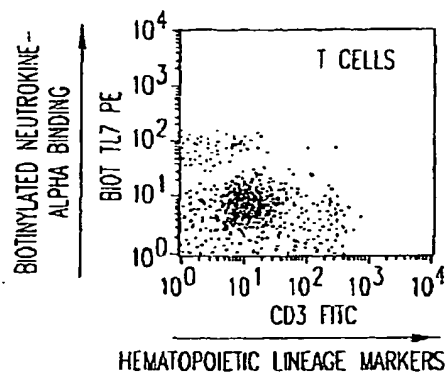


FIG.10A

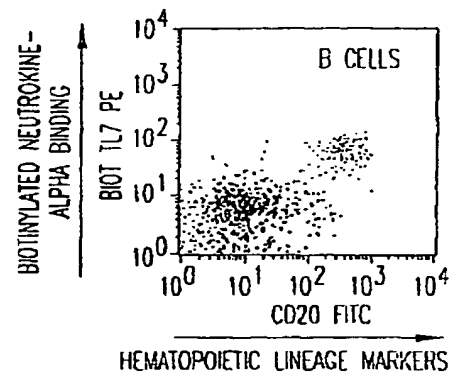


FIG.10B

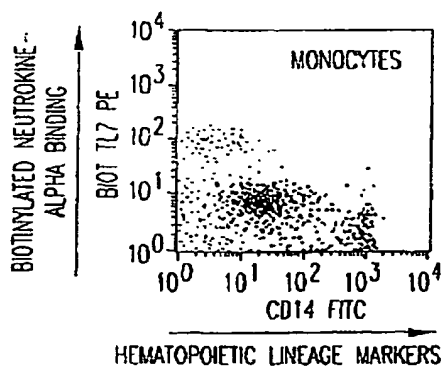


FIG.10C

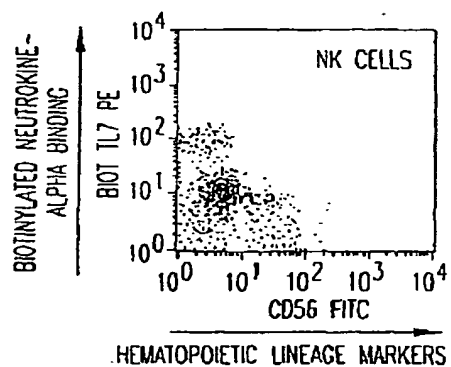


FIG.10D

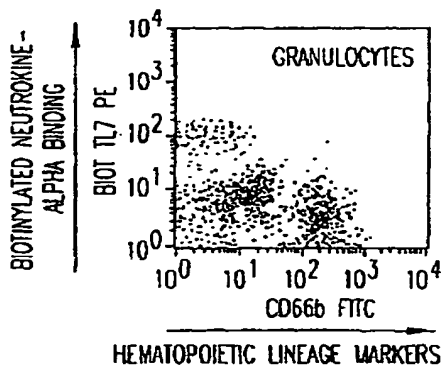


FIG.10E

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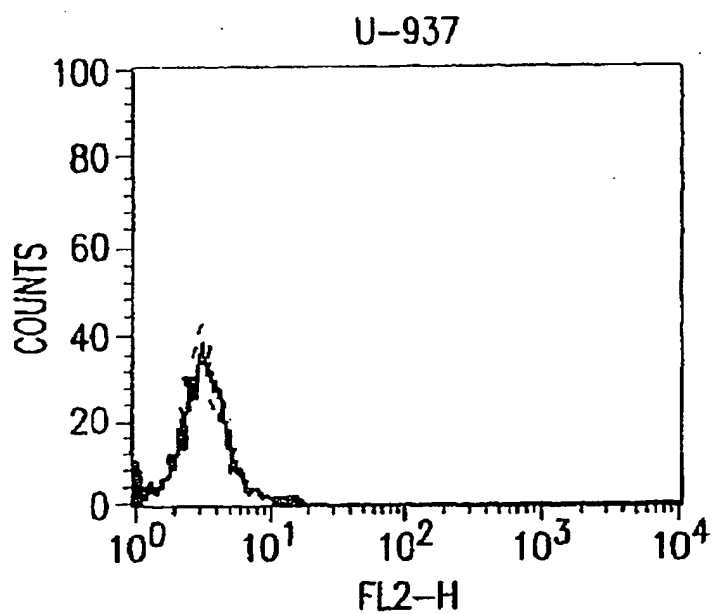


FIG.10F

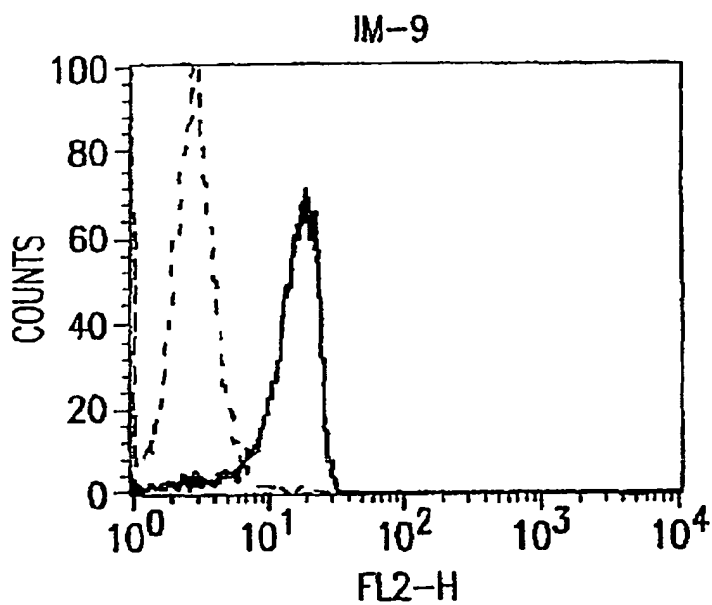


FIG.10G

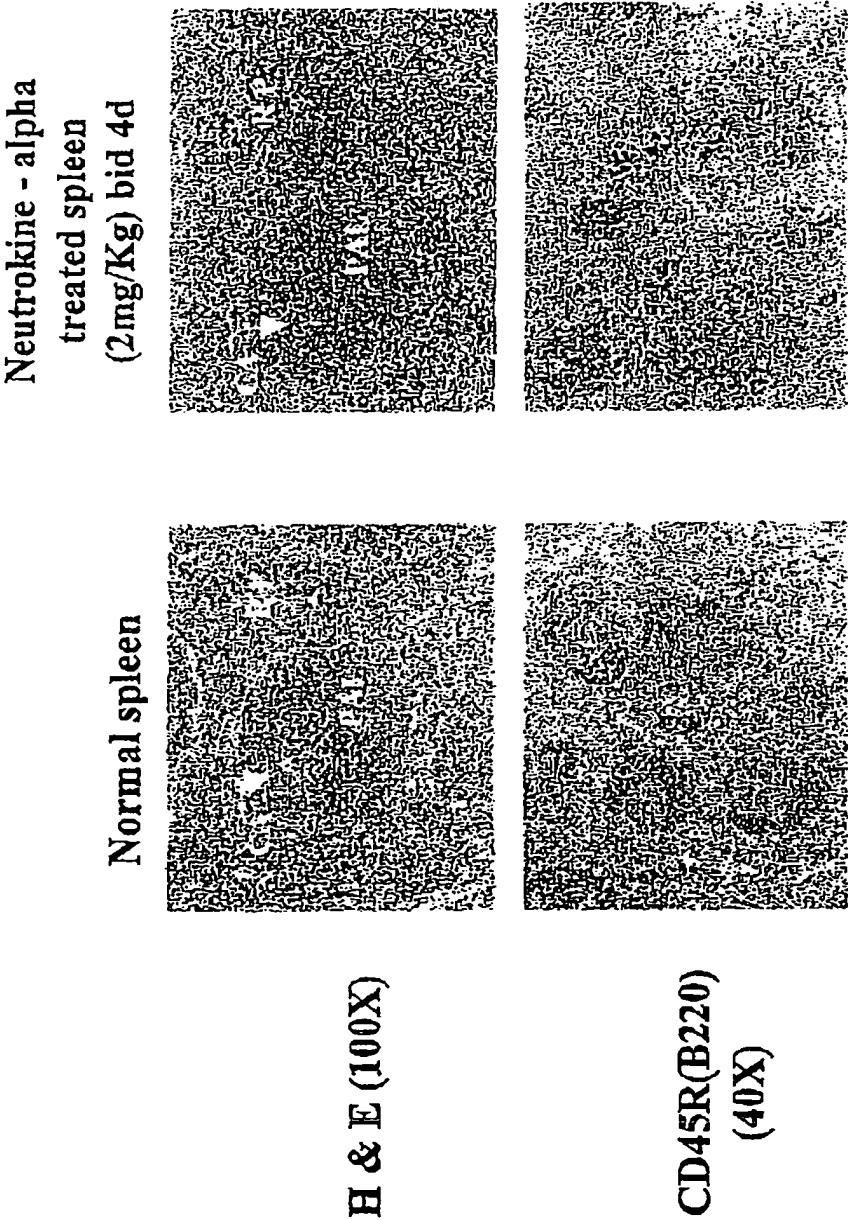


FIG.11A

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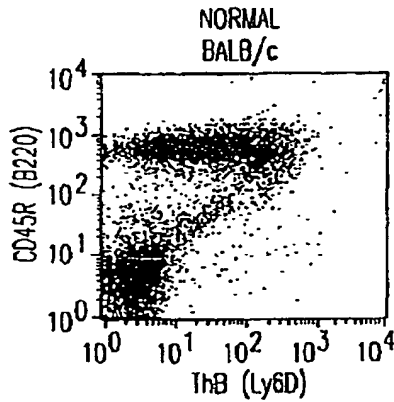


FIG. 11B

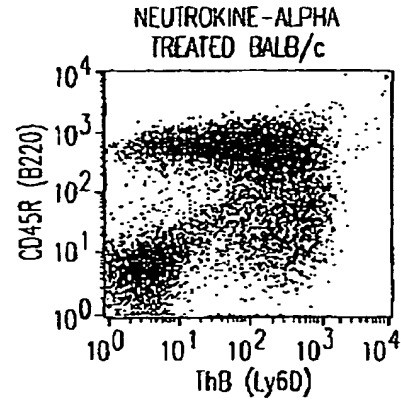


FIG. 11C

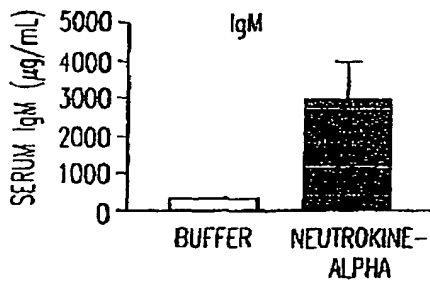


FIG. 11D

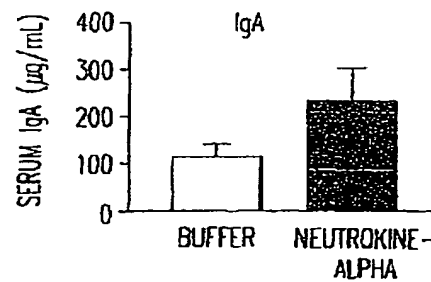


FIG. 11E

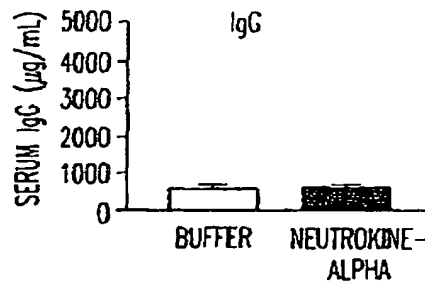


FIG. 11F

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1 METHODS OF INHIBITING B LYMPHOCYTES USING ANTIBODIES TO NEUTROKINE-ALPHA

This application is a continuation of application Ser. No. 09/507,968, filed Feb. 22, 2000 now U.S. Pat. No. 6,812,327; which claims the benefit of priority under 35 U.S.C. §119(e) based on the following U.S. provisional applications

U.S. application Ser. No.	Filing Date	U.S. application Ser. No.	Filing Date
60/122,388	Mar. 02, 1999	60/136,784	May 28, 1999
60/124,097	Mar. 12, 1999	60/142,659	Jul. 06, 1999
60/126,599	Mar. 26, 1999	60/145,824	Jul. 27, 1999
60/127,598	Apr. 02, 1999	60/167,239	Nov. 24, 1999
60/130,412	Apr. 16, 1999	60/168,624	Dec. 03, 1999
60/130,696	Apr. 23, 1999	60/171,108	Dec. 16, 1999
60/131,278	Apr. 27, 1999	60/171,626	Dec. 23, 1999
60/131,673	Apr. 29, 1999	60/176,015	Jan. 14, 2000

and which is also a continuation-in-part of copending application Ser. No. 09/255,794, filed Feb. 23, 1999; which in turn, is a continuation-in-part of copending application Ser. No. 09/005,874, filed Jan. 12, 1998; which is a continuation-in-part of PC1/US96/17957, filed Oct. 25, 1996, and claims the benefit of priority under 35 U.S.C. §119(e) of U.S. provisional application No. 60/036,100, filed Jan. 14, 1997. Each of the aforementioned non-provisional and provisional applications is hereby incorporated by reference in its entirety.

The present invention relates to a novel cytokine which has been designated Neutrokin-alpha ("Neutrokin-alpha"). In addition, an apparent splicing variant of Neutrokin-alpha has been identified and designated Neutrokin-alphaSV. In specific embodiments, the present invention provides nucleic acid molecules encoding Neutrokin-alpha and Neutrokin-alphaSV polypeptides. In additional embodiments, Neutrokin-alpha and Neutrokin-alphaSV polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same.

RELATED ART

Human tumor necrosis factors (TNF-alpha) and (TNF-beta, or lymphotoxin) are related members of a broad class of polypeptide mediators, which includes the interferons, interleukins and growth factors, collectively called cytokines (Beutler, B. and Cerami, A., *Annu. Rev. Immunol.* 7:625-655 (1989)). Sequence analysis of cytokine receptors has defined several subfamilies of membrane proteins (1) the Ig superfamily, (2) the hematopoietin (cytokine receptor superfamily) and (3) the tumor necrosis factor (TNF)/nerve growth factor (NGF) receptor superfamily (for review of TNF superfamily see, Gruss and Dower, *Blood* 85(12):3378-3404 (1995) and Aggarwal and Natarajan, *Eur. Cytokine Netw.* 7(2):93-124 (1996)). The TNF/NGF receptor superfamily contains at least 10 different proteins. Gruss and Dower, supra. Ligands for these receptors have been identified and belong to at least two cytokine superfamilies. Gruss and Dower, supra.

Tumor necrosis factor (a mixture of TNF-alpha and TNF-beta) was originally discovered as a result of its anti-tumor activity, however, now it is recognized as a pleiotropic cytokine capable of numerous biological activities including apoptosis of some transformed cell lines, mediation of cell activation and proliferation and also as playing important roles in immune regulation and inflammation.

2

To date, known members of the TNF-ligand superfamily include TNF-alpha, TNF-beta (lymphotoxin-alpha), LT-beta, OX40L, Fas ligand, CD30L, CD27L, CD40L, and 4-1BBL. The ligands of the TNF ligand superfamily are acidic, TNF-like molecules with approximately 20% sequence homology in the extracellular domains (range, 12%-36%) and exist mainly as membrane-bound forms with the biologically active form being a trimeric/multimeric complex. Soluble forms of the TNF ligand superfamily have only been identified so far for TNF, LT-beta, and Fas ligand (for a general review, see Gruss, H. and Dower, S. K., *Blood*, 85(12):3378-3404 (1995)), which is hereby incorporated by reference in its entirety. These proteins are involved in regulation of cell proliferation, activation, and differentiation, including control of cell survival or death by apoptosis or cytotoxicity (Armitage, R. J., *Curr. Opin. Immunol.* 6:407 (1994) and Smith, C. A., *Cell* 75:959 (1994)).

Tumor necrosis factor-alpha (TNF-alpha; also termed cachectin; hereinafter "TNF") is secreted primarily by monocytes and macrophages in response to endotoxin or other stimuli as a soluble homotrimer of 17 kDa protein subunits (Smith, R. A. et al., *J. Biol. Chem.* 262:6951-6954 (1987)). A membrane-bound 26 kD precursor form of TNF has also been described (Kriegler, M. et al., *Cell* 53:45-53 (1988)).

Accumulating evidence indicates that TNF is a regulatory cytokine with pleiotropic biological activities. These activities include: inhibition of lipoprotein lipase synthesis ("cachectin" activity) (Beutler, B. et al., *Nature* 316:552 (1985)), activation of polymorphonuclear leukocytes (Klebanoff, S. J. et al., *J. Immunol.* 136:4220 (1986); Perussia, B., et al., *J. Immunol.* 138:765 (1987)), inhibition of cell growth or stimulation of cell growth (Vilecek, J. et al., *J. Exp. Med.* 163:632 (1986); Suganman, B. J. et al., *Science* 230:943 (1985); Lachman, L. B. et al., *J. Immunol.* 138:2913 (1987)), cytotoxic action on certain transformed cell types (Lachman, L. B. et al., supra; Darzynkiewicz, Z. et al., *Canc. Res.* 44:83 (1984)), antiviral activity (Kohase, M. et al., *Cell* 45:659 (1986); Wong, G. H. W. et al., *Nature* 323:819 (1986)), stimulation of bone resorption (Bertolini, D. R. et al., *Nature* 319:516 (1986); Saklatvala, J., *Nature* 322:547 (1986)), stimulation of collagenase and prostaglandin E2 production (Dayer, J.-M. et al., *J. Exp. Med.* 162:2163 (1985)); and immunoregulatory actions, including activation of T cells (Yokota, S. et al., *J. Immunol.* 140:531 (1988)), B cells (Kehrl, J. H. et al., *J. Exp. Med.* 166:786 (1987)), monocytes (Philip, R. et al., *Nature* 323:86 (1986)), thymocytes (Ranges, G. E. et al., *J. Exp. Med.* 167:1472 (1988)), and stimulation of the cell-surface expression of major histocompatibility complex (MHC) class I and class II molecules (Collins, T. et al., *Proc. Natl. Acad. Sci. USA* 83:446 (1986); Pujol-Borrel, R. et al., *Nature* 326:304 (1987)).

TNF is noted for its pro-inflammatory actions which result in tissue injury, such as induction of procoagulant activity on vascular endothelial cells (Pober, J. S. et al., *J. Immunol.* 136:1680 (1986)), increased adherence of neutrophils and lymphocytes (Pober, J. S. et al., *J. Immunol.* 138:3319 (1987)), and stimulation of the release of platelet activating factor from macrophages, neutrophils and vascular endothelial cells (Camussi, G. et al., *J. Exp. Med.* 166:1390 (1987)).

Recent evidence implicates TNF in the pathogenesis of many infections (Cerami, A. et al., *Immunol. Today* 9:28 (1988)), immune disorders, neoplastic pathology, e.g., in cachexia accompanying some malignancies (Olioff, A. et al., *Cell* 50:555 (1987)), and in autoimmune pathologies and graft-versus host pathology (Piguet, P.-F. et al., *J. Exp. Med.* 166:1280 (1987)). The association of TNF with cancer and infectious pathologies is often related to the host's catabolic

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state. A major problem in cancer patients is weight loss, usually associated with anorexia. The extensive wasting which results is known as "cachexia" (Kem. K. A. et al. *J. Parent. Enter. Nutr.* 12:286-298 (1988)). Cachexia includes progressive weight loss, anorexia, and persistent erosion of body mass in response to a malignant growth. The cachectic state is thus associated with significant morbidity and is responsible for the majority of cancer mortality. A number of studies have suggested that TNF is an important mediator of the cachexia in cancer, infectious pathology, and in other catabolic states.

TNF is thought to play a central role in the pathophysiological consequences of Gram-negative sepsis and endotoxemic shock (Michie, H. R. et al., *Br. J. Surg.* 76:670-671 (1989); Debets, J. M. H. et al., *Second Vienna Shock Forum*, p.463-466 (1989); Simpson, S. Q. et al., *Crit. Care Clin.* 5:27-47 (1989)), including fever, malaise, anorexia, and cachexia. Endotoxin is a potent monocyte/macrophage activator which stimulates production and secretion of TNF (Kornbluth, S. K. et al., *J. Immunol.* 137:2585-2591 (1986)) and other cytokines. Because TNF could mimic many biological effects of endotoxin, it was concluded to be a central mediator responsible for the clinical manifestations of endotoxin-related illness. TNF and other monocyte-derived cytokines mediate the metabolic and neurohormonal responses to endotoxin (Michie, H. R. et al., *N. Eng. J. Med.* 318:1481-1486 (1988)). Endotoxin administration to human volunteers produces acute illness with flu-like symptoms including fever, tachycardia, increased metabolic rate and stress hormone release (Revhag, A. et al., *Arch. Surg.* 123:162-170 (1988)). Elevated levels of circulating TNF have also been found in patients suffering from Gram-negative sepsis (Waage, A. et al., *Lancet* 1:355-357 (1987); Hammerle, A. F. et al., *Second Vienna Shock Forum* p. 715-718 (1989); Debets, J. M. H. et al., *Crit. Care Med.* 17:489-497 (1989); Calandra, T. et al., *J. Infect. Dis.* 161:982-987 (1990)).

Passive immunotherapy directed at neutralizing TNF may have a beneficial effect in Gram-negative sepsis and endotoxemia, based on the increased TNF production and elevated TNF levels in these pathology states, as discussed above. Antibodies to a "modulator" material which was characterized as cachectin (later found to be identical to TNF) were disclosed by Cerami et al. (EPO Patent Publication 0,212, 489, Mar. 4, 1987). Such antibodies were said to be useful in diagnostic immunoassays and in therapy of shock in bacterial infections. Rubin et al. (EPO Patent Publication 0,218,868, Apr. 22, 1987) disclosed monoclonal antibodies to human TNF, the hybridomas secreting such antibodies, methods of producing such antibodies, and the use of such antibodies in immunoassay of TNF. Yone et al. (EPO Patent Publication 0,288,088, Oct. 26, 1988) disclosed anti-TNF antibodies, including mAbs, and their utility in immunoassay diagnosis of pathologies, in particular Kawasaki's pathology and bacterial infection. The body fluids of patients with Kawasaki's pathology (infantile acute febrile mucocutaneous lymph node syndrome; Kawasaki, T., *Allergy* 16:178 (1967); Kawasaki, T., *Shonika (Pediatrics)* 26:935 (1985)) were said to contain elevated TNF levels which were related to progress of the pathology (Yone et al., supra).

Other investigators have described mAbs specific for recombinant human TNF which had neutralizing activity in vitro (Liang, C-M. et al. *Biochem. Biophys. Res. Comm.* 137: 847-854 (1986); Meager, A. et al., *Hybridoma* 6:305-311 (1987); Fendly et al., *Hybridoma* 6:359-369 (1987); Bringman, T.S. et al., *Hybridoma* 6:489-507 (1987); Hirai, M. et al., *J. Immunol. Meth.* 96:57-62 (1987); Moller, A. et al. (*Cytokine* 2:162-169 (1990)). Some of these mAbs were used to map

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epitopes of human TNF and develop enzyme immunoassays (Fendly et al., supra; Hirai et al., supra; Moller et al., supra) and to assist in the purification of recombinant TNF (Bringman et al., supra). However, these studies do not provide a basis for producing TNF neutralizing antibodies that can be used for in vivo diagnostic or therapeutic uses in humans, due to immunogenicity, lack of specificity and/or pharmaceutical suitability.

Neutralizing antisera or mAbs to TNF have been shown in mammals other than man to abrogate adverse physiological changes and prevent death after lethal challenge in experimental endotoxemia and bacteremia. This effect has been demonstrated, e.g., in rodent lethality assays and in primate pathology model systems (Mathison, J. C. et al., *J. Clin. Invest.* 81:1925-1937 (1988); Beutler, B. et al., *Science* 229: 869-871 (1985); Tracey, K. J. et al., *Nature* 330:662-664 (1987); Shimamoto, Y. et al., *Immunol. Lett.* 17:311-318 (1988); Silva, A. T. et al., *J. Infect. Dis.* 162:421-427 (1990); Opal, S. M. et al., *J. Infect. Dis.* 161:1148-1152 (1990); Hinshaw, L. B. et al., *Circ. Shock* 30:279-292 (1990)).

To date, experience with anti-TNF mAb therapy in humans has been limited but shows beneficial therapeutic results, e.g., in arthritis and sepsis. See, e.g., Elliott, M. J. et al., *Baillieres Clin. Rheumatol.* 9:633-52 (1995); Feldmann M. et al., *Ann. N.Y. Acad. Sci. USA* 766:272-8 (1995); van der Poll, T. et al., *Shock* 3:1-12 (1995); Wherry et al., *Crit. Care Med.* 21:S436-40 (1993); Tracey K. J., et al., *Crit. Care Med.* 21:S415-22 (1993).

Mammalian development is dependent on both the proliferation and differentiation of cells as well as programmed cell death which occurs through apoptosis (Walker, et al., *Methods Achiev. Exp. Pathol.* 13:18 (1988)). Apoptosis plays a critical role in the destruction of immune thymocytes that recognize self antigens. Failure of this normal elimination process may play a role in autoimmune diseases (Ganamon et al., *Immunology Today* 12:193 (1991)).

Itoh et al. (*Cell* 66:233 (1991)) described a cell surface antigen, Fas/CD95 that mediates apoptosis and is involved in clonal deletion of T-cells. Fas is expressed in activated T-cells, B-cells, neutrophils and in thymus, liver, heart and lung and ovary in adult mice (Watanabe-Fukunaga et al., *J. Immunol.* 148:1274 (1992)) in addition to activated T-cells, B-cells, neutrophils. In experiments where a monoclonal Ab is cross-linked to Fas, apoptosis is induced (Yonehara et al., *J. Exp. Med.* 169:1747 (1989); Trauth et al., *Science* 245:301 (1989)). In addition, there is an example where binding of a monoclonal Ab to Fas is stimulatory to T-cells under certain conditions (Alderson et al., *J. Exp. Med.* 178:2231 (1993)).

Fas antigen is a cell surface protein of relative MW of 45 kDa. Both human and murine genes for Fas have been cloned by Watanabe-Fukunaga et al., (*J. Immunol.* 148:1274 (1992)) and Itoh et al. (*Cell* 66:233 (1991)). The proteins encoded by these genes are both transmembrane proteins with structural homology to the Nerve Growth Factor/Tumor Necrosis Factor receptor superfamily, which includes two TNF receptors, the low affinity Nerve Growth Factor receptor and CD40, CD27, CD30, and OX40.

Recently the Fas ligand has been described (Suda et al., *Cell* 75:1169 (1993)). The amino acid sequence indicates that Fas ligand is a type II transmembrane protein belonging to the TNF family. Thus, the Fas ligand polypeptide comprises three main domains: a short intracellular domain at the amino terminal end and a longer extracellular domain at the carboxy terminal end, connected by a hydrophobic transmembrane domain. Fas ligand is expressed in splenocytes and thymocytes, consistent with T-cell mediated cytotoxicity. The purified Fas ligand has a MW of 40 kDa.

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Recently, it has been demonstrated that Fas/Fas ligand interactions are required for apoptosis following the activation of T-cells (Ju et al., *Nature* 373:444 (1995); Brunner et al., *Nature* 373:441 (1995)). Activation of T-cells induces both proteins on the cell surface. Subsequent interaction between the ligand and receptor results in apoptosis of the cells. This supports the possible regulatory role for apoptosis induced by Fas/Fas ligand interaction during normal immune responses.

Accordingly, there is a need to provide cytokines similar to TNF that are involved in pathological conditions. Such novel cytokines may be used to make novel antibodies or other antagonists that bind these TNF-like cytokines for diagnosis and therapy of disorders related to TNF-like cytokines.

SUMMARY OF THE INVENTION

In accordance with one embodiment of the present invention, there is provided a novel extracellular domain of a Neutrokin-alpha polypeptide, and a novel extracellular domain of a Neutrokin-alphaSV polypeptide, as well as biologically active and diagnostically or therapeutically useful fragments, analogs and derivatives thereof.

In accordance with another embodiment of the present invention, there are provided isolated nucleic acid molecules encoding human Neutrokin-alpha or Neutrokin-alphaSV, including mRNAs, DNAs, cDNAs, genomic DNAs as well as analogs and biologically active and diagnostically or therapeutically useful fragments and derivatives thereof.

The present invention provides isolated nucleic acid molecules comprising, or alternatively, consisting of, a polynucleotide encoding a cytokine and an apparent splice variant thereof that are structurally similar to TNF and related cytokines and have similar biological effects and activities. This cytokine is named Neutrokin-alpha and the invention includes Neutrokin-alpha polypeptides having at least a portion of the amino acid sequence in FIGS. 1A and 1B (SEQ ID NO:2) or amino acid sequence encoded by the cDNA clone (HNEU15) deposited on Oct. 22, 1996 assigned ATCC number 97768. The nucleotide sequence determined by sequencing the deposited Neutrokin-alpha clone, which is shown in FIGS. 1A and 1B (SEQ ID NO:1), contains an open reading frame encoding a complete polypeptide of 285 amino acid residues including an N-terminal methionine, a predicted intracellular domain of about 46 amino acid residues, a predicted transmembrane domain of about 26 amino acids, a predicted extracellular domain of about 213 amino acids, and a deduced molecular weight for the complete protein of about 31 kDa. As for other type II transmembrane proteins, soluble forms of Neutrokin-alpha include all or a portion of the extracellular domain cleaved from the transmembrane domain and a polypeptide comprising the complete Neutrokin-alpha polypeptide lacking the transmembrane domain, i.e., the extracellular domain linked to the intracellular domain.

The apparent splice variant of Neutrokin-alpha is named Neutrokin-alphaSV and the invention includes Neutrokin-alphaSV polypeptides comprising, or alternatively, consisting of, at least a portion of the amino acid sequence in FIGS. 5A and 5B (SEQ ID NO:19) or amino acid sequence encoded by the cDNA clone HDPMC52 deposited on Dec. 10, 1998 and assigned ATCC number 203518. The nucleotide sequence determined by sequencing the deposited Neutrokin-alphaSV clone, which is shown in FIGS. 5A and 5B (SEQ ID NO:18), contains an open reading frame encoding a complete polypeptide of 266 amino acid residues including an N-terminal methionine, a predicted intracellular domain of

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about 46 amino acid residues, a predicted transmembrane domain of about 26 amino acids, a predicted extracellular domain of about 194 amino acids, and a deduced molecular weight for the complete protein of about 29 kDa. As for other type II transmembrane proteins, soluble forms of Neutrokin-alphaSV include all or a portion of the extracellular domain cleaved from the transmembrane domain and a polypeptide comprising the complete Neutrokin-alphaSV polypeptide lacking the transmembrane domain, i.e., the extracellular domain linked to the intracellular domain.

Thus, one embodiment of the invention provides an isolated nucleic acid molecule comprising, or alternatively consisting of, a polynucleotide having a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a full-length Neutrokin-alpha polypeptide having the complete amino acid sequence in FIGS. 1A and 1B (SEQ ID NO:2) or as encoded by the cDNA clone contained in the deposit having ATCC accession number 97768; (b) a nucleotide sequence encoding the predicted extracellular domain of the Neutrokin-alpha polypeptide having the amino acid sequence at positions 73 to 285 in FIGS. 1A and 1B (SEQ ID NO:2) or as encoded by the clone contained in the deposit having ATCC accession number 97768; (c) a nucleotide sequence encoding a fragment of the polypeptide of (b) having Neutrokin-alpha functional activity (e.g., biological activity); (d) a nucleotide sequence encoding a polypeptide comprising the Neutrokin-alpha intracellular domain (predicted to constitute amino acid residues from about 1 to about 46 in FIGS. 1A and 1B (SEQ ID NO:2)) or as encoded by the clone contained in the deposit having ATCC accession number 97768; (e) a nucleotide sequence encoding a polypeptide comprising the Neutrokin-alpha transmembrane domain (predicted to constitute amino acid residues from about 47 to about 72 in FIGS. 1A and 1B (SEQ ID NO:2) or as encoded by the cDNA clone contained in the deposit having ATCC accession number 97768; (f) a nucleotide sequence encoding a soluble Neutrokin-alpha polypeptide having the extracellular and intracellular domains but lacking the transmembrane domain; and (g) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), (c), (d), (e) or (f) above.

Further embodiments of the invention include isolated nucleic acid molecules that comprise, or alternatively consist of, a polynucleotide having a nucleotide sequence at least 80%, 85% or 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical, to any of the nucleotide sequences in (a), (b), (c), (d), (e), (f) or (g) above, or a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide in (a), (b), (c), (d), (e), (f) or (g) above. This polynucleotide which hybridizes does not hybridize under stringent hybridization conditions to a polynucleotide having a nucleotide sequence consisting of only A residues or of only T residues.

Another embodiment of the invention provides an isolated nucleic acid molecule comprising, or alternatively consisting of, a polynucleotide having a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a full-length Neutrokin-alphaSV polypeptide having the complete amino acid sequence in FIGS. 5A and 5B (SEQ ID NO:19) or as encoded by the cDNA clone contained in the ATCC Deposit deposited on Dec. 10, 1998 as ATCC Number 203518; (b) a nucleotide sequence encoding the predicted extracellular domain of the Neutrokin-alphaSV polypeptide having the amino acid sequence at positions 73 to 266 in FIGS. 1A and 1B (SEQ ID NO:2) or as encoded by the cDNA clone contained in ATCC 203518 deposited on Dec. 10, 1998; (c) a nucleotide sequence encoding a polypeptide

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comprising the Neurokinine-alphaSV intracellular domain (predicted to constitute amino acid residues from about 1 to about 46 in FIGS. 5A and 5B (SEQ ID NO:19)) or as encoded by the cDNA clone contained in ATCC[®] No. 203518 deposited on Dec. 10, 1998; (d) a nucleotide sequence encoding a polypeptide comprising the Neurokinine-alphaSV transmembrane domain (predicted to constitute amino acid residues from about 47 to about 72 in FIGS. 5A and 5B (SEQ ID NO:19)) or as encoded by the cDNA clone contained in ATCC[®] No. 203518 deposited on Dec. 10, 1998; (e) a nucleotide sequence encoding a soluble Neurokinine-alphaSV polypeptide having the extracellular and intracellular domains but lacking the transmembrane domain; and (f) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), (c), (d), or (e) above.

Further embodiments of the invention include isolated nucleic acid molecules that comprise, or alternatively consist of, a polynucleotide having a nucleotide sequence at least 80%, 85% or 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical, to any of the nucleotide sequences in (a), (b), (c), (d), (e) or (f) above, or a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide in (a), (b), (c), (d), (e) or (f) above. This polynucleotide which hybridizes does not hybridize under stringent hybridization conditions to a polynucleotide having a nucleotide sequence consisting of only A residues or of only T residues.

In one embodiment, the apparent splice variant of Neurokinine-alpha comprising, or alternatively consisting of, at least a portion of the amino acid sequence from Gly-142 to Leu-266 as shown in FIGS. 5A and 5B (SEQ ID NO:19) or amino acid sequence encoded by the cDNA clone HDPMC52 deposited on Dec. 10, 1998 and assigned ATCC Deposit No. 203518.

In additional embodiments, the nucleic acid molecules of the invention comprise, or alternatively consist of, a polynucleotide which encodes the amino acid sequence of an epitope-bearing portion of a Neurokinine-alpha or Neurokinine-alphaSV polypeptide having an amino acid sequence in (a), (b), (c), (d), (e), (f) or (g) above. A further nucleic acid embodiment of the invention relates to an isolated nucleic acid molecule comprising, or alternatively consisting of, a polynucleotide which encodes the amino acid sequence of a Neurokinine-alpha or Neurokinine-alphaSV polypeptide having an amino acid sequence which contains at least one amino acid addition, substitution, and/or deletion but not more than 50 amino acid additions, substitutions and/or deletions, even more preferably, not more than 40 amino acid additions, substitutions, and/or deletions, still more preferably, not more than 30 amino acid additions, substitutions, and/or deletions, and still even more preferably, not more than 20 amino acid additions, substitutions, and/or deletions. Of course, in order of ever-increasing preference, it is highly preferable for a polynucleotide which encodes the amino acid sequence of a Neurokinine-alpha or Neurokinine-alphaSV polypeptide to have an amino acid sequence which contains not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 or 1-100, 1-50, 1-25, 1-20, 1-15, 1-10, or 1-5 amino acid additions, substitutions and/or deletions. Conservative substitutions are preferable.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention, and to host cells containing the recombinant vectors, as well as to methods of making such vectors and host cells and for using them for production of Neurokinine-alpha polypeptides by recombinant techniques.

In accordance with a further embodiment of the present invention, there is provided a process for producing such

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polypeptides by recombinant techniques comprising culturing recombinant prokaryotic and/or eukaryotic host cells, containing a Neurokinine-alpha or Neurokinine-alphaSV nucleic acid sequence of the invention, under conditions promoting expression of said polypeptide and subsequent recovery of said polypeptide.

The invention further provides an isolated Neurokinine-alpha polypeptide comprising, or alternatively consisting of, an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of the full-length Neurokinine-alpha polypeptide having the complete amino acid sequence shown in FIGS. 1A and 1B (i.e., positions 1-285 of SEQ ID NO:2) or as encoded by the cDNA plasmid contained in the deposit having ATCC[®] accession number 97768; (b) the amino acid sequence of the full-length Neurokinine-alpha polypeptide having the complete amino acid sequence shown in SEQ ID NO:2 excepting the N-terminal methionine (i.e., positions 2 to 285 of SEQ ID NO:2); (c) a fragment of the polypeptide of (b) having Neurokinine-alpha functional activity (e.g., biological activity); (d) the amino acid sequence of the predicted extracellular domain of the Neurokinine-alpha polypeptide having the amino acid sequence at positions 73 to 285 in FIGS. 1A and 1B (SEQ ID NO:2) or as encoded by the cDNA plasmid contained in the deposit having ATCC[®] accession number 97768; (e) a nucleotide sequence encoding the Neurokinine-alpha polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2); (f) the amino acid sequence of the Neurokinine-alpha intracellular domain (predicted to constitute amino acid residues from about 1 to about 46 in FIGS. 1A and 1B (SEQ ID NO:2)) or as encoded by the cDNA plasmid contained in the deposit having ATCC[®] accession number 97768; (g) the amino acid sequence of the Neurokinine-alpha transmembrane domain (predicted to constitute amino acid residues from about 47 to about 72 in FIGS. 1A and 1B (SEQ ID NO:2)) or as encoded by the cDNA plasmid contained in the deposit having ATCC[®] accession number 97768; (h) the amino acid sequence of the soluble Neurokinine-alpha polypeptide having the extracellular and intracellular domains but lacking the transmembrane domain, wherein each of these domains is defined above; and (i) fragments of the polypeptide of (a), (b), (c), (d), (e), (f), (g) or (h). The polypeptides of the present invention also include polypeptides having an amino acid sequence at least 80% identical, more preferably at least 85% or 90% identical, and still more preferably 95%, 96%, 97%, 98% or 99% identical to those described in (a), (b), (c), (d), (e), (f), (g), (h) or (i) above, as well as polypeptides having an amino acid sequence with at least 80%, 85%, or 90% similarity, and more preferably at least 95% similarity, to those above. Additional embodiments of the invention relates to polypeptides which comprise, or alternatively consist of, the amino acid sequence of an epitope-bearing portion of a Neurokinine-alpha polypeptide having an amino acid sequence described in (a), (b), (c), (d), (e), (f), (g), (h) or (i) above. Polypeptides having the amino acid sequence of an epitope-bearing portion of a Neurokinine-alpha polypeptide of the invention include portions of such polypeptides with at least 4, at least 5, at least 6, at least 7, at least 8, and preferably at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 20, at least 25, at least 30, at least 40, at least 50, and more preferably at least about 30 amino acids to about 50 amino acids, although epitope-bearing polypeptides of any length up to and including the entire amino acid sequence of a polypeptide of the invention described above also are included in the invention.

Highly preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of a polynucleotide having a nucleotide

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sequence at least 80%, 85%, 90% identical and more preferably at least 95%, 96%, 97%, 98%, 99% or 100% identical to a polynucleotide sequence encoding the Neutrokinine-alpha polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2). Preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of a polynucleotide having a nucleotide sequence at least 90% identical to a polynucleotide sequence encoding the Neutrokinine-alpha polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2). More preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of a polynucleotide having a nucleotide sequence at least 95% identical to a polynucleotide sequence encoding the Neutrokinine-alpha polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2). More preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of a polynucleotide having a nucleotide sequence at least 96% identical to a polynucleotide sequence encoding the Neutrokinine-alpha polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2).

Additionally, more preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of a polynucleotide having a nucleotide sequence at least 97% to a polynucleotide sequence encoding the Neutrokinine-alpha polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2). Additionally, more preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of a polynucleotide having a nucleotide sequence at least 98% to a polynucleotide sequence encoding the Neutrokinine-alpha polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2). Additionally, more preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of a polynucleotide having a nucleotide sequence at least 99% identical to a polynucleotide sequence encoding the Neutrokinine-alpha polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2).

The present invention also encompasses the above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these polynucleotides and nucleic acid molecules are also encompassed by the invention.

The invention further provides an isolated Neutrokinine-alphaSV polypeptide comprising, or alternatively consisting of, an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of the full-length Neutrokinine-alphaSV polypeptide having the complete amino acid sequence shown in FIGS. 5A and 5B (i.e., positions 1-266 of SEQ ID NO:19) or as encoded by the cDNA clone contained in ATCC No. 203518 deposited on Dec. 10, 1998; (b) the amino acid sequence of the full-length Neutrokinine-alphaSV polypeptide having the complete amino acid sequence shown in SEQ ID NO:19 excepting the N-terminal methionine (i.e., positions 2 to 266 of SEQ ID NO:19); (c) the amino acid sequence of the predicted extracellular domain of the Neutrokinine-alphaSV polypeptide having the amino acid sequence at positions 73 to 266 in FIGS. 5A and 5B (SEQ ID NO:19) or as encoded by the cDNA clone contained in ATCC No. 203518 deposited on Dec. 10, 1998; (d) the amino acid sequence of the Neutrokinine-alphaSV intracellular domain (predicted to constitute amino acid residues from about 1 to

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about 46 in FIGS. 5A and 5B (SEQ ID NO:19)) or as encoded by the cDNA clone contained in ATCC No. 203518 deposited on Dec. 10, 1998; (e) the amino acid sequence of the Neutrokinine-alphaSV transmembrane domain (predicted to constitute amino acid residues from about 47 to about 72 in FIGS. 5A and 5B (SEQ ID NO:19)) or as encoded by the cDNA clone contained in ATCC No. 203518 deposited on Dec. 10, 1998; (f) the amino acid sequence of the soluble Neutrokinine-alphaSV polypeptide having the extracellular and intracellular domains but lacking the transmembrane domain, wherein each of these domains is defined above; and (g) fragments of the polypeptide of (a), (b), (c), (d), (e), or (f). The polypeptides of the present invention also include polypeptides having an amino acid sequence at least 80% identical, more preferably at least 85% or 90% identical, and still more preferably 95%, 96%, 97%, 98% or 99% identical to those described in (a), (b), (c), (d), (e), (f), or (g) above, as well as polypeptides having an amino acid sequence with at least 80%, 85%, or 90% similarity, and more preferably at least 95% similarity, to those above. Additional embodiments of the invention relates to polypeptides which comprise, or alternatively consist of, the amino acid sequence of an epitope-bearing portion of a Neutrokinine-alphaSV polypeptide having an amino acid sequence described in (a), (b), (c), (d), (e), (f), or (g) above. Peptides or polypeptides having the amino acid sequence of an epitope-bearing portion of a Neutrokinine-alphaSV polypeptide of the invention include portions of such polypeptides with at least 4, at least 5, at least 6, at least 7, at least 8, and preferably at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 20, at least 25, at least 30, at least 40, at least 50, and more preferably at least about 30 amino acids to about 50 amino acids, although epitope-bearing polypeptides of any length up to and including the entire amino acid sequence of a polypeptide of the invention described above also are included in the invention.

Certain non-exclusive embodiments of the invention relate to a polypeptide which has the amino acid sequence of an epitope-bearing portion of a Neutrokinine-alpha or Neutrokinine-alphaSV polypeptide having an amino acid sequence described in (a), (b), (c), (d), (e), (f), (g), (h) or (i) above. In other embodiments, the invention provides an isolated antibody that binds specifically (i.e., uniquely) to a Neutrokinine-alpha or Neutrokinine-alphaSV polypeptide having an amino acid sequence described in (a), (b), (c), (d), (e), (f), (g), (h) or (i) above.

The invention further provides methods for isolating antibodies that bind specifically (i.e., uniquely) to a Neutrokinine-alpha or Neutrokinine-alphaSV polypeptide having an amino acid sequence as described herein. Such antibodies are useful diagnostically or therapeutically as described below.

The invention also provides for pharmaceutical compositions comprising soluble Neutrokinine-alpha and/or Neutrokinine-alphaSV polypeptides, particularly human Neutrokinine-alpha and/or Neutrokinine-alphaSV polypeptides, and/or anti-Neutrokinine-alpha antibodies and/or anti-Neutrokinine-alphaSV antibodies which may be employed, for instance, to treat, prevent, prognose and/or diagnose tumor and tumor metastasis, infections by bacteria, viruses and other parasites, immunodeficiencies, inflammatory diseases, lymphadenopathy, autoimmune diseases, graft versus host disease, stimulate peripheral tolerance, destroy some transformed cell lines, mediate cell activation, survival and proliferation, mediate immune regulation and inflammatory responses, and to enhance or inhibit immune responses.

In certain embodiments, soluble Neutrokinine-alpha and/or Neutrokinine-alphaSV polypeptides of the invention, or agonists thereof, are administered, to treat, prevent, prognose

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and/or diagnose an immunodeficiency (e.g., severe combined immunodeficiency (SCID)-X linked, SCID-autosomal, adenosine deaminase deficiency (ADA deficiency), X-linked agammaglobulinemia (XLA), Bruton's disease, congenital agammaglobulinemia, X-linked infantile agammaglobulinemia, acquired agammaglobulinemia, adult onset agammaglobulinemia, late-onset agammaglobulinemia, dysgamma-globulinemia, hypogammaglobulinemia, transient hypogammaglobulinemia of infancy, unspecified hypogammaglobulinemia, agammaglobulinemia, common variable immunodeficiency (CVID) (acquired), Wiskott-Aldrich Syndrome (WAS), X-linked immunodeficiency with hyper IgM, non X-linked immunodeficiency with hyper IgM, selective IgA deficiency, IgG subclass deficiency (with or without IgA deficiency), antibody deficiency with normal or elevated Igs, immunodeficiency with thymoma, Ig heavy chain deletions, kappa chain deficiency, B cell lymphoproliferative disorder (BLPD), selective IgM immunodeficiency, recessive agammaglobulinemia (Swiss type), reticular dysgenesis, neonatal neutropenia, severe congenital leukopenia, thymic aplasia/aplasia or dysplasia with immunodeficiency, ataxia-telangiectasia, short limbed dwarfism, X-linked lymphoproliferative syndrome (XLP), Nezelof syndrome-combined immunodeficiency with Igs, purine nucleoside phosphorylase deficiency (PNP), MHC Class II deficiency (Bare Lymphocyte Syndrome) and severe combined immunodeficiency,) or conditions associated with an immunodeficiency.

In a specific embodiment, Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides or polynucleotides of the invention, or agonists thereof, are administered to treat, prevent, prognose and/or diagnose common variable immunodeficiency.

In a specific embodiment, Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides or polynucleotides of the invention, or agonists thereof, are administered to treat, prevent, prognose and/or diagnose X-linked agammaglobulinemia.

In another specific embodiment, Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides or polynucleotides of the invention, or agonists thereof, are administered to treat, prevent, prognose and/or diagnose severe combined immunodeficiency (SCID).

In another specific embodiment, Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides or polynucleotides of the invention, or agonists thereof, are administered to treat, prevent, prognose and/or diagnose Wiskott-Aldrich syndrome.

In another specific embodiment, Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides or polynucleotides of the invention, or agonists thereof, are administered to treat, prevent, prognose and/or diagnose X-linked Ig deficiency with hyper IgM.

In another embodiment, Neutrokin-alpha antagonists and/or Neutrokin-alphaSV antagonists (e.g., an anti-Neutrokin-alpha antibody), are administered to treat, prevent, prognose and/or diagnose an autoimmune disease (e.g., rheumatoid arthritis, systemic lupus erythematosus, idiopathic thrombocytopenia purpura, autoimmune hemolytic anemia, autoimmune neonatal thrombocytopenia, autoimmune cytopenia, hemolytic anemia, antiphospholipid syndrome, dermatitis, allergic encephalomyelitis, myocarditis, relapsing polychondritis, rheumatic heart disease, glomerulonephritis (e.g., IgA nephropathy), Multiple Sclerosis, Neuritis, Uveitis, Ophthalmia, Polyendocrinopathies, Purpura (e.g., Henoch-Schoenlein purpura), Reiter's Disease, Stiff-Man Syndrome, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune inflammatory eye, autoimmune thyroiditis, hypothyroidism

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(i.e., Hashimoto's thyroiditis, Goodpasture's syndrome, Pemphigus. Receptor autoimmunities such as, for example, (a) Graves' Disease, (b) Myasthenia Gravis, and (c) insulin resistance, autoimmune hemolytic anemia, autoimmune thrombocytopenic purpura, scleroderma with anti-collagen antibodies, mixed connective tissue disease, polymyositis/dermatomyositis, pernicious anemia, idiopathic Addison's disease, infertility, glomerulonephritis such as primary glomerulonephritis and IgA nephropathy, bullous pemphigoid, Sjogren's syndrome, diabetes mellitus, and adrenergic drug resistance (including adrenergic drug resistance with asthma or cystic fibrosis), chronic active hepatitis, primary biliary cirrhosis, other endocrine gland failure, vitiligo, vasculitis, post-MI, cardiomyopathy syndrome, urticaria, atopic dermatitis, asthma, inflammatory myopathies, and other inflammatory, granulomatous, degenerative, and atrophic disorders) or conditions associated with an autoimmune disease. In a specific preferred embodiment, rheumatoid arthritis is treated, prevented, prognosed and/or diagnosed using anti-Neutrokin-alpha antibodies and/or anti-Neutrokin-alphaSV antibodies and/or other antagonist of the invention. In another specific preferred embodiment, systemic lupus erythematosus is treated, prevented, prognosed, and/or diagnosed using anti-Neutrokin-alpha antibodies and/or anti-Neutrokin-alphaSV and/or other antagonist of the invention. In another specific preferred embodiment, idiopathic thrombocytopenia purpura is treated, prevented, prognosed, and/or diagnosed using anti-Neutrokin-alpha antibodies and/or anti-Neutrokin-alphaSV and/or other antagonist of the invention. In another specific preferred embodiment, IgA nephropathy is treated, prevented, prognosed and/or diagnosed using anti-Neutrokin-alpha antibodies and/or anti-Neutrokin-alphaSV and/or other antagonist of the invention. In a preferred embodiment, the autoimmune diseases and disorders and/or conditions associated with the diseases and disorders recited above are treated, prevented, prognosed and/or diagnosed using anti-Neutrokin-alpha antibodies and/or anti-Neutrokin-alphaSV antibodies.

The invention further provides compositions comprising a Neutrokin-alpha or Neutrokin-alphaSV polynucleotide, a Neutrokin-alpha or Neutrokin-alphaSV polypeptide, and/or an anti-Neutrokin-alpha antibody or anti-Neutrokin-alphaSV antibody, for administration to cells in vitro, to cells ex vivo, and to cells in vivo, or to a multicellular organism. In preferred embodiments, the compositions of the invention comprise a Neutrokin-alpha and/or Neutrokin-alphaSV polynucleotide for expression of a Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide in a host organism for treatment of disease. In a most preferred embodiment, the compositions of the invention comprise a Neutrokin-alpha and/or Neutrokin-alphaSV polynucleotide for expression of a Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide in a host organism for treatment of an immunodeficiency and/or conditions associated with an immunodeficiency. Particularly preferred in this regard is expression in a human patient for treatment of a dysfunction associated with aberrant endogenous activity of a Neutrokin-alpha or Neutrokin-alphaSV gene (e.g., expression to enhance the normal B-cell function by expanding B-cell numbers or increasing B cell lifespan).

The present invention also provides a screening method for identifying compounds capable of enhancing or inhibiting a cellular response induced by Neutrokin-alpha and/or Neutrokin-alphaSV which involves contacting cells which express Neutrokin-alpha and/or Neutrokin-alphaSV with the candidate compound, assaying a cellular response, and comparing the cellular response to a standard cellular

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response, the standard being assayed when contact is made in absence of the candidate compound; whereby, an increased cellular response over the standard indicates that the compound is an agonist and a decreased cellular response over the standard indicates that the compound is an antagonist.

In another embodiment, a method for identifying Neutrokinine-alpha and/or Neutrokinine-alphaSV receptors is provided, as well as a screening assay for agonists and antagonists using such receptors. This assay involves determining the effect a candidate compound has on Neutrokinine-alpha and/or Neutrokinine-alphaSV binding to the Neutrokinine-alpha and/or Neutrokinine-alphaSV receptor. In particular, the method involves contacting a Neutrokinine-alpha and/or Neutrokinine-alphaSV receptor with a Neutrokinine-alpha and/or Neutrokinine-alphaSV polypeptide of the invention and a candidate compound and determining whether Neutrokinine-alpha and/or Neutrokinine-alphaSV polypeptide binding to the Neutrokinine-alpha and/or Neutrokinine-alphaSV receptor is increased or decreased due to the presence of the candidate compound. The antagonists may be employed to prevent septic shock, inflammation, cerebral malaria, activation of the HIV virus, graft-host rejection, bone resorption, rheumatoid arthritis, cachexia (wasting or malnutrition), immune system function, lymphoma, and autoimmune disorders (e.g., rheumatoid arthritis and systemic lupus erythematosus).

The present inventors have discovered that Neutrokinine-alpha is expressed not only in cells of monocytic lineage, but also in kidney, lung, peripheral leukocyte, bone marrow, T cell lymphoma, B cell lymphoma, activated T cells, stomach cancer, smooth muscle, macrophages, and cord blood tissue. The present inventors have further discovered that Neutrokinine-alphaSV appears to be expressed highly only in primary dendritic cells. For a number of disorders of these tissues and cells, such as tumor and tumor metastasis, infection of bacteria, viruses and other parasites, immunodeficiencies (e.g., chronic variable immunodeficiency), septic shock, inflammation, cerebral malaria, activation of the HIV virus, graft-host rejection, bone resorption, rheumatoid arthritis, autoimmune diseases (e.g., rheumatoid arthritis and systemic lupus erythematosus) and cachexia (wasting or malnutrition). It is believed that significantly higher or lower levels of Neutrokinine-alpha and/or Neutrokinine-alphaSV gene expression can be detected in certain tissues (e.g., bone marrow) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) taken from an individual having such a disorder, relative to a "standard" Neutrokinine-alpha and/or Neutrokinine-alphaSV gene expression level, i.e., the Neutrokinine-alpha and/or Neutrokinine-alphaSV expression level in tissue or bodily fluids from an individual not having the disorder. Thus, the invention provides a diagnostic method useful during diagnosis of a disorder, which involves: (a) assaying Neutrokinine-alpha and/or Neutrokinine-alphaSV gene expression level in cells or body fluid of an individual; (b) comparing the Neutrokinine-alpha and/or Neutrokinine-alphaSV gene expression level with a standard Neutrokinine-alpha and/or Neutrokinine-alphaSV gene expression level, whereby an increase or decrease in the assayed Neutrokinine-alpha and/or Neutrokinine-alphaSV gene expression level compared to the standard expression level is indicative of a disorder.

An additional embodiment of the invention is related to a method for treating an individual in need of an increased or constitutive level of Neutrokinine-alpha and/or Neutrokinine-alphaSV activity in the body comprising administering to such an individual a composition comprising a therapeutically effective amount of an isolated Neutrokinine-alpha and/or Neutrokinine-alphaSV polypeptide of the invention or an agonist thereof.

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A still further embodiment of the invention is related to a method for treating an individual in need of a decreased level of Neutrokinine-alpha and/or Neutrokinine-alphaSV activity in the body comprising, administering to such an individual a composition comprising a therapeutically effective amount of an Neutrokinine-alpha and/or Neutrokinine-alphaSV antagonist. Preferred antagonists for use in the present invention are Neutrokinine-alpha-specific and/or Neutrokinine-alphaSV-specific antibodies.

BRIEF DESCRIPTION OF THE FIGURES

The following drawings are illustrative of embodiments of the invention and are not meant to limit the scope of the invention as encompassed by the claims.

FIGS. 1A and 1B show the nucleotide (SEQ ID NO:1) and deduced amino acid (SEQ ID NO:2) sequences of Neutrokinine-alpha. Amino acids 1 to 46 represent the predicted intracellular domain, amino acids 47 to 72 the predicted transmembrane domain (the double-underlined sequence), and amino acids 73 to 285, the predicted extracellular domain (the remaining sequence). Potential asparagine-linked glycosylation sites are marked in FIGS. 1A and 1B with a bolded asparagine symbol (N) in the Neutrokinine-alpha amino acid sequence and a bolded pound sign (#) above the first nucleotide encoding that asparagine residue in the Neutrokinine-alpha nucleotide sequence. Potential N-linked glycosylation sequences are found at the following locations in the Neutrokinine-alpha amino acid sequence: N-124 through Q-127 (N-124, S-125, S-126, Q-127) and N-242 through C-245 (N-242, N-243, S-244, C-245).

Regions of high identity between Neutrokinine-alpha, Neutrokinine-alphaSV, TNF-alpha, TNF-beta, LT-beta, and the closely related Fas Ligand (an alignment of these sequences is presented in FIGS. 2A, 2B, 2C, and 2D) are underlined in FIGS. 1A and 1B. These regions are not limiting and are labeled as Conserved Domain (CD)-I, CD-II, CD-III, CD-IV, CD-V, CD-VI, CD-VII, CD-VIII, CD-IX, CD-X, and CD-XI in FIGS. 1A and 1B.

FIGS. 2A, 2B, 2C, and 2D show the regions of identity between the amino acid sequences of Neutrokinine-alpha (SEQ ID NO:2) and Neutrokinine-alphaSV (SEQ ID NO:19), and TNF-alpha ("TNFalpha" in FIGS. 2A, 2B, 2C, and 2D; GenBank No. Z15026; SEQ ID NO:3), TNF-beta ("TNFbeta" in FIGS. 2A, 2B, 2C, and 2D; GenBank No. Z15026; SEQ ID NO:4), Lymphotoxin-beta ("LTbeta" in FIGS. 2A, 2B, 2C, and 2D; GenBank No. L11016; SEQ ID NO:5), and FAS ligand ("FASL" in FIGS. 2A, 2B, 2C, and 2D; GenBank No. U11821; SEQ ID NO:6), determined by the "MegAlign" routine which is part of the computer program called "DNA*STAR." Residues that match the consensus are shaded.

FIG. 3 shows an analysis of the Neutrokinine-alpha amino acid sequence. Alpha, beta, turn and coil regions; hydrophilicity and hydrophobicity; amphipathic regions; flexible regions; antigenic index and surface probability are shown, as predicted for the amino acid sequence of SEQ ID NO:2 using the default parameters of the recited computer programs. In the "Antigenic Index—Jameson-Wolf" graph, the indicate location of the highly antigenic regions of Neutrokinine-alpha i.e., regions from which epitope-bearing peptides of the invention may be obtained. Antigenic polypeptides include from about Phe-115 to about Leu-147, from about Ile-150 to about Tyr-163, from about Ser-171 to about Phe-194, from about Glu-223 to about Tyr-246, and from about Ser-271 to about Phe-278, of the amino acid sequence of SEQ ID NO:2.

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The data presented in FIG. 3 are also represented in tabular form in Table I. The columns are labeled with the headings "Res", "Position", and Roman Numerals I-XIV. The column headings refer to the following features of the amino acid sequence presented in FIG. 3, and Table I: "Res": amino acid residue of SEQ ID NO:2 and FIGS. 1A and 1B; "Position": position of the corresponding residue within SEQ ID NO:2 and FIGS. 1A and 1B; I: Alpha, Regions-Garnier-Robson; II: Alpha, Regions-Chou-Fasman; III: Beta, Regions-Garnier-Robson; IV: Beta, Regions-Chou-Fasman; V: Turn, Regions-Garnier-Robson; VI: Turn, Regions-Chou-Fasman; VII: Coil, Regions-Garnier-Robson; VIII: Hydrophilicity Plot-Kyte-Doolittle; IX: Hydrophobicity Plot-Hopp-Woods; X: Alpha, Amphipathic Regions-Eisenberg; XI: Beta, Amphipathic Regions-Eisenberg; XII: Flexible Regions-Karplus-Schulz; XIII: Antigenic Index-Jameson-Wolf; and XIV: Surface Probability Plot-Emili.

FIGS. 4A, 4B, and 4C show the alignment of the Neutrokin-alpha nucleotide sequence (SEQ ID NO:1) determined from the human cDNA clone (HNEU15) deposited in ATCC No. 97768 with related human cDNA clones of the invention which have been designated HSOAD55 (SEQ ID NO:7), HSLAH84 (SEQ ID NO:8) and HLTBM08 (SEQ ID NO:9).

FIGS. 5A and 5B show the nucleotide (SEQ ID NO:18) and deduced amino acid (SEQ ID NO:19) sequences of the Neutrokin-alphaSV protein. Amino acids 1 to 46 represent the predicted intracellular domain, amino acids 47 to 72 the predicted transmembrane domain (the double-underlined sequence), and amino acids 73 to 266, the predicted extracellular domain (the remaining sequence). Potential asparagine-linked glycosylation sites are marked in FIGS. 5A and 5B with a bolded asparagine symbol (N) in the Neutrokin-alphaSV amino acid sequence and a bolded pound sign (#) above the first nucleotide encoding that asparagine residue in the Neutrokin-alphaSV nucleotide sequence. Potential N-linked glycosylation sequences are found at the following locations in the Neutrokin-alphaSV amino acid sequence: N-124 through Q-127 (N-124, S-125, S-126, Q-127) and N-223 through C-226 (N-223, N-224, S-225, C-226). Antigenic polypeptides include from about Pro-32 to about Leu-47, from about Glu-116 to about Ser-143, from about Phe-153 to about Tyr-173, from about Pro-218 to about Tyr-227, from about Ala-232 to about Gln-241, from about Ile-244 to about Ala-249, and from about Ser-252 to about Val-257 of the amino acid sequence of SEQ ID NO:19.

Regions of high identity between Neutrokin-alpha, Neutrokin-alphaSV, TNF-alpha, TNF-beta, LT-beta, and the closely related Fas ligand (an alignment of these sequences is presented in FIGS. 2A, 2B, 2C, and 2D) are underlined in FIGS. 1A and 1B. These conserved regions (of Neutrokin-alpha and Neutrokin-alphaSV) are labeled as Conserved Domain (CD)-I, (CD)-II, (CD)-III, (CD)-V, (CD)-VI, (CD)-VII, (CD)-VIII, (CD)-IX, (CD)-X, and (CD)-XI in FIGS. 5A and 5B. Neutrokin-alphaSV does not contain the sequence of CD-IV described in the legend of FIGS. 1A and 1B.

An additional alignment of the Neutrokin-alpha polypeptide sequence (SEQ ID NO:2) with APRIL, TNF-alpha, and LT-alpha is presented in FIGS. 7A-1 and 7A-2. In FIGS. 7A-1 and 7A-2, beta sheet regions are indicated as described below in the legend to FIGS. 7A-1 and 7A-2.

FIG. 6 shows an analysis of the Neutrokin-alphaSV amino acid sequence. Alpha, beta, turn and coil regions; hydrophilicity and hydrophobicity; amphipathic regions; flexible regions; antigenic index and surface probability are shown, as predicted for the amino acid sequence of SEQ ID NO:19 using the default parameters of the recited computer

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programs. The location of the highly antigenic regions of the Neutrokin-alpha protein, i.e., regions from which epitope-bearing peptides of the invention may be obtained is indicated in the "Antigenic Index Jameson-Wolf" graph. Antigenic polypeptides include, but are not limited to, a polypeptide comprising amino acid residues from about Pro-32 to about Leu-47, from about Glu-116 to about Ser-143, from about Phe-153 to about Tyr-173, from about Pro-218 to about Tyr-227, from about Ser-252 to about Thr-258, from about Ala-232 to about Gln-241, from about Ile-244 to about Ala-249, and from about Ser-252 to about Val-257, of the amino acid sequence of SEQ ID NO:19.

The data shown in FIG. 6 can be easily represented in tabular format similar to the data shown in Table I. Such a tabular representation of the exact data disclosed in FIG. 6 can be generated using the MegAlign component of the DNA*STAR computer sequence analysis package set on default parameters. This is the identical program that was used to generate FIGS. 3 and 6 of the present application.

FIGS. 7A-1 and 7A-2. The amino acid sequence of Neutrokin-alpha and alignment of its predicted ligand-binding domain with those of APRIL, TNF-alpha, and LT-alpha (specifically, amino acid residues 115-250 of the human APRIL polypeptide (SEQ ID NO:20; ATCC Accession No. AF046888), amino acid residues 88-233 of TNF-alpha (SEQ ID NO:3; GenBank Accession No. Z15026), and LT-alpha (also designated TNF-beta) amino acid residues 62-205 of SEQ ID NO:4; GenBank Accession No. Z15026)). The predicted membrane-spanning region of Neutrokin-alpha is indicated and the site of cleavage of Neutrokin-alpha is depicted with an arrow. Sequences overlaid with lines (A thru H) represent predicted beta-pleated sheet regions.

FIG. 7B. Expression of Neutrokin-alpha mRNA. Northern hybridization analysis was performed using the Neutrokin-alpha orf as a probe on blots of poly (A)+ RNA (Clontech) from a spectrum of human tissue types and a selection of cancer cell lines. A 2.6 kb Neutrokin-alpha mRNA was detected at high levels in placenta, heart, lung, fetal liver, thymus, and pancreas. The 2.6 kb Neutrokin-alpha mRNA was also detected in HL-60 and K562 cell lines.

FIGS. 8A, 8B, and 8C. Neutrokin-alpha expression increases following activation of human monocytes by IFN-gamma. FIGS. 8A and 8B. Flow cytometric analysis of Neutrokin-alpha protein expression on in vitro cultured monocytes. Purified monocytes were cultured for 3 days in presence or absence of IFN-gamma (100 U/ml). Cells were then stained with a Neutrokin-alpha-specific mAb (2E5) (solid lines) or an isotype-matched control (IgG1) (dashed lines). Comparable results were obtained with monocytes purified from three different donors in three independent experiments. FIG. 8C. Neutrokin-alpha-specific TaqMan primers were prepared and used to assess the relative Neutrokin-alpha mRNA expression levels in unstimulated and IFN-gamma (100 U/mL) treated monocytes. Nucleotide sequences of the TaqMan primers are as follows: (a) Probe: 5'-CCA CCA GCT CCA GGA GAA GGC AAC TC-3' (SEQ ID NO:24); (b) 5' amplification primer: 5'-ACC GCG GGA CTG AAA ATC T-3' (SEQ ID NO:25); and (c) 3' amplification primer: 5'-CAC GCT TAT TTC TGC TGT TCT GA-3' (SEQ ID NO:26).

FIGS. 9A and 9B. Neutrokin-alpha is a potent B lymphocyte stimulator. FIG. 9A. The biological activity of Neutrokin-alpha was assessed in a standard B-lymphocyte co-stimulation assay utilizing *Staphylococcus aureus* cowan 1 SAC as the priming agent. SAC alone yielded background counts of 1427+/-316. Values are reported as mean+/-standard deviation of triplicate wells. Similar results were

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obtained using recombinant Neutrokin- α purified from stable CHO transfectants and transiently transfected HEK 293T cells. FIG. 9B. Proliferation of tonsillar B cells with Neutrokin- α and co-stimulation with anti-IgM. The bioassay was performed as described for SAC with the exception that individual wells were pre-coated with goat anti-human IgM antibody at 10 micrograms/ml. in PBS.

FIGS. 10A, 10B, 10C, 10D, 10E, 10F and 10G. Neutrokin- α receptor expression among normal human peripheral blood mononuclear cells and tumor cell lines. FIGS. 10A, 10B, 10C, 10D and 10E. Human peripheral blood nucleated cells were obtained from normal volunteers and isolated by density gradient centrifugation. Cells were stained with biotinylated Neutrokin- α followed by PE-conjugated streptavidin or FITC or PerCP coupled mAbs specific for CD3, CD20, CD14, CD56, and CD66b. Cells were analyzed on a Becton Dickinson FACScan using the CellQuest software. Data represent one of four independent experiments. FIGS. 10F and 10G. Neutrokin- α binding to histiocytic cell line U-937 and the myeloma line IM-9.

FIGS. 11A, 11B, 11C, 11D, 11E, and 11F. In vivo effects of Neutrokin- α administration in BALB/cAnNCr mice. FIG. 11A. Formalin-fixed spleens were paraffin embedded and 5 micrometer sections stained with hematoxylin and eosin (upper panels). The lower panels are sections taken from the same animals stained with anti-CD45R(B220) mAb and developed with horseradish-peroxidase coupled rabbit anti-rat Ig (mouse adsorbed) and the substrate diaminobenzidine tetrahydrochloride (DAB). Slides were counter-stained with Mayer's hematoxylin. CD45R(B220) expressing cells appear brown. FIGS. 11B and 11C. Flow cytometric analyses of normal (left panel) and Neutrokin- α -treated (right panel) stained with PE-CD45R(B220) and FITC-ThB (Ly6D). FIGS. 11D, 11E, and 11F. Serum IgM, IgG, and IgA levels in normal and Neutrokin- α treated mice.

DETAILED DESCRIPTION

The present invention provides isolated nucleic acid molecules comprising a polynucleotide encoding a Neutrokin- α polypeptides having the amino acid sequences shown in FIGS. 1A and 1B (SEQ ID NO:2), which was determined by sequencing a cDNA clone. The nucleotide sequence shown in FIGS. 1A and 1B (SEQ ID NO:1) was obtained by sequencing the HNEDU15 clone, which was deposited on Oct. 22, 1996 at the American Type Culture Collection, 10801 University Boulevard, Manassas, Va. 20110-2209, and assigned ATCC Accession No. 97768. The deposited clone is contained in the pBluescript SK(-) plasmid (Stratagene, La Jolla, Calif.).

The present invention also provides isolated nucleic acid molecules comprising a polynucleotide encoding Neutrokin- α SV polypeptides having the amino acid sequences shown in FIGS. 5A and 5B (SEQ ID NO:19), which was determined by sequencing a cDNA clone. The nucleotide sequence shown in FIGS. 5A and 5B (SEQ ID NO:18) was obtained by sequencing the HDPMS2 clone, which was deposited on Dec. 10, 1998 at the American Type Culture Collection, and assigned ATCC Accession No. 203518. The deposited clone is contained in the pBluescript SK(-) plasmid (Stratagene, La Jolla, Calif.).

The Neutrokin- α and Neutrokin- α polypeptides of the present invention share sequence homology with the translation products of the human mRNAs for TNF- α , TNF- β , LT β , Fas ligand, APRIL, and LT α . (See, FIGS. 2A, 2B, 2C, 2D, 7A-1 and 7A-2). As noted above, TNF- α is thought to be an important cytokine that plays a

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role in cytotoxicity, necrosis, apoptosis, costimulation, proliferation, lymph node formation, immunoglobulin class switch, differentiation, antiviral activity, and regulation of adhesion molecules and other cytokines and growth factors.

Nucleic Acid Molecules

Unless otherwise indicated, all nucleotide sequences determined by sequencing a DNA molecule herein were determined using an automated DNA sequencer (such as the Model 373 from Applied Biosystems, Inc., Foster City, Calif.), and all amino acid sequences of polypeptides encoded by DNA molecules determined herein were predicted by translation of a DNA sequence determined as above. Therefore, as is known in the art for any DNA sequence determined by this automated approach, any nucleotide sequence determined herein may contain some errors. Nucleotide sequences determined by automation are typically at least about 90% identical, more typically at least about 95% to at least about 99.9% identical to the actual nucleotide sequence of the sequenced DNA molecule. The actual sequence can be more precisely determined by other approaches including manual DNA sequencing methods well known in the art. As is also known in the art, a single insertion or deletion in a determined nucleotide sequence compared to the actual sequence will cause a frame shift in translation of the nucleotide sequence such that the predicted amino acid sequence encoded by a determined nucleotide sequence will be completely different from the amino acid sequence actually encoded by the sequenced DNA molecule, beginning at the point of such an insertion or deletion.

By "nucleotide sequence" of a nucleic acid molecule or polynucleotide is intended, for a DNA molecule or polynucleotide, a sequence of deoxyribonucleotides, and for an RNA molecule or polynucleotide, the corresponding sequence of ribonucleotides (A, G, C and U), where each thymidine deoxyribonucleotide (T) in the specified deoxyribonucleotide sequence is replaced by the ribonucleotide uridine (U).

Using the information provided herein, such as the nucleotide sequence in FIGS. 1A and 1B, a nucleic acid molecule of the present invention encoding a Neutrokin- α polypeptide may be obtained using standard cloning and screening procedures, such as those for cloning cDNAs using mRNA as starting material. Illustrative of the invention, the nucleic acid molecule described in FIGS. 1A and 1B (SEQ ID NO:1) was discovered in a cDNA library derived from neutrophils. Expressed sequence tags corresponding to a portion of the Neutrokin- α cDNA were also found in kidney, lung, peripheral leukocyte, bone marrow, T cell lymphoma, B cell lymphoma, activated T cells, stomach cancer, smooth muscle, macrophages, and cord blood tissue. In addition, using the nucleotide information provided in FIGS. 5A and 5B, a nucleic acid molecule of the present invention encoding a Neutrokin- α SV polypeptide may be obtained using standard cloning and screening procedures, such as those for cloning cDNAs using mRNA as starting material. Illustrative of the invention, the nucleic acid molecule described in FIGS. 5A and 5B (SEQ ID NO:18) was discovered in a cDNA library derived from primary dendritic cells.

The Neutrokin- α plasmid HNEDU15 deposited as ATCC Accession No. 97768 contains an open reading frame encoding a protein of about 285 amino acid residues, a predicted intracellular domain of about 46 amino acids (amino acid residues from about 1 to about 46 in FIGS. 1A and 1B (SEQ ID NO:2)), a predicted transmembrane domain of about 26 amino acids (underlined amino acid residues from about 47 to about 72 in FIGS. 1A and 1B (SEQ ID NO:2)), a predicted extracellular domain of about 213 amino acids

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(amino acid residues from about 73 to about 285 in FIGS. 1A and 1B (SEQ ID NO:2)); and a deduced molecular weight of about 31 kDa. The Neutrokin- α polypeptide shown in FIGS. 1A and 1B (SEQ ID NO:2) is about 20% similar and about 10% identical to human TNF- α , which can be accessed on GenBank as Accession No. 339764.

The Neutrokin- α SV plasmid 11DPMC52, deposited as ATCC Accession No. 203518, contains a predicted open reading frame encoding a protein of about 266 amino acid residues, a predicted intracellular domain of about 46 amino acids (amino acid residues from about 1 to about 46 in FIGS. 5A and 5B (SEQ ID NO:19)), a predicted transmembrane domain of about 26 amino acids (underlined amino acid residues from about 47 to about 72 in FIGS. 5A and 5B (SEQ ID NO:19)), a predicted extracellular domain of about 194 amino acids (amino acid residues from about 73 to about 266 in FIGS. 5A and 5B (SEQ ID NO:19)); and a deduced molecular weight of about 29 kDa. The Neutrokin- α SV polypeptide shown in FIGS. 5A and 5B (SEQ ID NO:19) is about 33.9% similar and about 22.0% identical to human TNF- α which can be accessed on GenBank as Accession No. 339764.

As one of ordinary skill would appreciate, due to the possibilities of sequencing errors discussed above, the actual complete Neutrokin- α and/or Neutrokin- α SV polypeptides encoded by the deposited cDNAs, which comprise about 285 and 266 amino acids, respectively, may be somewhat shorter. In particular, the determined Neutrokin- α and Neutrokin- α SV coding sequences contain a common second methionine codon which may serve as an alternative start codon for translation of the open reading frame, at nucleotide positions 210-212 in FIGS. 1A and 1B (SEQ ID NO:1) and at nucleotide positions 64-66 in FIGS. 5A and 5B (SEQ ID NO:18). More generally, the actual open reading frame may be anywhere in the range of ± 20 amino acids, more likely in the range of ± 10 amino acids, of that predicted from either the first or second methionine codon from the N-terminus shown in FIGS. 1A and 1B (SEQ ID NO:1) and in FIGS. 5A and 5B (SEQ ID NO:18). It will further be appreciated that, the polypeptide domains described herein have been predicted by computer analysis, and accordingly, that depending on the analytical criteria used for identifying various functional domains, the exact "address" of the extracellular, intracellular and transmembrane domains of the Neutrokin- α and Neutrokin- α SV polypeptides may differ slightly. For example, the exact location of the Neutrokin- α and Neutrokin- α SV extracellular domains in FIGS. 1A and 1B (SEQ ID NO:2) and FIGS. 5A and 5B (SEQ ID NO:19) may vary slightly (e.g., the address may "shift" by about 1 to about 20 residues, more likely about 1 to about 5 residues) depending on the criteria used to define the domain. In this case, the ends of the transmembrane domains and the beginning of the extracellular domains were predicted on the basis of the identification of the hydrophobic amino acid sequence in the above indicated positions, as shown in FIGS. 3 and 6 and in Table I. In any event, as discussed further below, the invention further provides polypeptides having various residues deleted from the N-terminus and/or C-terminus of the complete polypeptides, including polypeptides lacking one or more amino acids from the N-termini of the extracellular domains described herein, which constitute soluble forms of the extracellular domains of the Neutrokin- α and Neutrokin- α SV polypeptides.

As indicated, nucleic acid molecules and polynucleotides of the present invention may be in the form of RNA, such as mRNA, or in the form of DNA, including, for instance, cDNA

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and genomic DNA obtained by cloning or produced synthetically. The DNA may be double-stranded or single-stranded. Single-stranded DNA or RNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

By "isolated" nucleic acid molecule(s) is intended a nucleic acid molecule (DNA or RNA), which has been removed from its native environment. For example, recombinant DNA molecules contained in a vector are considered isolated for the purposes of the present invention. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells or purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include in vivo or in vitro RNA transcripts of the DNA molecules of the present invention. However, a nucleic acid contained in a clone that is a member of a library (e.g., a genomic or cDNA library) that has not been isolated from other members of the library (e.g., in the form of a homogeneous solution containing the clone and other members of the library) or a chromosome isolated or removed from a cell or a cell lysate (e.g., a "chromosome spread", as in a karyotype), is not "isolated" for the purposes of this invention. As discussed further herein, isolated nucleic acid molecules according to the present invention may be produced naturally, recombinantly, or synthetically.

Isolated nucleic acid molecules of the present invention include DNA molecules comprising, or alternatively consisting of, an open reading frame (ORF) with an initiation codon at positions 147-149 of the nucleotide sequence shown in FIGS. 1A and 1B (SEQ ID NO:1). In addition, isolated nucleic acid molecules of the invention include DNA molecules which comprise, or alternatively consist of, a sequence substantially different from those described above, but which due to the degeneracy of the genetic code, still encode the Neutrokin- α protein. Of course, the genetic code is well known in the art. Thus, it would be routine for one skilled in the art to generate the degenerate variants described above. In another embodiment, the invention provides isolated nucleic acid molecules comprising, or alternatively consisting of, a sequence encoding the Neutrokin- α polypeptide having an amino acid sequence encoded by the cDNA contained in the plasmid having ATCC accession number 97768. Preferably, this nucleic acid molecule comprises, or alternatively consists of, a sequence encoding the extracellular domain the mature or soluble polypeptide sequence of the polypeptide encoded by the cDNA contained in the plasmid having ATCC accession number 97768.

Isolated nucleic acid molecules of the present invention also include DNA molecules comprising an open reading frame (ORF) with an initiation codon at positions 1-3 of the nucleotide sequence shown in FIGS. 5A and 5B (SEQ ID NO:18). In addition, isolated nucleic acid molecules of the invention include DNA molecules which comprise, or alternatively consist of, a sequence substantially different from those described above, but which due to the degeneracy of the genetic code, still encodes the Neutrokin- α SV polypeptide. Of course, the genetic code is well known in the art. Thus, it would be routine for one skilled in the art to generate the degenerate variants described above. In another embodiment, the invention provides isolated nucleic acid molecules comprising, or alternatively consisting of, a sequence encoding the Neutrokin- α SV polypeptide having an amino acid encoded by the cDNA contained in the plasmid having ATCC accession number 203518. Preferably, this nucleic acid molecule comprises, or alternatively consists of, a sequence encoding the extracellular domain or the mature

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soluble polypeptide sequence of the polypeptide encoded by the cDNA contained in the plasmid having ATCC accession number 203518.

The invention further provides an isolated nucleic acid molecule comprising, or alternatively consisting of, the nucleotide sequence shown in FIGS. 1A and 1B (SEQ ID NO:1) or the nucleotide sequence of the Neutrokin- α cDNA contained in the plasmid having ATCC accession number 97768, or a nucleic acid molecule having a sequence complementary to one of the above sequences. In addition, the invention provides an isolated nucleic acid molecule comprising, or alternatively, consisting of, the nucleotide sequence shown in FIGS. 5A and 5B (SEQ ID NO:18) or the nucleotide sequence of the Neutrokin- α SV cDNA contained in the plasmid having ATCC accession number 203518, or a nucleic acid molecule having a sequence complementary to one of the above sequences. Such isolated molecules, particularly DNA molecules, have uses which include, but are not limited to, as probes for gene mapping by in situ hybridization with chromosomes, and for detecting expression of the Neutrokin- α and Neutrokin- α SV in human tissue, for instance, by Northern or Western blot analysis.

In one embodiment, the polynucleotides of the invention comprise, or alternatively consist of, the sequence shown in SEQ ID NO:22. The sequence provided as SEQ ID NO:22 was constructed from several overlapping mouse EST sequences obtained from GenBank (A1182472, AA422749, AA254047, and A1122485). The EST sequences were aligned to generate the Neutrokin- α -like polynucleotide sequence provided as SEQ ID NO:22. The amino acid sequence resulting from the translation of SEQ ID NO:22 is provided as SEQ ID NO:23. Fragments, variants, and derivatives of the sequences provided as SEQ ID NO:22 and SEQ ID NO:23 are also encompassed by the invention.

In another embodiment, the polynucleotides of the invention comprise, or alternatively consist of, the sequence shown in SEQ ID NO:27, and/or a sequence encoding the amino acid sequence disclosed in SEQ ID NO:28, fragments, variants, and derivatives thereof. These polynucleotides are also encompassed by the invention. For example, certain embodiments of the invention are directed to polynucleotides comprising, or alternatively consisting of, a sequence encoding a polypeptide sequence that is at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98%, or 99% identical to amino acids 68-219 of SEQ ID NO:28. The amino acid sequence resulting from the translation of SEQ ID NO:27 is provided as SEQ ID NO:28. Polypeptides comprising, or alternatively consisting of, the amino acid sequence of SEQ ID NO:28, and fragments, variants, and derivatives of the sequence provided as SEQ ID NO:28 are also encompassed by the invention. For example, certain embodiments of the invention are directed to polypeptides comprising, or alternatively consisting of, a polypeptide sequence that is at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98%, or 99% identical to amino acids 68-219 of SEQ ID NO:28. A nucleic acid molecule having the sequence provided as SEQ ID NO:27 was obtained by RT-PCR from cynomolgous monkey (i.e., *Macaca irus*) PBMC using two degenerate primers. Briefly, total RNA was prepared from cynomolgous monkey PBMC by using Trizol (available from Life Technologies, Inc., Rockville, Md.) according to the manufacturer's protocol. Then a single stranded cDNA was synthesized from the cynomolgous monkey PBMC preparation using standard methods with an oligo-dT primer. Neutrokin- α -specific primers were designed based on the conserved region between the mouse and human Neutrokin- α molecules (SEQ ID NOs:22 and 1, respectively).

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A cynomolgous monkey Neutrokin- α nucleic acid molecule was then generated by PCR using the cDNA template in combination with the following two degenerate oligonucleotide primers. 5' primer: 5'-TAC CAG ITG GCIGCC ITG CAA G-3' (SEQ ID NO:35) and 3' primer: 5'-GTIACA GCA GTT TIA IIG CAC C-3' (SEQ ID NO:36). In the sequence of the degenerate primers (SEQ ID NOs:35 and 36), "I" represents deoxyinosine or dideoxyinosine.

In another embodiment, the polynucleotides of the invention comprise, or alternatively consist of, the sequence shown in SEQ ID NO:29, and/or a sequence encoding the amino acid sequence disclosed in SEQ ID NO:30, fragments, variants, and derivatives thereof. These polynucleotides are also encompassed by the invention. For example, certain embodiments of the invention are directed to polynucleotides comprising, or alternatively consisting of, a sequence encoding a polypeptide sequence that is at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98%, or 99% identical to amino acids 68-219 of SEQ ID NO:30. The amino acid sequence resulting from the translation of SEQ ID NO:29 is provided as SEQ ID NO:30. Polypeptides comprising, or alternatively consisting of, the amino acid sequence of SEQ ID NO:30, and fragments, variants, and derivatives of the sequences provided as SEQ ID NO:29 and SEQ ID NO:30 are also encompassed by the invention. For example, certain embodiments of the invention are directed to polypeptides comprising, or alternatively consisting of, a polypeptide sequence that is at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98%, or 99% identical to amino acids 68-219 of SEQ ID NO:30. A nucleic acid molecule having the sequence provided as SEQ ID NO:29 was obtained by RT-PCR from rhesus monkey PBMC using two degenerate primers. Briefly, total RNA was prepared from rhesus monkey PBMC by using Trizol (available from Life Technologies, Inc., Rockville, Md.) according to the manufacturer's protocol. Then a single stranded cDNA was synthesized from the rhesus monkey PBMC preparation using standard methods with an oligo-dT primer. Neutrokin- α -specific primers were designed based on the conserved region between the mouse and human Neutrokin- α molecules (SEQ ID NOs:22 and 1, respectively). A rhesus monkey Neutrokin- α nucleic acid molecule was then generated by PCR using the cDNA template in combination with the following two degenerate oligonucleotide primers. 5' primer: 5'-TAC CAG ITG GCIGCC ITG CAA G-3' (SEQ ID NO:35) and 3' primer: 5'-GTIACA GCA GTT TIA IIG CAC C-3' (SEQ ID NO:36). In the sequence of the degenerate primers (SEQ ID NOs:35 and 36), "I" represents deoxyinosine or dideoxyinosine.

The invention also provides nucleic acid molecules having nucleotide sequences related to extensive portions of SEQ ID NO:1 and SEQ ID NO:18 which have been determined from the following related cDNA clones: HSOAD55 (SEQ ID NO:7), HSLAH84 (SEQ ID NO:8), and HLTBM08 (SEQ ID NO:9).

The present invention is further directed to nucleic acid molecules encoding portions of the nucleotide sequences described herein, as well as to fragments of the isolated nucleic acid molecules described herein. In one embodiment, the invention provides a polynucleotide having a nucleotide sequence representing the portion of SEQ ID NO:1 which consists of the nucleotides at positions 1-1001 of SEQ ID NO:1. In another embodiment, the invention provides a polynucleotide having a nucleotide sequence representing the portion of SEQ ID NO:18 which consists of positions 1-798 of SEQ ID NO:18.

The present invention is further directed to fragments of the nucleic acid molecules (i.e. polynucleotides) described

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herein. By a fragment of a nucleic acid molecule having, for example, the nucleotide sequence of the cDNA contained in the plasmid having ATCC accession number 97768, a nucleotide sequence encoding the polypeptide sequence encoded by the cDNA contained in the plasmid having ATCC accession number 97768, the nucleotide sequence of SEQ ID NO:1, a nucleotide sequence encoding the polypeptide sequence of SEQ ID NO:2, the nucleotide sequence of the cDNA contained in the plasmid having ATCC accession number 203518, a nucleotide sequence encoding the polypeptide sequence encoded by the cDNA contained in the plasmid having ATCC accession number 203518, the nucleotide sequence of SEQ ID NO:18, a nucleotide sequence encoding the polypeptide sequence of SEQ ID NO:20, or the complementary strand thereto, is intended fragments at least 15 nt, and more preferably at least 20 nt or at least 25 nt, still more preferably at least 30 nt, and even more preferably, at least 40, 50, 100, 150, 200, 250, 300, 325, 350, 375, 400, 450, or 500 nt in length. These fragments have numerous uses which include, but are not limited to, diagnostic probes and primers as discussed herein. Of course, larger fragments, such as those of 501-1500 nt in length are also useful according to the present invention as are fragments corresponding to most, if not all, of the nucleotide sequences of the cDNA contained in the plasmid having ATCC accession number 97768, the nucleotide sequence of SEQ ID NO:1, the nucleotide sequences of the cDNA contained in the plasmid having ATCC accession number 203518, and the nucleotide sequence of SEQ ID NO:18. Preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding polypeptides comprising, or alternatively, consisting of, epitope-bearing portions of the Neutrokine-alpha and/or Neutrokine-alphaSV polypeptide as identified in FIGS. 1A and 1B (SEQ ID NO:2) and in FIGS. 5A and 5B (SEQ ID NO:19), respectively, and described in more detail below. Polypeptides encoded by these polynucleotide fragments are also encompassed by the invention.

Also by a fragment of a nucleic acid molecule having, for example, the nucleotide sequence of SEQ ID NO:21, the nucleotide sequence of SEQ ID NO:22, the nucleotide sequence of SEQ ID NO:27, the nucleotide sequence of SEQ ID NO:29, a nucleotide sequence encoding the polypeptide sequence of SEQ ID NO:23, a nucleotide sequence encoding the polypeptide sequence of SEQ ID NO:28, a nucleotide sequence encoding the polypeptide sequence of SEQ ID NO:30, or the complementary strands thereof, is intended fragments at least 15 nt, and more preferably at least 20 nt or at least 25 nt, still more preferably at least 30 nt, and even more preferably, at least 40, 50, 100, 150, 200, 250, 300, 325, 350, 375, 400, 450, or 500 nt in length. These fragments have numerous uses which include, but are not limited to, diagnostic probes and primers as discussed herein. Of course, larger fragments, such as those of 501-1500 nt in length are also useful according to the present invention as are fragments corresponding to most, if not all, of the nucleotide sequence of SEQ ID NO:21, the nucleotide sequence of SEQ ID NO:22, the nucleotide sequence of SEQ ID NO:27, the nucleotide sequence of SEQ ID NO:29, a nucleotide sequence encoding the polypeptide sequence of SEQ ID NO:23, a nucleotide sequence encoding the polypeptide sequence of SEQ ID NO:28, a nucleotide sequence encoding the polypeptide sequence of SEQ ID NO:30, or the complementary strands thereof. Polypeptides encoded by these polynucleotide fragments are also encompassed by the invention.

Representative examples of Neutrokine-alpha polynucleotide fragments of the invention include, for example, fragments that comprise, or alternatively, consist of, a sequence

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from about nucleotide 1 to 50, 51 to 100, 101 to 146, 147 to 200, 201 to 250, 251 to 300, 301 to 350, 351 to 400, 401 to 450, 451 to 500, 501 to 550, 551 to 600, 600 to 650, 651 to 700, 701 to 750, 751 to 800, 800 to 850, 851 to 900, 901 to 950, 951 to 1000, 1001 to 1050, and/or 1051 to 1082, of SEQ ID NO:1, or the complementary strand thereto, or the cDNA contained in the plasmid having ATCC accession number 97768. In this context "about" includes the particularly recited ranges, and ranges that are larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini.

Representative examples of Neutrokine-alphaSV polynucleotide fragments of the invention include, for example, fragments that comprise, or alternatively, consist of, a sequence from about nucleotide 1 to 50, 51 to 100, 101 to 150, 151 to 200, 201 to 250, 251 to 300, 301 to 350, 351 to 400, 401 to 450, 451 to 500, 501 to 550, 551 to 600, 600 to 650, 651 to 700, 701 to 750, 751 to 800, 800 to 850, and/or 851 to 900 of SEQ ID NO:18, or the complementary strand thereto, or the cDNA contained in the plasmid having ATCC accession number 203518. In this context "about" includes the particularly recited ranges, and ranges that are larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini.

In certain preferred embodiments, polynucleotide of the invention comprise, or alternatively, consist of, nucleotide residues 571-627, 580-627, 590-627, 600-627, 610-627, 571-620, 580-620, 590-620, 600-620, 571-610, 580-610, 590-610, 571-600, 580-600, and/or 571-590 of SEQ ID NO:1.

In certain other preferred embodiments, polynucleotides of the invention comprise, or alternatively, consist of nucleotide residues 1-879, 25-879, 50-879, 75-879, 100-879, 125-879, 150-879, 175-879, 200-879, 225-879, 250-879, 275-879, 300-879, 325-879, 350-879, 375-879, 400-879, 425-879, 450-879, 475-879, 500-879, 525-879, 550-879, 575-879, 600-879, 625-879, 650-879, 675-879, 700-879, 725-879, 750-879, 775-879, 800-879, 825-879, 850-879, 1-850, 25-850, 50-850, 75-850, 100-850, 125-850, 150-850, 175-850, 200-850, 225-850, 250-850, 275-850, 300-850, 325-850, 350-850, 375-850, 400-850, 425-850, 450-850, 475-850, 500-850, 525-850, 550-850, 575-850, 600-850, 625-850, 650-850, 675-850, 700-850, 725-850, 750-850, 775-850, 800-850, 825-850, 1-825, 25-825, 50-825, 75-825, 100-825, 125-825, 150-825, 175-825, 200-825, 225-825, 250-825, 275-825, 300-825, 325-825, 350-825, 375-825, 400-825, 425-825, 450-825, 475-825, 500-825, 525-825, 550-825, 575-825, 600-825, 625-825, 650-825, 675-825, 700-825, 725-825, 750-825, 775-825, 800-825, 1-800, 25-800, 50-800, 75-800, 100-800, 125-800, 150-800, 175-800, 200-800, 225-800, 250-800, 275-800, 300-800, 325-800, 350-800, 375-800, 400-800, 425-800, 450-800, 475-800, 500-800, 525-800, 550-800, 575-800, 600-800, 625-800, 650-800, 675-800, 700-800, 725-800, 750-800, 775-800, 1-775, 25-775, 50-775, 75-775, 100-775, 125-775, 150-775, 175-775, 200-775, 225-775, 250-775, 275-775, 300-775, 325-775, 350-775, 375-775, 400-775, 425-775, 450-775, 475-775, 500-775, 525-775, 550-775, 575-775, 600-775, 625-775, 650-775, 675-775, 700-775, 725-775, 750-775, 1-750, 25-750, 50-750, 75-750, 100-750, 125-750, 150-750, 175-750, 200-750, 225-750, 250-750, 275-750, 300-750, 325-750, 350-750, 375-750, 400-750, 425-750, 450-750, 475-750, 500-750, 525-750, 550-750, 575-750, 600-750, 625-750, 650-750, 675-750, 700-750, 725-750, 1-725, 25-725, 50-725, 75-725, 100-725, 125-725, 150-725, 175-725, 200-725, 225-725, 250-725, 275-725, 300-725, 325-725, 350-725, 375-725, 400-725, 425-725, 450-725, 475-725, 500-725, 525-725, 550-725, 575-725, 600-725, 625-725, 650-

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725-675-725, 700-725, 1-700, 25-700, 50-700, 75-700, 100-700, 125-700, 150-700, 175-700, 200-700, 225-700, 250-700, 275-700, 300-700, 325-700, 350-700, 375-700, 400-700, 425-700, 450-700, 475-700, 500-700, 525-700, 550-700, 575-700, 600-700, 625-700, 650-700, 675-700, 1-675, 25-675, 50-675, 75-675, 100-675, 125-675, 150-675, 175-675, 200-675, 225-675, 250-675, 275-675, 300-675, 325-675, 350-675, 375-675, 400-675, 425-675, 450-675, 475-675, 500-675, 525-675, 550-675, 575-675, 600-675, 625-675, 650-675, 1-650, 25-650, 50-650, 75-650, 100-650, 125-650, 150-650, 175-650, 200-650, 225-650, 250-650, 275-650, 300-650, 325-650, 350-650, 375-650, 400-650, 425-650, 450-650, 475-650, 500-650, 525-650, 550-650, 575-650, 600-650, 625-650, 1-625, 25-625, 50-625, 75-625, 100-625, 125-625, 150-625, 175-625, 200-625, 225-625, 250-625, 275-625, 300-625, 325-625, 350-625, 375-625, 400-625, 425-625, 450-625, 475-625, 500-625, 525-625, 550-625, 575-625, 600-625, 1-600, 25-600, 50-600, 75-600, 100-600, 125-600, 150-600, 175-600, 200-600, 225-600, 250-600, 275-600, 300-600, 325-600, 350-600, 375-600, 400-600, 425-600, 450-600, 475-600, 500-600, 525-600, 550-600, 575-600, 1-575, 25-575, 50-575, 75-575, 100-575, 125-575, 150-575, 175-575, 200-575, 225-575, 250-575, 275-575, 300-575, 325-575, 350-575, 375-575, 400-575, 425-575, 450-575, 475-575, 500-575, 525-575, 550-575, 1-550, 25-550, 50-550, 75-550, 100-550, 125-550, 150-550, 175-550, 200-550, 225-550, 250-550, 275-550, 300-550, 325-550, 350-550, 375-550, 400-550, 425-550, 450-550, 475-550, 500-550, 525-550, 1-525, 25-525, 50-525, 75-525, 100-525, 125-525, 150-525, 175-525, 200-525, 225-525, 250-525, 275-525, 300-525, 325-525, 350-525, 375-525, 400-525, 425-525, 450-525, 475-525, 500-525, 1-500, 25-500, 50-500, 75-500, 100-500, 125-500, 150-500, 175-500, 200-500, 225-500, 250-500, 275-500, 300-500, 325-500, 350-500, 375-500, 400-500, 425-500, 450-500, 475-500, 1-475, 25-475, 50-475, 75-475, 100-475, 125-475, 150-475, 175-475, 200-475, 225-475, 250-475, 275-475, 300-475, 325-475, 350-475, 375-475, 400-475, 425-475, 450-475, 1-450, 25-450, 50-450, 75-450, 100-450, 125-450, 150-450, 175-450, 200-450, 225-450, 250-450, 275-450, 300-450, 325-450, 350-450, 375-450, 400-450, 425-450, 1-425, 25-425, 50-425, 75-425, 100-425, 125-425, 150-425, 175-425, 200-425, 225-425, 250-425, 275-425, 300-425, 325-425, 350-425, 375-425, 400-425, 1-400, 25-400, 50-400, 75-400, 100-400, 125-400, 150-400, 175-400, 200-400, 225-400, 250-400, 275-400, 300-400, 325-400, 350-400, 375-400, 1-375, 25-375, 50-375, 75-375, 100-375, 125-375, 150-375, 175-375, 200-375, 225-375, 250-375, 275-375, 300-375, 325-375, 350-375, 1-350, 25-350, 50-350, 75-350, 100-350, 125-350, 150-350, 175-350, 200-350, 225-350, 250-350, 275-350, 300-350, 325-350, 1-325, 25-325, 50-325, 75-325, 100-325, 125-325, 150-325, 175-325, 200-325, 225-325, 250-325, 275-325, 300-325, 1-300, 25-300, 50-300, 75-300, 100-300, 125-300, 150-300, 175-300, 200-300, 225-300, 250-300, 275-300, 1-275, 25-275, 50-275, 75-275, 100-275, 125-275, 150-275, 175-275, 200-275, 225-275, 250-275, 1-250, 25-250, 50-250, 75-250, 100-250, 125-250, 150-250, 175-250, 200-250, 225-250, 1-225, 25-225, 50-225, 75-225, 100-225, 125-225, 150-225, 175-225, 200-225, 1-200, 25-200, 50-200, 75-200, 100-200, 125-200, 150-200, 175-200, 1-175, 25-175, 50-175, 75-175, 100-175, 125-175, 150-175, 1-150, 25-150, 50-150, 75-150, 100-150, 125-150, 1-125, 25-125, 50-125, 75-125, 100-125, 1-100, 25-100, 50-100, 75-100, 1-75, 25-75, 50-75, 1-50, 25-50, and/or 1-25 of SEQ ID NO:18.

In certain additional preferred embodiments, polynucleotides of the invention comprise, or alternatively, consist of

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nucleotide residues 400-627, 425-627, 450-627, 475-627, 500-627, 525-627, 550-627, 575-627, 600-627, 400-600, 425-600, 450-600, 475-600, 500-600, 525-600, 550-600, 575-600, 400-575, 425-575, 450-575, 475-575, 500-575, 525-575, 550-575, 400-550, 425-550, 450-550, 475-550, 500-550, 525-550, 400-500, 425-500, 450-500, 475-500, 400-475, 425-475, 450-475, 400-450, 425-450, 571-800, 600-800, 625-800, 650-800, 675-800, 700-800, 725-800, 750-800, 775-800, 571-775, 600-775, 625-775, 650-775, 675-775, 700-775, 725-775, 750-775, 571-750, 600-750, 625-750, 650-750, 675-750, 700-750, 725-750, 571-725, 600-725, 625-725, 650-725, 675-725, 700-725, 571-700, 600-700, 625-700, 650-700, 675-700, 571-675, 600-675, 625-675, 650-675, 571-650, 600-650, 625-650, 571-625, 600-625, and/or 571-600 of SEQ ID NO:1.

In additional preferred embodiments, polynucleotides of the invention comprise, or alternatively, consist of nucleotide residues 147-500, 147-450, 147-400, 147-350, 200-500, 200-450, 200-400, 200-350, 250-500, 250-450, 250-400, 250-350, 300-500, 300-450, 300-400, 300-350, 350-500, 350-450, 350-400, 350-350, 400-500, 400-450, 400-400, 400-350, 425-500, 425-450, 425-400, 425-350, 450-500, 450-450, 450-400, 450-350, 450-300, 450-250, 450-200, 450-150, 450-100, 450-50, 450-0, 500-500, 500-450, 500-400, 500-350, 500-300, 500-250, 500-200, 500-150, 500-100, 500-50, 500-0, 550-500, 550-450, 550-400, 550-350, 550-300, 550-250, 550-200, 550-150, 550-100, 550-50, 550-0, 600-500, 600-450, 600-400, 600-350, 600-300, 600-250, 600-200, 600-150, 600-100, 600-50, 600-0, 650-500, 650-450, 650-400, 650-350, 650-300, 650-250, 650-200, 650-150, 650-100, 650-50, 650-0, 700-500, 700-450, 700-400, 700-350, 700-300, 700-250, 700-200, 700-150, 700-100, 700-50, 700-0, 750-500, 750-450, 750-400, 750-350, 750-300, 750-250, 750-200, 750-150, 750-100, 750-50, 750-0, 800-500, 800-450, 800-400, 800-350, 800-300, 800-250, 800-200, 800-150, 800-100, 800-50, 800-0, 850-500, 850-450, 850-400, 850-350, 850-300, 850-250, 850-200, 850-150, 850-100, 850-50, 850-0, 900-500, 900-450, 900-400, 900-350, 900-300, 900-250, 900-200, 900-150, 900-100, 900-50, 900-0, 950-500, 950-450, 950-400, 950-350, 950-300, 950-250, 950-200, 950-150, 950-100, 950-50, 950-0, 1000-500, 1000-450, 1000-400, 1000-350, 1000-300, 1000-250, 1000-200, 1000-150, 1000-100, 1000-50, 1000-0, 1050-500, 1050-450, 1050-400, 1050-350, 1050-300, 1050-250, 1050-200, 1050-150, 1050-100, 1050-50, 1050-0, and/or 1050-0 of SEQ ID NO:1.

Preferably, the polynucleotide fragments of the invention encode a polypeptide which demonstrates a Neutrokin- α and/or Neutrokin- α SV functional activity. By a polypeptide demonstrating "functional activity" is meant, a polypeptide capable of displaying one or more known functional activities associated with a full-length and/or secreted Neutrokin- α polypeptide and/or Neutrokin- α SV polypeptide. Such functional activities include, but are not limited to, biological activity (e.g., ability to stimulate B cell proliferation, survival, differentiation, and/or activation), antigenicity [ability to bind or compete with a Neutrokin- α and/or Neutrokin- α SV polypeptide for binding to an anti-Neutrokin- α and/or anti-Neutrokin- α SV antibody], immunogenicity (ability to generate antibody which binds to a Neutrokin- α and/or Neutrokin- α SV polypeptide), ability to form multimers with Neutrokin- α and/or Neutrokin- α SV polypeptides of the invention, and ability to bind to a receptor or ligand for a Neutrokin- α and/or Neutrokin- α SV polypeptide.

In additional specific embodiments, the polynucleotide fragments of the invention encode a polypeptide comprising, or alternatively, consisting of the predicted intracellular domain (amino acids 1 to 46 of SEQ ID NO:2), the predicted transmembrane domain (amino acids 47 to 72 of SEQ ID NO:2), the predicted extracellular domain (amino acids 73 to 285 of SEQ ID NO:2), or the predicted TNF conserved domain (amino acids 191 to 284 of SEQ ID NO:2) of Neutrokin- α . In additional embodiments, the polynucleotide fragments of the invention encode a polypeptide comprising, or alternatively, consisting of any combination of 1, 2, 3, or all 4 of the above recited domains. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

In additional specific embodiments, the polynucleotide fragments of the invention encode a polypeptide comprising, or alternatively, consisting of the predicted intracellular domain (amino acids 1 to 46 of SEQ ID NO:19), the predicted

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transmembrane domain (amino acids 47 to 72 of SEQ ID NO:19), the predicted extracellular domain (amino acids 73 to 266 of SEQ ID NO:19), or the predicted TNF conserved domain (amino acids 172 to 265 of SEQ ID NO:19) of Neurokinine- α SV. In additional embodiments, the polynucleotide fragments of the invention encode a polypeptide comprising, or alternatively, consisting of any combination of 1, 2, 3, or all 4 of the above recited domains. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

In another embodiment, polynucleotide fragments of the invention comprise, or alternatively consist of, polynucleotides which encode an amino acid sequence selected from residues Met-1 to Lys-113, Leu-114 to Thr-141, Ile-142 to Lys-160, Gly-161 to Gln-198, Val-199 to Ala-248, and Gly-250 to Leu-285 of SEQ ID NO:2. Moreover, polynucleotides that encode any combination of two, three, four, five or more of these amino acid sequences are also encompassed by the invention. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

In another embodiment, polynucleotide fragments of the invention comprise, or alternatively consist of, polynucleotides which encode an amino acid sequence selected from residues Met-1 to Lys-113, Leu-114 to Thr-141, Gly-142 to Gln-179, Val-180 to Ala-229, and Gly-230 to Leu-266 of SEQ ID NO:19. Moreover, polynucleotides that encode any combination of two, three, four, five or more of these amino acid sequences are also encompassed by the invention. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

In another embodiment, polynucleotide fragments of the invention comprise, or alternatively consist of, polynucleotides which encode an amino acid sequence selected from residues Met-1 to Lys-106, Leu-107 to Thr-134, Glu-135 to Asn-165, Ile-167 to Lys-184, Gly-185 to Gln-224, Val-225 to Ala-272, and Gly-273 to Leu-309 of SEQ ID NO:23. Moreover, polynucleotides that encode any combination of two, three, four, five or more of these amino acid sequences are also encompassed by the invention. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

In another embodiment, polynucleotide fragments of the invention comprise, or alternatively consist of, polynucleotides which encode an amino acid sequence selected from residues Tyr-1 to Lys-47, Leu-48 to Thr-75, Ile-76 to Lys-94, Gly-95 to Gln-132, Val-133 to Ala-182, and Gly-183 to Ala-219 of SEQ ID NO:28. Moreover, polynucleotides that encode any combination of two, three, four, five or more of these amino acid sequences are also encompassed by the invention. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

In another embodiment, polynucleotide fragments of the invention comprise, or alternatively consist of, polynucleotides which encode an amino acid sequence selected from residues Tyr-1 to Lys-47, Leu-48 to Thr-75, Ile-76 to Lys-94, Gly-95 to Gln-132, Val-133 to Ala-182, and Gly-183 to Ala-219 of SEQ ID NO:30. Moreover, polynucleotides that encode any combination of two, three, four, five or more of these amino acid sequences are also encompassed by the invention. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

In another embodiment, the polynucleotides of the invention comprise, or alternatively consist of, the sequence shown in SEQ ID NO:21. The sequence shown as SEQ ID NO:21 encodes a polypeptide consisting of an initiating methionine residue linked to residues Ala-134 through Leu-285 of the Neurokinine- α polypeptide sequence shown as SEQ ID

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NO:2. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

In certain additional preferred embodiments, polynucleotides of the invention comprise, or alternatively, consist of nucleotide residues 1-459, 15-459, 30-459, 45-459, 60-459, 75-459, 90-459, 105-459, 120-459, 135-459, 150-459, 165-459, 180-459, 195-459, 210-459, 225-459, 240-459, 255-459, 270-459, 285-459, 300-459, 315-459, 330-459, 345-459, 360-459, 375-459, 390-459, 405-459, 420-459, 435-459, 450-459, 1-450, 15-450, 30-450, 45-450, 60-450, 75-450, 90-450, 105-450, 120-450, 135-450, 150-450, 165-450, 180-450, 195-450, 210-450, 225-450, 240-450, 255-450, 270-450, 285-450, 300-450, 315-450, 330-450, 345-450, 360-450, 375-450, 390-450, 405-450, 420-450, 435-450, 1-435, 15-435, 30-435, 45-435, 60-435, 75-435, 90-435, 105-435, 120-435, 135-435, 150-435, 165-435, 180-435, 195-435, 210-435, 225-435, 240-435, 255-435, 270-435, 285-435, 300-435, 315-435, 330-435, 345-435, 360-435, 375-435, 390-435, 405-435, 420-435, 1-420, 15-420, 30-420, 45-420, 60-420, 75-420, 90-420, 105-420, 120-420, 135-420, 150-420, 165-420, 180-420, 195-420, 210-420, 225-420, 240-420, 255-420, 270-420, 285-420, 300-420, 315-420, 330-420, 345-420, 360-420, 375-420, 390-420, 405-420, 1-405, 15-405, 30-405, 45-405, 60-405, 75-405, 90-405, 105-405, 120-405, 135-405, 150-405, 165-405, 180-405, 195-405, 210-405, 225-405, 240-405, 255-405, 270-405, 285-405, 300-405, 315-405, 330-405, 345-405, 360-405, 375-405, 390-405, 1-390, 15-390, 30-390, 45-390, 60-390, 75-390, 90-390, 105-390, 120-390, 135-390, 150-390, 165-390, 180-390, 195-390, 210-390, 225-390, 240-390, 255-390, 270-390, 285-390, 300-390, 315-390, 330-390, 345-390, 360-390, 375-390, 1-375, 15-375, 30-375, 45-375, 60-375, 75-375, 90-375, 105-375, 120-375, 135-375, 150-375, 165-375, 180-375, 195-375, 210-375, 225-375, 240-375, 255-375, 270-375, 285-375, 300-375, 315-375, 330-375, 345-375, 360-375, 1-360, 15-360, 30-360, 45-360, 60-360, 75-360, 90-360, 105-360, 120-360, 135-360, 150-360, 165-360, 180-360, 195-360, 210-360, 225-360, 240-360, 255-360, 270-360, 285-360, 300-360, 315-360, 330-360, 345-360, 1-345, 15-345, 30-345, 45-345, 60-345, 75-345, 90-345, 105-345, 120-345, 135-345, 150-345, 165-345, 180-345, 195-345, 210-345, 225-345, 240-345, 255-345, 270-345, 285-345, 300-345, 315-345, 330-345, 1-330, 15-330, 30-330, 45-330, 60-330, 75-330, 90-330, 105-330, 120-330, 135-330, 150-330, 165-330, 180-330, 195-330, 210-330, 225-330, 240-330, 255-330, 270-330, 285-330, 300-330, 315-330, 1-315, 15-315, 30-315, 45-315, 60-315, 75-315, 90-315, 105-315, 120-315, 135-315, 150-315, 165-315, 180-315, 195-315, 210-315, 225-315, 240-315, 255-315, 270-315, 285-315, 300-315, 1-300, 15-300, 30-300, 45-300, 60-300, 75-300, 90-300, 105-300, 120-300, 135-300, 150-300, 165-300, 180-300, 195-300, 210-300, 225-300, 240-300, 255-300, 270-300, 285-300, 1-285, 15-285, 30-285, 45-285, 60-285, 75-285, 90-285, 105-285, 120-285, 135-285, 150-285, 165-285, 180-285, 195-285, 210-285, 225-285, 240-285, 255-285, 270-285, 1-270, 15-270, 30-270, 45-270, 60-270, 75-270, 90-270, 105-270, 120-270, 135-270, 150-270, 165-270, 180-270, 195-270, 210-270, 225-270, 240-270, 255-270, 1-255, 15-255, 30-255, 45-255, 60-255, 75-255, 90-255, 105-255, 120-255, 135-255, 150-255, 165-255, 180-255, 195-255, 210-255, 225-255, 240-255, 1-240, 15-240, 30-240, 45-240, 60-240, 75-240, 90-240, 105-240, 120-240, 135-240, 150-240, 165-240, 180-240, 195-240, 210-240, 225-240, 1-225, 15-225, 30-225, 45-225, 60-225, 75-225, 90-225, 105-225, 120-225, 135-225, 150-225, 165-225, 180-225, 195-225, 210-225, 1-210, 15-210, 30-210, 45-210, 60-210, 75-210, 90-210, 105-210, 120-210, 135-210,

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150-210, 165-210, 180-210, 195-210, 1-195, 15-195, 30-195, 45-195, 60-195, 75-195, 90-195, 105-195, 120-195, 135-195, 150-195, 165-195, 180-195, 1-180, 15-180, 30-180, 45-180, 60-180, 75-180, 90-180, 105-180, 120-180, 135-180, 150-180, 165-180, 1-165, 15-165, 30-165, 45-165, 60-165, 75-165, 90-165, 105-165, 120-165, 135-165, 150-165, 1-150, 15-150, 30-150, 45-150, 60-150, 75-150, 90-150, 105-150, 120-150, 135-150, 1-135, 15-135, 30-135, 45-135, 60-135, 75-135, 90-135, 105-135, 120-135, 1-120, 15-120, 30-120, 45-120, 60-120, 75-120, 90-120, 105-120, 1-105, 15-105, 30-105, 45-105, 60-105, 75-105, 90-105, 1-90, 15-90, 30-90, 45-90, 60-90, 75-90, 1-75, 15-75, 30-75, 45-75, 60-75, 1-60, 15-60, 30-60, 45-60, 1-45, 15-45, 30-45, 1-30, and/or 15-30 of SEQ ID NO: 21. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

Accordingly, specific embodiments of the invention are directed to polynucleotides encoding polypeptides which comprise, or alternatively consist of, the amino acid sequence of beta pleated sheet region A, A', B, B', C, D, E, F, G, or H disclosed in FIGS. 7A-1 and 7A-2 and described in Example 6. Additional embodiments of the invention are directed to polynucleotides encoding Neutrokin-alpha polypeptides which comprise, or alternatively consist of, any combination of 1, 2, 3, 4, 5, 6, 7, 8, 9 or all 10 of beta pleated sheet regions A-H disclosed in FIGS. 7A-1 and 7A-2 and described in Example 6. Additional preferred embodiments of the invention are directed to polypeptides which comprise, or alternatively consist of, the Neutrokin-alpha amino acid sequence of beta pleated sheet region A, A', B, B', C, D, E, F, G, or H disclosed in FIGS. 7A-1 and 7A-2 and described in Example 6. Additional embodiments of the invention are directed to Neutrokin-alpha polypeptides which comprise, or alternatively consist of, any combination of 1, 2, 3, 4, 5, 6, 7, 8, 9 or all 10 of beta pleated sheet regions A through H disclosed in FIGS. 7A-1 and 7A-2 and described in Example 6.

In certain other preferred embodiments, polynucleotides of the invention comprise, or alternatively consist of, nucleotide residues 34-57, 118-123, 133-141, 151-159, 175-216, 232-255, 280-315, 328-357, 370-393, and/or 430-456 of SEQ ID NO: 21. Polypeptides encoded by these polynucleotides are also encompassed by the invention. These polynucleotide and polypeptide fragments correspond to the predicted beta-pleated sheet regions shown in FIGS. 7A-1 and 7A-2. In certain embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence at least 90%, 95%, 96%, 97%, 98% or 99% identical to the polynucleotide sequence encoding one, two, three, four, five, six, seven, eight, nine or ten of the beta-pleated sheet regions described above. The present invention also encompasses the above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these polynucleotide sequences are also encompassed by the invention. In another embodiment, the invention provides an isolated nucleic acid molecule comprising a polynucleotide which hybridizes under stringent hybridization conditions to one, two, three, four, five, six, seven, eight, nine or ten of the beta-pleated sheet polynucleotides of the invention described above. The meaning of the phrase "stringent conditions" as used herein is described infra.

In further preferred embodiments, polynucleotides of the invention comprise, or alternatively consist of, nucleotide residues 576-599, 660-665, 675-683, 693-701, 717-758, 774-803, 822-857, 870-899, 912-935, and/or 972-998 of SEQ ID NO: 1. Polypeptides encoded by these polynucleotide fragments are also encompassed by the invention. These poly-

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nucleotide and polypeptide fragments correspond to the predicted beta-pleated sheet regions shown in FIGS. 7A-1 and 7A-2.

In additional preferred embodiments, polynucleotides of the invention comprise, or alternatively consist of, nucleotide residues 457-462, 472-480, 490-498, 514-555, 571-600, 619-654, 667-696, 699-732, and/or 769-795 of SEQ ID NO: 18. Polypeptides encoded by these polynucleotide fragments are also encompassed by the invention. These polynucleotide and polypeptide fragments correspond to the predicted beta-pleated sheet regions shown in FIGS. 7A-1 and 7A-2.

In yet further preferred embodiments, polynucleotides of the invention comprise, or alternatively consist of, nucleotide residues 124-129, 139-147, 157-165, 181-222, 238-267, 286-321, 334-363, 376-399, and/or 436-462 of SEQ ID NO: 22. Polypeptides encoded by these polynucleotide fragments are also encompassed by the invention. These polynucleotide and polypeptide fragments correspond to the predicted beta-pleated sheet regions shown in FIGS. 7A-1 and 7A-2. Polypeptides comprising, or alternatively, consisting of the amino acid sequence of any combination of one, two, three, four, five, six, seven, eight, nine, ten, or all of these regions are encompassed by the invention.

The relative positions of several intron/exon boundaries were determined for the mouse Neutrokin-alpha (SEQ ID NO: 22 and SEQ ID NO: 23) based on sequence analysis of mouse genomic DNA. The apparent second exon from the 5' end of the mouse Neutrokin-alpha genomic clone (preliminarily designated "Exon 2") consists of Tyr-187 to Gln-222 of the sequence shown in SEQ ID NO: 23. The apparent third exon from the 5' end of the mouse Neutrokin-alpha genomic clone (preliminarily designated "Exon 3") comprises Val-223 to Gly-273 of the sequence shown in SEQ ID NO: 23.

Thus, in one embodiment, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, the amino acid sequence of residues Tyr-187 to Gln-222 of SEQ ID NO: 23. The present invention is also directed to nucleic acid molecules comprising, or alternatively, consisting of, a polynucleotide sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to the polynucleotide sequence encoding the mouse Neutrokin-alpha polypeptides described above. The present invention also encompasses the above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these nucleic acids and/or polynucleotide sequences are also encompassed by the invention.

In another embodiment, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, the amino acid sequence of residues Val-223 to Gly-273 of SEQ ID NO: 23. The present invention is also directed to nucleic acid molecules comprising, or alternatively, consisting of, a polynucleotide sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to the polynucleotide sequence encoding the mouse Neutrokin-alpha polypeptides described above. The present invention also encompasses the above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these nucleic acids and/or polynucleotide sequences are also encompassed by the invention.

Moreover, the relative positions of the corresponding intron/exon boundaries were determined for human Neutrokin-alpha (SEQ ID NO: 1 and SEQ ID NO: 2) based on an alignment of the sequences of mouse and human Neutrokin-alpha polypeptides. The apparent second exon from the 5' end of human Neutrokin-alpha (also preliminarily designated "Exon 2") consists of Tyr-163 to Gln-198 of the sequence shown in SEQ ID NO: 2. The apparent third exon from the 5'

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end of human Neutrokin-alpha (also preliminarily designated "Exon 3") consists of, Val-199 to Gly-249 of the sequence shown in SEQ ID NO:2.

Thus, in one embodiment, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, the amino acid sequence of residues Tyr-163 to Gln-198 of SEQ ID NO:2. The present invention is also directed to nucleic acid molecules comprising, or alternatively, consisting of, a polynucleotide sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to the polynucleotide sequence encoding the Neutrokin-alpha polypeptides described above. The present invention also encompasses the above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these nucleic acids and/or polynucleotide sequences are also encompassed by the invention.

In another embodiment, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, the amino acid sequence of residues Val-199 to Gly-249 of SEQ ID NO:2. The present invention is also directed to nucleic acid molecules comprising, or alternatively, consisting of, a polynucleotide sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to the polynucleotide sequence encoding the Neutrokin-alpha polypeptides described above. The present invention also encompasses the above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these nucleic acids and/or polynucleotide sequences are also encompassed by the invention.

The functional activity of Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides, and fragments, variants derivatives, and analogs thereof, can be assayed by various methods as described herein and as are well known in the art.

For example, in one embodiment where one is assaying for the ability to bind or compete with full-length Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide for binding to anti-Neutrokin-alpha and/or anti-Neutrokin-alphaSV antibody or binding to Neutrokin-alpha receptor(s) and/or Neutrokin-alphaSV receptor(s) on B cells, various immunoassays known in the art can be used, including but not limited to, competitive and non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitation reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention.

In another embodiment, where a Neutrokin-alpha and/or Neutrokin-alphaSV ligand is identified, or the ability of a polypeptide fragment, variant or derivative of the invention to multimerize is being evaluated, binding can be assayed, e.g., by means well-known in the art, such as, for example, reducing and non-reducing gel chromatography, protein affinity chromatography, and affinity blotting. See generally, Phizicky, E., et al., 1995, *Microbiol. Rev.* 59:94-123. In another

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embodiment, physiological correlates of Neutrokin-alpha and/or Neutrokin-alphaSV binding to its substrates (signal transduction) can be assayed.

In addition, assays described herein (see, e.g., Examples 6 and 7) and otherwise known in the art may routinely be applied to measure the ability of Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides and fragments, variants derivatives and analogs thereof to elicit Neutrokin-alpha and/or Neutrokin-alphaSV related biological activity (e.g., to stimulate, or alternatively to inhibit (in the case of Neutrokin-alpha and/or Neutrokin-alphaSV antagonists) B cell proliferation, differentiation and/or activation and/or to extend B cell survival in vitro or in vivo).

Other methods will be known to the skilled artisan and are within the scope of the invention.

In additional embodiments, the polynucleotides of the invention encode polypeptides comprising, or alternatively consisting of, functional attributes of Neutrokin-alpha and Neutrokin-alphaSV. Preferred embodiments of the invention in this regard include fragments that comprise, or alternatively consist of, alpha-helix and alpha-helix forming regions ("alpha-regions"), beta-sheet and beta-sheet forming regions ("beta-regions"), turn and turn-forming regions ("turn-regions"), coil and coil-forming regions ("coil-regions"), hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions and high antigenic index regions of Neutrokin-alpha and Neutrokin-alphaSV polypeptides.

It is believed one or more of the beta pleated sheet regions of Neutrokin-alpha disclosed in FIGS. 7A-1 and 7A-2 is important for dimerization and also for interactions between Neutrokin-alpha and its ligands.

Certain preferred regions in this regard are set out in FIG. 3 (Table I). The data presented in FIG. 3 and that presented in Table I, merely present a different format of the same results obtained when the amino acid sequence of SEQ ID NO:2 is analyzed using the default parameters of the DNA*STAR computer algorithm.

The above-mentioned preferred regions set out in FIG. 3 and in Table I include, but are not limited to, regions of the aforementioned types identified by analysis of the amino acid sequence set out in FIGS. 1A and 1B. As set out in FIG. 3 and in Table I, such preferred regions include Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions, Chou-Fasman alpha-regions, beta-regions, and coil-regions, Kyte-Doolittle hydrophilic regions and hydrophobic regions, Eisenberg alpha- and beta-amphipathic regions, Karplus-Schultz flexible regions, Emini surface-forming regions and Jameson-Wolf regions of high antigenic index. Among highly preferred polynucleotides in this regard are those that encode polypeptides comprising, or alternatively consisting of, regions of Neutrokin-alpha and/or Neutrokin-alphaSV that combine several structural features, such as several (e.g., 1, 2, 3 or 4) of the features set out above. Polypeptides encoded by the polynucleotides are also encompassed by the invention.

Additionally, the data presented in columns VIII, IX, XIII, and XIV of Table I can routinely be used to determine regions of Neutrokin-alpha which exhibit a high degree of potential for antigenicity (column VIII of Table I represents hydrophilicity according to Kyte-Doolittle; column IX of Table I represents hydrophobicity according to Hopp-Woods; column XIII of Table I represents antigenic index according to Jameson-Wolf; and column XIV of Table I represents surface probability according to Emini). Regions of high antigenicity are determined from the data presented in columns VIII, IX, XIII, and/or XIV by choosing values which represent regions of

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the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response. The data presented in FIG. 6 can also routinely be presented in a similar tabular format by simply examining the amino acid sequence disclosed in FIG. 6 (SEQ ID NO:19)

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using the modules and algorithms of the DNA*STAR set on default parameters. As above, the amino acid sequence presented in FIG. 6 can also be used to determine regions of Neutrokin-alpha which exhibit a high degree of potential for antigenicity whether presented as a Figure (as in FIG. 6) or a table (as in Table I).

TABLE I

Res Position	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
Met	1	A	0.73	-0.71	.	.	.	0.95	1.39
Asp	2	A	I	1.12	-0.66	*	.	.	1.15	1.56
Asp	3	A	T	1.62	-1.09	*	.	.	1.15	2.12
Ser	4	A	T	2.01	-1.51	*	.	.	1.15	4.19
Thr	5	A	T	2.40	-2.13	.	.	F	1.30	4.35
Glu	6	A	A	2.70	-1.73	*	*	F	0.90	4.51
Arg	7	A	A	2.81	-1.34	*	*	F	0.90	4.51
Glu	8	A	A	2.60	-1.73	*	*	F	0.90	6.12
Gln	9	A	A	1.99	-1.53	*	*	F	0.90	2.91
Ser	10	A	.	.	B	.	.	2.60	-1.04	*	*	F	0.90	2.15
Arg	11	A	.	.	B	.	.	1.33	-0.66	*	*	F	0.90	1.66
Leu	12	A	.	.	B	.	.	0.41	-0.09	*	*	F	0.45	0.51
Thr	13	A	.	.	B	.	.	0.46	0.20	*	*	F	-0.15	0.32
Ser	14	A	A	0.50	-0.19	*	*	.	0.30	0.32
Cys	15	A	A	0.91	-0.19	*	*	.	0.30	0.78
Leu	16	A	A	0.80	-0.87	*	*	F	0.90	1.06
Lys	17	A	A	1.61	1.36	.	*	F	0.90	1.37
Lys	18	A	A	1.32	-1.74	.	*	F	0.90	4.44
Arg	19	A	A	1.67	-1.70	.	*	F	0.90	5.33
Glu	20	A	A	1.52	-2.39	.	*	F	0.90	5.33
Glu	21	A	A	2.38	-1.70	.	*	F	0.90	2.20
Met	22	A	A	2.33	-1.70	.	*	F	0.90	2.24
Lys	23	A	A	1.62	-1.70	*	*	F	0.90	2.24
Leu	24	A	A	0.66	-1.13	*	*	F	0.75	0.69
Lys	25	A	A	0.36	-0.49	.	*	F	0.45	0.52
Glu	26	A	A	.	B	.	.	-0.53	-0.71	*	*	.	0.60	0.35
Cys	27	A	A	.	B	.	.	-0.74	-0.03	*	*	.	0.30	0.30
Val	28	A	A	.	B	.	.	-1.00	-0.03	*	*	.	0.30	0.12
Ser	29	A	A	.	B	.	.	-0.08	0.40	*	*	.	-0.30	0.11
Ile	30	A	.	.	B	.	.	-0.08	0.40	*	*	.	-0.30	0.40
Leu	31	A	.	.	B	.	.	-0.08	-0.17	*	*	.	0.45	1.08
Pro	32	.	.	.	B	.	C	0.29	-0.81	*	.	F	1.10	1.39
Arg	33	.	.	.	T	.	.	0.93	-0.81	.	*	F	1.50	2.66
Lys	34	.	.	.	T	.	.	0.93	-1.07	.	.	F	1.84	4.98
Glu	35	C	.	0.97	-1.37	*	*	F	1.98	4.32
Ser	36	T	C	1.89	-1.16	*	*	F	2.52	1.64
Pro	37	T	C	1.80	-1.16	*	*	F	2.86	1.60
Ser	38	.	.	.	T	T	.	1.39	-0.77	.	.	F	3.40	1.24
Val	39	A	.	.	.	T	.	1.39	-0.39	.	*	F	2.36	1.24
Arg	40	A	1.39	-0.77	*	*	F	2.46	1.60
Ser	41	A	1.34	-1.20	*	*	F	2.46	2.00
Ser	42	.	.	.	T	T	.	1.60	-1.16	.	*	F	3.06	2.67
Lys	43	.	.	.	T	T	.	1.09	-1.80	.	*	F	3.06	2.72
Asp	44	.	.	.	T	T	.	1.13	-1.11	*	*	F	3.40	1.67
Gly	45	A	.	.	.	T	.	0.43	-0.81	*	*	F	2.66	1.03
Lys	46	A	A	0.14	-0.70	.	.	F	1.77	0.52
Leu	47	A	A	0.13	-0.20	*	.	.	0.98	0.31
Leu	48	A	A	-0.72	0.29	*	.	.	0.04	0.46
Ala	49	A	A	-1.53	0.54	.	*	.	-0.60	0.19
Ala	50	A	A	-2.00	1.23	.	.	.	-0.60	0.19
Thr	51	A	A	-2.63	1.23	.	.	.	-0.60	0.19
Leu	52	A	A	-2.63	1.04	.	.	.	-0.60	0.19
Leu	53	A	A	-2.63	1.23	.	.	.	-0.60	0.15
Leu	54	A	A	-2.34	1.41	.	.	.	-0.60	0.09
Ala	55	A	A	-2.42	1.31	.	.	.	-0.60	0.14
Leu	56	A	A	-2.78	1.20	.	.	.	-0.60	0.09
Leu	57	A	.	.	.	T	.	-2.78	1.09	.	.	.	-0.20	0.06
Ser	58	A	.	.	.	T	.	-2.28	1.09	.	.	.	-0.20	0.05
Cys	59	A	.	.	.	T	.	-2.32	1.07	.	.	.	-0.20	0.09
Cys	60	A	.	.	.	T	.	-2.59	1.03	.	.	.	-0.20	0.08
Leu	61	.	.	B	B	.	.	-2.08	0.99	.	.	.	-0.60	0.04
Thr	62	.	.	B	B	.	.	-1.97	0.99	.	.	.	-0.60	0.11
Val	63	.	.	B	B	.	.	-1.91	1.20	.	.	.	-0.60	0.17
Val	64	.	.	B	B	.	.	-1.24	1.39	.	.	.	-0.60	0.33
Ser	65	.	.	B	B	.	.	-1.43	1.10	.	.	.	-0.60	0.40
Phe	66	A	.	.	B	.	.	-1.21	1.26	.	.	.	-0.60	0.40
Tyr	67	A	.	.	B	.	.	-1.49	1.11	.	.	.	-0.60	0.54
Gln	68	A	.	.	B	.	.	-1.44	0.97	.	.	.	-0.60	0.41
Val	69	A	.	.	B	.	.	-0.59	1.27	.	.	.	-0.60	0.39
Ala	70	A	.	.	B	.	.	-0.63	0.89	.	.	.	-0.60	0.43

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TABLE I-continued

Res Position	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
Ala	71	A	.	B	.	.	.	0.07	0.56	.	*	.	-0.60	0.25
Leu	72	A	.	.	.	T	.	-0.50	0.16	.	*	.	0.19	0.55
Gln	73	A	.	.	.	T	.	-1.09	0.20	.	.	F	0.25	0.45
Gly	74	A	.	.	.	T	.	-0.53	0.20	.	.	F	0.25	0.45
Asp	75	A	.	.	.	T	.	-0.76	0.09	.	*	F	0.25	0.73
Leu	76	A	A	-0.06	0.09	.	*	F	-0.15	0.35
Ala	77	A	A	0.17	-0.31	.	*	.	0.30	0.69
Ser	78	A	A	0.17	-0.24	.	*	.	0.30	0.42
Leu	79	A	A	-0.30	-0.24	.	*	.	0.30	0.88
Arg	80	A	A	-0.30	-0.24	.	*	.	0.30	0.72
Ala	81	A	A	0.17	-0.34	.	*	.	0.30	0.93
Glu	82	A	A	0.72	-0.30	.	*	.	0.45	1.11
Leu	83	A	A	0.99	-0.49	.	*	.	0.30	0.77
Gln	84	A	A	1.21	0.01	.	*	.	-0.15	1.04
Gly	85	A	A	1.10	0.01	.	*	.	-0.30	0.61
His	86	A	A	1.73	0.01	.	*	.	-0.15	1.27
His	87	A	A	0.92	-0.67	.	*	.	0.75	1.47
Ala	88	A	A	1.52	-0.39	.	*	.	0.45	1.22
Glu	89	A	A	0.93	-0.39	.	.	.	0.45	1.39
Lys	90	A	A	0.93	-0.39	.	*	F	0.60	1.05
Leu	91	A	.	.	.	T	.	0.38	-0.46	.	*	.	0.85	1.01
Pro	92	A	.	.	.	T	.	0.97	-0.46	.	.	.	0.70	0.59
Ala	93	A	.	.	.	T	.	0.67	-0.03	.	.	.	0.70	0.29
Gly	94	A	.	.	.	T	.	-0.14	0.47	.	.	.	-0.20	0.36
Ala	95	A	-0.14	0.21	.	*	.	-0.10	0.36
Gly	96	A	0.08	-0.21	.	.	F	0.65	0.71
Ala	97	A	-0.06	-0.21	.	.	F	0.65	0.72
Pro	98	A	-0.28	-0.21	.	*	F	0.65	0.71
Lys	99	A	A	0.67	-0.03	.	.	F	0.45	0.59
Ala	100	A	A	0.66	-0.46	.	.	F	0.60	1.01
Gly	101	A	A	0.41	-0.96	.	.	F	0.90	1.13
Leu	102	A	A	0.79	-0.89	.	.	F	0.75	0.57
Glu	103	A	A	0.41	-0.46	.	*	F	0.45	0.88
Glu	104	A	A	-0.49	-0.46	.	*	F	0.45	0.89
Ala	105	A	A	-0.21	-0.24	.	.	.	0.30	0.81
Pro	106	A	A	-0.46	-0.44	.	.	.	0.30	0.67
Ala	107	A	A	0.01	0.06	.	.	.	-0.30	0.39
Val	108	A	A	-0.80	0.49	.	*	.	-0.60	0.38
Thr	109	A	A	-0.76	0.67	.	*	.	-0.60	0.20
Ala	110	A	A	-1.06	0.24	.	*	.	-0.30	0.40
Gly	111	A	A	-1.54	0.43	.	*	.	-0.60	0.38
Leu	112	A	A	-0.96	0.57	.	*	.	-0.60	0.23
Lys	113	.	A	B	.	.	.	-0.31	0.09	.	*	.	-0.30	0.39
Ile	114	.	A	B	.	.	.	-0.21	0.01	.	*	.	-0.30	0.61
Phe	115	.	A	B	.	.	.	-0.21	0.01	.	*	.	0.15	1.15
Glu	116	.	A	.	.	.	C	-0.08	-0.17	.	*	F	1.25	0.58
Pro	117	.	A	.	.	.	C	0.39	0.26	.	*	F	1.10	1.28
Pro	118	C	0.34	-0.00	.	.	F	2.20	1.47
Ala	119	T	C	0.89	-0.79	.	*	F	3.00	1.47
Pro	120	T	C	1.59	-0.36	.	*	F	2.25	0.94
Gly	121	.	.	.	T	T	.	1.29	-0.39	.	*	F	2.15	0.98
Glu	122	.	.	.	T	T	.	1.20	-0.43	.	.	F	2.00	1.30
Gly	123	C	.	1.41	-0.54	.	.	F	1.60	1.12
Asn	124	.	.	.	T	C	.	2.00	-0.57	.	.	F	1.50	1.97
Ser	125	.	.	.	T	C	.	1.91	-0.60	.	*	F	1.50	1.82
Ser	126	.	.	.	T	C	.	2.37	-0.21	.	*	F	1.54	2.47
Gln	127	.	.	.	T	C	.	2.37	-0.64	.	*	F	2.18	3.01
Asn	128	C	.	2.76	-0.64	.	.	F	2.32	3.61
Ser	129	.	.	.	T	C	.	2.87	-1.03	.	.	F	2.86	5.39
Arg	130	.	.	.	T	T	.	2.58	-1.41	.	*	F	3.40	6.09
Asn	131	.	.	.	T	T	.	2.02	-1.31	.	*	F	3.06	3.83
Lys	132	.	.	.	T	T	.	2.02	-1.07	.	*	F	2.72	2.12
Arg	133	.	.	.	T	.	.	1.68	-1.06	.	*	F	2.18	1.88
Ala	134	C	.	1.77	-0.63	.	*	F	1.64	1.15
Val	135	C	.	1.66	-0.60	.	*	F	1.49	0.89
Gln	136	C	.	1.66	-0.60	.	*	F	1.83	0.79
Gly	137	.	.	.	T	C	.	1.30	-0.60	.	*	F	2.52	1.35
Pro	138	.	.	.	T	C	.	0.33	-0.61	.	*	F	2.86	2.63
Glu	139	.	.	.	T	T	.	0.61	-0.61	.	*	F	3.40	1.13
Glu	140	A	.	.	.	T	.	1.47	-0.53	.	*	F	2.66	1.64
Thr	141	A	1.47	-0.56	.	.	F	2.12	1.84
Val	142	A	1.14	-0.99	.	.	F	1.78	1.77
Thr	143	A	.	.	.	T	.	0.54	-0.41	.	.	F	1.19	0.55
Gln	144	A	.	.	.	T	.	0.54	0.27	.	*	F	0.25	0.31
Asp	145	A	.	.	.	T	.	-0.27	0.19	.	*	F	0.25	0.73
Cys	146	A	.	.	.	T	.	-0.84	0.23	.	*	.	0.10	0.42
Ileu	147	A	A	-0.58	0.43	.	*	.	-0.60	0.17
Gln	148	A	A	-0.27	0.53	.	*	.	-0.60	0.10

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TABLE I-continued

Res	Position	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
Leu	149	A	A	-0.57	0.53	*	*	.	-0.30	0.52
Ile	150	A	A	-0.57	0.34	*	.	.	0.30	0.52
Ala	151	.	A	C	-0.21	-0.34	.	*	.	1.40	0.52
Asp	152	T	F	.	0.39	-0.26	.	*	F	2.45	0.91
Ser	153	T	C	0.08	-0.51	.	.	F	3.00	2.00
Glu	154	T	C	-0.60	-0.71	.	.	F	2.70	2.86
Thr	155	T	C	0.89	-0.53	*	.	F	2.40	1.20
Pro	156	.	.	.	B	.	.	C	1.52	-0.13	*	.	F	1.56	1.55
Thr	157	.	.	.	B	F	.	.	1.18	-0.51	*	.	F	1.92	1.79
Ile	158	A	.	.	B	.	.	.	1.18	-0.09	.	.	F	1.08	1.25
Gln	159	F	T	.	0.93	-0.19	.	.	F	2.04	1.07
Lys	160	F	T	.	0.93	0.14	*	.	F	1.60	1.16
Gly	161	T	T	.	0.44	0.14	*	.	F	1.44	2.38
Ser	162	T	T	.	-0.10	0.24	*	.	F	1.28	1.19
Tyr	163	.	.	.	B	T	.	.	0.58	0.49	*	.	.	0.12	0.44
Thr	164	.	.	B	B	.	.	.	0.29	0.91	*	.	.	-0.44	0.69
Phe	165	.	.	B	B	.	.	.	-0.57	1.40	*	.	.	-0.60	0.54
Val	166	.	.	B	B	.	.	.	-1.03	1.70	.	.	.	-0.60	0.29
Pro	167	.	.	B	B	.	.	.	-1.03	1.63	.	.	.	-0.60	0.16
Trp	168	A	.	.	B	.	.	.	-1.49	1.53	.	*	.	-0.60	0.25
Leu	169	A	.	.	B	.	.	.	-1.13	1.53	.	.	.	-0.60	0.29
Leu	170	A	.	.	B	.	.	.	-0.32	0.89	*	.	.	-0.30	0.38
Ter	171	A	0.19	0.46	*	.	.	0.20	0.71
Phe	172	T	.	.	0.10	-0.03	*	.	.	1.80	0.85
Lys	173	T	T	.	-0.20	-0.53	*	.	F	2.60	1.38
Arg	174	T	C	.	-0.20	-0.51	.	.	F	3.00	1.04
Gly	175	T	C	0.61	-0.21	.	.	F	2.25	0.99
Ser	176	A	T	.	0.91	-1.00	*	.	F	2.05	0.86
Ala	177	A	A	1.66	-1.00	*	.	F	1.35	0.76
Leu	178	A	A	1.61	-1.00	.	.	F	1.20	1.54
Glu	179	A	A	1.50	-1.43	.	.	F	0.90	1.98
Glu	180	A	A	1.89	-1.41	*	.	F	0.90	3.16
Lys	181	A	A	1.50	-1.91	*	.	F	0.90	7.66
Glu	182	A	A	1.08	-1.91	.	.	F	0.90	3.10
Asn	183	A	A	1.63	-1.23	*	.	F	0.90	1.48
Lys	184	A	A	1.08	-0.59	*	.	F	0.75	0.55
Ile	185	A	A	1.08	-0.59	*	.	.	0.60	0.63
Leu	186	A	A	0.72	-0.59	*	.	.	0.60	0.68
Val	187	A	A	0.38	-0.50	*	.	.	0.30	0.49
Lys	188	A	A	0.13	-0.07	*	.	F	0.45	0.69
Glu	189	A	.	.	.	T	.	.	-0.61	0.00	*	.	F	0.40	1.32
Thr	190	.	.	.	T	T	.	.	-0.42	0.10	.	*	F	0.80	1.54
Gly	191	.	.	.	T	T	.	.	-0.50	0.24	*	.	F	0.65	0.67
Tyr	192	.	.	.	T	T	.	.	0.11	0.93	*	.	.	0.20	0.27
Phe	193	.	.	B	B	.	.	.	-0.28	1.69	.	.	.	-0.60	0.29
Phe	194	.	.	B	B	.	.	.	-0.28	1.63	.	*	.	-0.60	0.29
Ile	195	.	.	B	B	.	.	.	-0.82	1.60	.	.	.	-0.60	0.32
Tyr	196	.	.	B	B	.	.	.	-1.29	1.49	.	.	.	-0.60	0.28
Gly	197	.	.	.	D	T	.	.	-1.29	1.39	.	.	.	-0.20	0.26
Gln	198	.	.	.	B	T	.	.	-0.90	1.36	.	.	.	-0.20	0.59
Val	199	.	.	.	B	.	.	C	-0.20	1.16	.	.	.	-0.40	0.54
Leu	200	.	.	.	B	.	.	C	0.73	0.40	.	.	.	-0.10	0.92
Tyr	201	.	.	.	T	T	.	.	0.67	-0.03	.	.	.	1.25	1.06
Thr	202	.	.	.	T	T	.	.	0.77	0.06	.	.	F	0.80	2.06
Asp	203	.	.	.	T	T	.	.	0.18	0.17	.	.	F	0.80	3.91
Lys	204	A	.	.	.	F	.	.	0.43	-0.01	.	.	F	1.00	2.52
Thr	205	A	A	0.90	-0.16	.	.	F	0.60	1.73
Tyr	206	A	A	1.11	-0.21	.	.	.	0.45	1.03
Ala	207	A	A	0.61	0.29	.	.	.	-0.30	0.70
Met	208	A	A	-0.28	0.97	.	.	.	-0.60	0.40
Gly	209	A	A	.	B	.	.	.	-0.32	1.17	*	.	.	-0.60	0.18
His	210	A	A	.	B	.	.	.	0.10	0.81	*	.	.	-0.60	0.31
Leu	211	A	A	.	B	.	.	.	0.39	0.31	.	.	.	-0.30	0.61
Ile	212	A	A	.	B	.	.	.	1.02	-0.30	.	.	.	0.45	1.22
Gln	213	A	A	.	B	.	.	.	0.77	-0.73	*	.	.	0.75	1.80
Arg	214	A	A	.	B	.	.	.	1.08	-0.59	.	*	F	0.90	1.62
Lys	215	A	A	.	D	.	.	.	0.26	-0.77	*	.	F	0.90	3.14
Lys	216	A	A	.	B	.	.	.	0.37	-0.81	*	.	F	0.90	1.35
Val	217	.	A	B	B	.	.	.	0.91	-0.43	*	.	.	0.30	0.60
His	218	.	A	B	B	.	.	.	0.91	-0.00	*	.	.	0.30	0.29
Val	219	.	A	B	B	.	.	.	0.80	-0.00	*	.	.	0.30	0.25
Phe	220	.	.	B	B	.	.	.	-0.06	-0.00	*	.	.	0.30	0.57
Gly	221	A	.	.	D	.	.	.	-0.40	0.04	.	*	.	-0.30	0.35
Asp	222	A	-0.36	-0.07	*	.	.	0.50	0.63
Glu	223	A	-1.18	-0.03	*	.	.	0.50	0.60
Leu	224	A	.	.	B	.	.	.	-0.63	-0.17	.	.	.	0.30	0.45
Ser	225	A	.	.	B	.	.	.	-0.74	-0.11	.	.	.	0.30	0.39
Leu	226	A	.	.	B	.	.	.	-1.10	0.57	.	*	.	-0.60	0.18

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TABLE I-continued

Res Position	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
Val	227	A	.	B	.	.	.	-0.99	1.36	.	*	.	-0.60	0.19
Thr	228	A	.	B	.	.	.	-1.66	0.67	*	*	.	-0.60	0.28
Leu	229	A	.	B	.	.	.	-1.73	0.86	*	.	.	-0.60	0.18
Phe	230	A	.	B	.	.	.	-1.43	0.86	*	.	.	-0.60	0.17
Arg	231	A	.	B	.	.	.	-0.67	0.61	*	.	.	-0.60	0.21
Cys	232	.	.	B	T	.	.	-0.37	0.53	*	.	.	-0.20	0.41
Ile	233	.	.	B	T	.	.	-0.27	0.46	*	.	.	-0.20	0.46
Glu	234	.	.	B	T	.	.	0.54	0.10	*	.	.	0.10	0.37
Asn	235	.	.	B	.	C	.	0.93	0.10	*	.	.	0.05	1.19
Met	236	.	.	B	.	C	.	0.01	0.01	*	.	F	0.20	2.44
Pro	237	.	.	B	.	C	.	0.47	0.01	*	.	F	0.44	1.16
Glu	238	.	.	.	T	.	.	1.36	0.04	*	.	F	1.08	1.12
Thr	239	C	.	1.36	0.04	*	.	F	1.12	1.82
Leu	240	C	.	1.06	-0.17	*	.	F	1.96	1.89
Pro	241	.	.	.	T	.	.	0.99	-0.21	.	.	F	2.40	1.46
Asn	242	.	.	.	T	.	.	0.96	0.36	.	.	F	1.41	0.54
Asn	243	.	.	.	T	T	.	0.66	0.63	.	.	F	1.22	1.03
Ser	244	.	.	.	T	T	.	0.38	0.33	.	.	F	1.13	0.89
Cys	245	.	.	.	T	T	.	0.84	0.40	.	.	.	0.74	0.56
Tyr	246	.	.	.	T	T	.	0.17	0.43	.	.	.	0.20	0.35
Ser	247	A	-0.42	0.71	.	.	.	-0.40	0.18
Ala	248	A	A	-0.38	0.83	.	.	.	0.60	0.34
Gly	249	A	A	-0.89	0.26	.	.	.	-0.30	0.43
Ile	250	A	A	-0.22	0.19	*	.	.	-0.30	0.27
Ala	251	A	A	0.02	-0.20	*	.	.	0.30	0.46
Lys	252	A	A	-0.02	-0.70	.	.	.	0.60	0.80
Leu	253	A	A	0.57	-0.70	.	.	F	0.90	1.13
Glu	254	A	A	0.91	-1.39	.	.	F	0.90	1.87
Glu	255	A	A	0.99	-1.89	.	.	F	0.90	1.62
Gly	256	A	A	1.58	-1.20	.	*	F	0.90	1.62
Asp	257	A	A	0.72	-1.49	.	*	I	0.90	1.62
Glu	258	A	A	0.94	-0.80	*	*	F	0.75	0.77
Leu	259	A	A	0.06	-0.30	*	*	.	0.30	0.79
Gln	260	A	A	-0.16	-0.04	*	.	.	0.30	0.33
Leu	261	A	A	0.30	0.39	*	.	.	-0.30	0.30
Ala	262	A	A	0.30	0.39	*	.	.	-0.30	0.30
Ile	263	A	A	0.30	-0.30	*	.	.	0.30	0.70
Pro	264	A	.	.	.	T	.	0.52	-0.30	.	*	F	1.00	1.37
Arg	265	A	.	.	.	T	.	0.52	-0.49	*	*	F	1.00	1.37
Glu	266	A	.	.	.	T	.	0.44	-0.59	*	*	F	1.30	3.38
Asn	267	A	.	.	.	T	.	0.73	-0.59	*	*	F	1.30	1.53
Ala	268	A	0.81	-0.63	*	*	.	0.95	1.05
Gln	269	A	1.02	0.06	*	*	.	-0.10	0.50
Ile	270	A	0.57	0.06	.	*	.	0.15	0.52
Ser	271	C	.	0.57	0.09	*	.	.	0.60	0.51
Leu	272	C	.	-0.29	-0.41	*	*	F	1.60	0.49
Asp	273	.	.	.	T	T	.	-0.01	-0.17	.	*	F	2.25	0.52
Gly	274	.	.	.	T	T	.	-0.71	-0.37	.	*	F	2.50	0.56
Asp	275	.	.	.	T	T	.	-0.52	0.03	.	*	F	1.65	0.59
Val	276	A	.	.	.	T	.	-0.57	0.13	.	*	F	1.00	0.30
Thr	277	A	.	B	.	.	.	-0.34	0.56	.	*	.	-0.10	0.30
Phe	278	A	.	B	.	.	.	-1.16	0.63	.	*	.	-0.35	0.18
Phe	279	A	.	B	.	.	.	-0.77	1.31	.	*	.	-0.60	0.20
Gly	280	A	A	-1.58	0.67	.	*	.	-0.60	0.28
Ala	281	A	A	-1.53	0.87	.	*	.	-0.60	0.27
Leu	282	A	A	-1.61	0.77	.	*	.	-0.60	0.26
Lys	283	A	A	-1.30	0.41	.	*	.	-0.60	0.33
Leu	284	A	A	-0.99	0.41	.	*	.	-0.60	0.42
Leu	285	A	A	-1.03	0.34	.	*	.	-0.30	0.65

Additional preferred nucleic acid fragments of the present invention include nucleic acid molecules comprising, or alternatively, consisting of a sequence encoding one or more epitope-bearing portions of Neutrokin- α . In particular, such nucleic acid fragments of the present invention include nucleic acid molecules comprising, or alternatively consisting of, a sequence encoding a polypeptide selected from: from about Phe-115 to about Leu-147, from about Ile-150 to about Tyr-163, from about Ser-171 to about Phe-194, from about Glu-223 to about Tyr-246, and from about Ser-271 to about Phe-278, of the amino acid sequence of SEQ ID NO:2. In this context, "about" means the particularly recited ranges and ranges larger or smaller by several, a few, 5, 4, 3, 2 or 1 amino acid residues at either or both the amino- and carboxy-

termini. Polypeptides encoded by these nucleic acid molecules are also encompassed by the invention. Polypeptide fragments which bear antigenic epitopes of the Neutrokin- α may be easily determined by one of skill in the art using the above-described analysis of the Jameson-Wolf antigenic index, as shown in FIG. 3. Methods for determining other such epitope-bearing portions of Neutrokin- α are described in detail below.

Additional preferred nucleic acid fragments of the present invention include nucleic acid molecules comprising, or alternatively consisting of a sequence encoding one or more epitope-bearing portions of Neutrokin- α SV. In particular, such nucleic acid fragments of the present invention include nucleic acid molecules comprising, or alternatively

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consisting of a sequence encoding a polypeptide selected from about Pro-32 to about Leu-47, from about Glu-116 to about Ser-143, from about Phe-153 to about Tyr-173, from about Pro-218 to about Tyr-227, from about Ser-252 to about Thr-258, from about Ala-232 to about Gln-241, from about Ile-244 to about Ala-249, and from about Ser-252 to about Val-257, of the amino acid sequence of SEQ ID NO:19. In this context, "about" means the particularly recited ranges and ranges larger or smaller by several, a few, 5, 4, 3, 2 or 1 amino acid residues at either or both the amino- and carboxy-termini. Polypeptides encoded by these nucleic acid molecules are also encompassed by the invention. Polypeptide fragments which bear antigenic epitopes of the Neutrokin-alpha may be easily determined by one of skill in the art using the above-described analysis of the Jameson-Wolf antigenic index. Methods for determining other such epitope-bearing portions of Neutrokin-alphaSV are described in detail below.

In specific embodiments, the polynucleotides of the invention are less than 100,000 kb, 50,000 kb, 10,000 kb, 1,000 kb, 500 kb, 400 kb, 350 kb, 300 kb, 250 kb, 200 kb, 175 kb, 150 kb, 125 kb, 100 kb, 75 kb, 50 kb, 40 kb, 30 kb, 25 kb, 20 kb, 15 kb, 10 kb, 7.5 kb, or 5 kb in length.

In further embodiments, polynucleotides of the invention comprise at least 15, at least 30, at least 50, at least 100, or at least 250, at least 500, or at least 1000 contiguous nucleotides of Neutrokin-alpha coding sequence, but consist of less than or equal to 1000 kb, 500 kb, 250 kb, 200 kb, 150 kb, 100 kb, 75 kb, 50 kb, 30 kb, 25 kb, 20 kb, 15 kb, 10 kb, or 5 kb of genomic DNA that flanks the 5' or 3' coding nucleotide set forth in FIGS. 1A and 1B (SEQ ID NO:1) or FIGS. 5A and 5B (SEQ ID NO:18). In further embodiments, polynucleotides of the invention comprise at least 15, at least 30, at least 50, at least 100, or at least 250, at least 500, or at least 1000 contiguous nucleotides of Neutrokin-alpha coding sequence, but do not comprise all or a portion of any Neutrokin-alpha intron. In another embodiment, the nucleic acid comprising Neutrokin-alpha coding sequence does not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the Neutrokin-alpha gene in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

In another embodiment, the invention provides an isolated nucleic acid molecule comprising a polynucleotide which hybridizes under stringent hybridization conditions to a portion of the polynucleotide in a nucleic acid molecule of the invention described above, for instance, the sequence complementary to the coding and/or noncoding sequence depicted in FIGS. 1A and 1B (SEQ ID NO:1), the sequence of the cDNA clone contained in the deposit having ATCC accession no. 97768, the sequence complementary to the coding sequence and/or noncoding sequence depicted in FIGS. 5A and 5B (SEQ ID NO:18), the sequence of the cDNA clone contained in the deposit having ATCC accession no. 203518, the sequence complementary to the coding sequence and/or noncoding sequence (i.e., transcribed, untranslated) depicted in SEQ ID NO:21, the sequence complementary to the coding sequence and/or noncoding sequence depicted in SEQ ID NO:22, the sequence complementary to the coding sequence and/or noncoding sequence depicted in SEQ ID NO:27, the sequence complementary to the coding sequence and/or noncoding sequence depicted in SEQ ID NO:29, or fragments (such as, for example, the open reading frame or a fragment thereof) of these sequences, as described herein. By "stringent hybridization conditions" is intended overnight incubation at 42° C. in a solution comprising: 50% formamide,

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5xSSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5xDenhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1xSSC at about 65° C.

By a polynucleotide which hybridizes to a "portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridizing to at least about 15 nucleotides (nt), and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably about 30-70 (e.g., 40, 50, or 60) nucleotides, and even more preferably about any integer in the range of 30-70 or 80-150 nucleotides, or the entire length of the reference polynucleotide. These have uses, which include, but are not limited to, diagnostic probes and primers as discussed above and in more detail below. By a portion of a polynucleotide of "at least about 20 nt in length," for example, is intended to include the particularly recited ranges, larger or smaller by several (i.e. 5, 4, 3, 2, 1, or 0) amino acids, at either extreme or at both extremes of the nucleotide sequence of the reference polynucleotide (e.g., the sequence of one or both of the deposited cDNAs, the complementary strand of the nucleotide sequence shown in FIGS. 1A and 1B (SEQ ID NO:1), the complementary strand of the nucleotide sequence shown in FIGS. 5A and 5B (SEQ ID NO:18), the complementary strand of the nucleotide sequence shown in SEQ ID NO:21, the complementary strand of the nucleotide sequence shown in SEQ ID NO:22, the complementary strand of the nucleotide sequence shown in SEQ ID NO:27 and/or the complementary strand of the nucleotide sequence shown in SEQ ID NO:29). Of course, a polynucleotide which hybridizes only to a poly A sequence (such as the 3' terminal poly (A) tract of the Neutrokin-alpha cDNA shown in FIGS. 1A and 1B (SEQ ID NO:1), the 3' terminal poly(A) tract of the Neutrokin-alphaSV cDNA shown in FIGS. 5A and 5B (SEQ ID NO:18) or the 3' terminal poly(A) tract of the Neutrokin-alphaSV cDNA shown in SEQ ID NO:22), or to a complementary stretch of T (or U) residues, would not be included in a polynucleotide of the invention used to hybridize to a portion of a nucleic acid of the invention, since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

As indicated, nucleic acid molecules of the present invention which encode a Neutrokin-alpha polypeptide or a Neutrokin-alphaSV polypeptide may include, but are not limited to, polynucleotides encoding the amino acid sequence of the respective extracellular domains of the polypeptides, by themselves; and the coding sequence for the extracellular domains of the respective polypeptides and additional sequences, such as those encoding the intracellular and transmembrane domain sequences, or a pre-, pro- or prepro-protein sequence; the coding sequence of the respective extracellular domains of the polypeptides, with or without the aforementioned additional coding sequences.

Also encoded by nucleic acids of the invention are the above protein sequences together with additional, non-coding sequences, including for example, but not limited to, introns and non-coding 5' and 3' sequences, such as the transcribed, non-translated sequences that play a role in transcription, mRNA processing, including splicing and polyadenylation signals, for example, ribosome binding and stability of mRNA; an additional coding sequence which codes for additional amino acids, such as those which provide additional functionalities.

Thus, the sequence encoding the polypeptide may be fused to a marker sequence, such as a sequence encoding a peptide

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which facilitates purification of the fused polypeptide. In certain preferred embodiments of this embodiment of the invention, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, Calif. 91311), among others, many of which are commercially available. As described in Gientz et al., *Proc. Natl. Acad. Sci. USA* 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. The "HA" tag is another peptide useful for purification which corresponds to an epitope derived from the influenza hemagglutinin protein, which has been described by Wilson et al., *Cell* 37: 767 (1984). As discussed below, other such fusion proteins include the Neurokinine-alpha or the Neurokinine-alphaSV polypeptides fused to Fc at the N- or C-terminus.

The present invention further relates to variants of the nucleic acid molecules of the present invention, which encode portions, analogs or derivatives of the Neurokinine-alpha or Neurokinine-alphaSV polypeptides of SEQ ID NO:2. Variants may occur naturally, such as a natural allelic variant. By an "allelic variant" is intended one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. *Genes II*, Lewin, B., ed., John Wiley & Sons, New York (1985). Non-naturally occurring variants may be produced using art-known mutagenesis techniques, which include, but are not limited to oligonucleotide mediated mutagenesis, alanine scanning, PCR mutagenesis, site directed mutagenesis (see e.g., Carter et al., *Nucl. Acids Res.* 13:4331 (1986); and Zoller et al., *Nucl. Acids Res.* 10:6487 (1982)), cassette mutagenesis (see e.g., Wells et al., *Gene* 34:315 (1985)), restriction selection mutagenesis (see e.g., Wells et al., *Philos. Trans. R. Soc. London SerA* 317:415 (1986)).

Such variants include those produced by nucleotide substitutions, deletions or additions. The substitutions, deletions or additions may involve one or more nucleotides. The variants may be altered in coding regions, non-coding regions, or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the Neurokinine-alpha and/or Neurokinine-alphaSV polypeptides or portions thereof. Also especially preferred in this regard are conservative substitutions.

Additional embodiments of the invention are directed to isolated nucleic acid molecules comprising a polynucleotide which encodes the amino acid sequence of a Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide (e.g., a Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide fragment described herein) having an amino acid sequence which contains at least one conservative amino acid substitution, but not more than 50 conservative amino acid substitutions, even more preferably, not more than 40 conservative amino acid substitutions, still more preferably, not more than 30 conservative amino acid substitutions, and still even more preferably, not more than 20 conservative amino acid substitutions, 10-20 conservative amino acid substitutions, 5-10 conservative amino acid substitutions, 1-5 conservative amino acid substitutions, 3-5 conservative amino acid substitutions, or 1-3 conservative amino acid substitutions. Of course, in order of ever-increasing preference, it is highly preferable for a polynucleotide which encodes the amino acid sequence of a Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide to have an amino acid sequence which contains not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 conservative amino acid substitutions.

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Further embodiments include an isolated nucleic acid molecule comprising, or alternatively consisting of, a polynucleotide having a nucleotide sequence at least 80%, 85%, or 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical to a polynucleotide selected from the group consisting of: (a) a nucleotide sequence encoding the Neurokinine-alpha polypeptide having the complete amino acid sequence in FIGS. 1A and 1B (i.e., positions 1 to 285 of SEQ ID NO:2); (b) a nucleotide sequence encoding the Neurokinine-alpha polypeptide having the complete amino acid sequence in SEQ ID NO:2 excepting the N-terminal methionine (i.e., positions 2 to 285 of SEQ ID NO:2); (c) a fragment of the polypeptide of (b) having Neurokinine-alpha functional activity (e.g., antigenic or biological activity); (d) a nucleotide sequence encoding the predicted extracellular domain of the Neurokinine-alpha polypeptide having the amino acid sequence at positions 73-285 in FIGS. 1A and 1B (SEQ ID NO:2); (e) a nucleotide sequence encoding the Neurokinine-alpha polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2); (f) a nucleotide sequence encoding the Neurokinine-alpha polypeptide having the complete amino acid sequence encoded by the cDNA clone contained in the deposit having ATCC accession number 97768; (g) a nucleotide sequence encoding the extracellular domain of the Neurokinine-alpha polypeptide having the amino acid sequence encoded by the cDNA contained in the deposit having ATCC accession number 97768; and (h) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), or (h) above. The present invention also encompasses the above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these polynucleotides and nucleic acid molecules are also encompassed by the invention.

Highly preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of a polynucleotide having a nucleotide sequence at least 80%, 85%, 90% identical and more preferably at least 95%, 96%, 97%, 98%, 99% or 100% identical to a polynucleotide sequence encoding the Neurokinine-alpha polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2). Preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of a polynucleotide having a nucleotide sequence at least 90% identical to a polynucleotide sequence encoding the Neurokinine-alpha polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2). More preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of a polynucleotide having a nucleotide sequence at least 95% identical to a polynucleotide sequence encoding the Neurokinine-alpha polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2). More preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of a polynucleotide having a nucleotide sequence at least 96% identical to a polynucleotide sequence encoding the Neurokinine-alpha polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2).

Additionally, more preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of a polynucleotide having a nucleotide sequence at least 97% to a polynucleotide sequence encoding the Neurokinine-alpha polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ

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ID NO:2). Additionally, more preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of a polynucleotide having a nucleotide sequence at least 98% to a polynucleotide sequence encoding the Neurokinine-alpha polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2). Additionally, more preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of a polynucleotide having a nucleotide sequence at least 99% identical to a polynucleotide sequence encoding the Neurokinine-alpha polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2).

A further embodiment of the invention relates to an isolated nucleic acid molecule comprising a polynucleotide which encodes the amino acid sequence of a Neurokinine-alphaSV polypeptide (e.g., a Neurokinine-alphaSV polypeptide fragment described herein) having an amino acid sequence which contains at least one conservative amino acid substitution, but not more than 50 conservative amino acid substitutions, even more preferably, not more than 40 conservative amino acid substitutions, still more preferably not more than 30 conservative amino acid substitutions, and still even more preferably not more than 20 conservative amino acid substitutions. Of course, in order of ever-increasing preference, it is highly preferable for a polynucleotide which encodes the amino acid sequence of a Neurokinine-alpha polypeptide to have an amino acid sequence which contains not more than 7-10, 5-10, 3-7, 3-5, 2-5, 1-5, 1-3, 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 conservative amino acid substitutions.

Further embodiments include an isolated nucleic acid molecule comprising, or alternatively, consisting of a polynucleotide having a nucleotide sequence at least 80%, 85% or 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical to a polynucleotide selected from the group consisting of: (a) a nucleotide sequence encoding the Neurokinine-alphaSV polypeptide having the complete amino acid sequence in FIGS. 5A and 5B (i.e., positions 1 to 266 of SEQ ID NO:19); (b) a nucleotide sequence encoding the Neurokinine-alphaSV polypeptide having the complete amino acid sequence in SEQ ID NO:19 excepting the N-terminal methionine (i.e., positions 2 to 266 of SEQ ID NO:2); (c) a nucleotide sequence encoding the predicted extracellular domain of the Neurokinine-alphaSV polypeptide having the amino acid sequence at positions 73-285 in FIGS. 5A and 5B (SEQ ID NO:19); (d) a nucleotide sequence encoding the Neurokinine-alphaSV polypeptide having the complete amino acid sequence encoded by the cDNA clone contained in the deposit having ATCC accession number 203518; (e) a nucleotide sequence encoding the extracellular domain of the Neurokinine-alphaSV polypeptide having the amino acid sequence encoded by the cDNA clone contained in the deposit having ATCC accession number 203518; and (f) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), (c), (d) or (e), above.

Further, the invention includes a polynucleotide comprising, or alternatively, consisting of, a sequence at least 90%, or at least 95%, identical to any portion of at least about 10 contiguous nucleotides, about 20 contiguous nucleotides, about 25 contiguous nucleotides, or about 30 contiguous nucleotides, preferably at least about 40 nucleotides, or at least about 50 nucleotides, of the sequence from nucleotide 1 to nucleotide 1082 in FIGS. 1A and 1B (SEQ ID NO:1), preferably excluding the nucleotide sequences determined from the above-listed 4 cDNA clones and the nucleotide sequences from nucleotide 797 to 1082, 810 to 1082, and 346 to 542. The invention also includes a polynucleotide comprising,

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ing, or alternatively consisting of, a sequence at least 90%, or at least 95%, identical to any portion of at least about 10 contiguous nucleotides, about 20 contiguous nucleotides, about 25 contiguous nucleotides, or about 30 contiguous nucleotides, preferably at least about 40 nucleotides, or at least about 50 nucleotides, of the sequence in FIGS. 5A and 5B (SEQ ID NO:18), preferably excluding the nucleotide sequences determined from the above-listed 4 cDNA clones. The invention also includes a polynucleotide comprising, or alternatively consisting of a sequence at least 90%, or at least 95%, identical to any portion of at least about 10 contiguous nucleotides, about 20 contiguous nucleotides, about 25 contiguous nucleotides, or about 30 contiguous nucleotides, preferably at least about 40 nucleotides, or at least about 50 nucleotides, of the sequence in SEQ ID NO:21, preferably excluding the nucleotide sequences determined from the above-listed 4 cDNA clones. The invention also includes a polynucleotide comprising a sequence at least 90%, or at least 95%, identical to any portion of at least about 10 contiguous nucleotides, about 20 contiguous nucleotides, about 25 contiguous nucleotides, or about 30 contiguous nucleotides, preferably at least about 40 nucleotides, or at least about 50 nucleotides, of the sequence in SEQ ID NO:22, preferably excluding the nucleotide sequences determined from the above-listed 4 cDNA clones. The invention also includes a polynucleotide comprising a sequence at least 90%, or at least 95%, identical to any portion of at least about 10 contiguous nucleotides, about 20 contiguous nucleotides, about 25 contiguous nucleotides, or about 30 contiguous nucleotides, preferably at least about 40 nucleotides, or at least about 50 nucleotides, of the sequence in SEQ ID NO:27, preferably excluding the nucleotide sequences determined from the above-listed 4 cDNA clones. The invention also includes a polynucleotide comprising a sequence at least 90%, or at least 95%, identical to any portion of at least about 10 contiguous nucleotides, about 20 contiguous nucleotides, about 25 contiguous nucleotides, or about 30 contiguous nucleotides, preferably at least about 40 nucleotides, or at least about 50 nucleotides, of the sequence in SEQ ID NO:29, preferably excluding the nucleotide sequences determined from the above-listed 4 cDNA clones. In this context "about" includes the particularly recited ranges, larger or smaller by several (i.e. 5, 4, 3, 2 or 1) amino acids, at either extreme or at both extremes.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence encoding a Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five mismatches per each 100 nucleotides of the reference nucleotide sequence encoding the Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence. The reference (query) sequence may be the entire nucleotide sequence encoding Neurokinine-alpha or Neurokinine-alphaSV, as shown in FIGS. 1A and 1B (SEQ ID

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NO:1) and FIGS. 5A and 5B (SEQ ID NO:18), respectively, or any Neutrokin- α such as, for example, the Neutrokin- α polynucleotides shown as SEQ ID NOs:21, 22, 27, or 28, or any Neutrokin- α or Neutrokin- α SV polynucleotide fragment as described herein.

As a practical matter, whether any particular nucleic acid molecule is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the nucleotide sequences shown in FIGS. 1A and 1B, or the nucleotide sequences shown in FIGS. 5A and 5B, or to the nucleotide sequence of the deposited cDNA clones, or to any Neutrokin- α polynucleotide such as, for example, the Neutrokin- α polynucleotides shown as SEQ ID NOs:21, 22, 27, or 28, or fragments thereof, can be determined conventionally using known computer programs such as the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, Wis. 53711). Bestfit uses the local homology algorithm of Smith and Waterman to find the best segment of homology between two sequences (Advances in Applied Mathematics 2:482-489 (1981)). When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference nucleotide sequence and that gaps in homology of up to 5% of the total number of nucleotides in the reference sequence are allowed.

In a specific embodiment, the identity between a reference (query) sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, is determined using the FASTDB computer program based on the algorithm of Brutlag and colleagues (Comp. App. Biosci. 6:237-245 (1990)). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter. According to this embodiment, if the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction is made to the results to take into consideration the fact that the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. A determination of whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of this embodiment. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score. For example, a 90 base subject sequence is aligned to a 100 base query sequence to

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determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are made for the purposes of this embodiment.

The present application is directed to nucleic acid molecules at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequences (i.e., polynucleotides) disclosed herein (e.g., those disclosed in FIGS. 1A and 1B (SEQ ID NO:1) or to the nucleic acid sequence of the deposited cDNAs), irrespective of whether they encode a polypeptide having Neutrokin- α and/or Neutrokin- α SV functional activity (e.g., biological activity). In addition, the present application is also directed to nucleic acid molecules at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence shown in FIGS. 5A and 5B (SEQ ID NO:18) or to the nucleic acid sequence of the deposited cDNA, irrespective of whether they encode a polypeptide having Neutrokin- α SV activity. Moreover, the present application is also directed to nucleic acid molecules at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98%, 99% identical to the nucleic acid sequence shown in SEQ ID NOs:21, 22, 27 or 28, irrespective of whether they encode a polypeptide having Neutrokin- α activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having Neutrokin- α and/or Neutrokin- α SV activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe or a polymerase chain reaction (PCR) primer. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having Neutrokin- α and/or Neutrokin- α SV activity include, inter alia, (1) isolating the Neutrokin- α and/or Neutrokin- α SV gene or allelic variants thereof in a cDNA library; (2) in situ hybridization (e.g., "FISH") to metaphase chromosomal spreads to provide precise chromosomal location of the Neutrokin- α and/or Neutrokin- α SV gene, as described in Verma et al., *Human Chromosomes: A Manual of Basic Techniques*, Pergamon Press, New York (1988); and Northern Blot analysis for detecting Neutrokin- α and/or Neutrokin- α SV mRNA expression in specific tissues.

Preferred, however, are nucleic acid molecules having sequences at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequences disclosed herein (e.g., the nucleotide sequence shown in FIGS. 1A and 1B (SEQ ID NO:1) and the nucleic acid sequence of the deposited cDNAs, or fragments thereof), which do, in fact, encode a polypeptide having Neutrokin- α and/or Neutrokin- α SV polypeptide functional activity (e.g., biological activity). Also preferred are nucleic acid molecules having sequences at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence shown in FIGS. 5A and 5B (SEQ ID NO:18) or to the nucleic

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acid sequence of the deposited cDNA which do, in fact, encode a polypeptide having Neutrokinine-alpha and/or Neutrokinine-alphaSV polypeptide functional activity (e.g., biological activity). Also preferred are nucleic acid molecules having sequences at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence shown SEQ ID NOs:21, 22, 27, or 28, which do, in fact, encode a polypeptide having Neutrokinine-alpha and/or Neutrokinine-alphaSV polypeptide functional activity (e.g., biological activity).

By "a polypeptide having Neutrokinine-alpha polypeptide functional activity" (e.g., biological activity) and "a polypeptide having Neutrokinine-alphaSV polypeptide functional activity" (e.g., biological activity) are intended polypeptides exhibiting activity similar, but not necessarily identical, to an activity of the extracellular domain or the full-length Neutrokinine-alpha or Neutrokinine-alphaSV polypeptides of the invention, as measured in a particular functional assay (e.g., immunological or biological assay). For example, Neutrokinine-alpha and/or Neutrokinine-alphaSV polypeptide functional activity can be measured by the ability of a polypeptide sequence described herein to form multimers (e.g., homodimers and homotrimers) with the complete Neutrokinine-alpha and/or Neutrokinine-alphaSV or extracellular domain of Neutrokinine-alpha and/or Neutrokinine-alphaSV, and to bind a Neutrokinine-alpha and/or Neutrokinine-alphaSV ligand Neutrokinine-alpha and/or Neutrokinine-alphaSV polypeptide functional activity can be also be measured by determining the ability of a polypeptide of the invention to induce lymphocyte (e.g., B cell) proliferation, differentiation or activation and/or to extend B cell survival. These functional assays can be routinely performed using techniques described herein (e.g., see Example 6) and otherwise known in the art. Additionally, Neutrokinine-alpha or Neutrokinine-alphaSV polypeptides of the present invention modulate cell proliferation, cytotoxicity, cell survival and cell death. An in vitro cell proliferation, cytotoxicity, cell survival, and cell death assay for measuring the effect of a protein on certain cells can be performed by using reagents well known and commonly available in the art for detecting cell replication and/or death. For instance, numerous such assays for TNF-related protein activities are described in the various references in this disclosure. Briefly, an example of such an assay involves collecting human or animal (e.g., mouse) cells and mixing with (1) transfected host cell-supernatant containing Neutrokinine-alpha protein (or a candidate polypeptide) or (2) nontransfected host cell-supernatant control, and measuring the effect on cell numbers or viability after incubation of certain period of time. Such cell proliferation and/or survival modulation activities as can be measure in this type of assay are useful for treating tumor, tumor metastasis, infections, autoimmune diseases, inflammation and other immune-related diseases.

Neutrokinine-alpha modulates cell proliferation and differentiation in a dose-dependent manner in the above-described assay. Accordingly, it is preferred that "a polypeptide having Neutrokinine-alpha polypeptide functional activity" (e.g., biological activity) includes polypeptides that also exhibit any of the same cell modulatory (particularly immunomodulatory) activities in the above-described assays in a dose-dependent manner. Although the degree of dose-dependent activity need not be identical to that of the Neutrokinine-alpha polypeptides, preferably, "a polypeptide having Neutrokinine-alpha polypeptide functional activity" will exhibit substantially similar dose-dependence in a given activity as compared to the Neutrokinine-alpha polypeptides (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold

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less and, preferably, not more than about tenfold less activity relative to the reference Neutrokinine-alpha polypeptides).

In certain preferred embodiments, "a polypeptide having Neutrokinine-alpha polypeptide functional activity" (e.g., biological activity) and "a polypeptide having Neutrokinine-alphaSV polypeptide functional activity" (e.g., biological activity) includes polypeptides that also exhibit any of the same B cell (or other cell type) modulatory (particularly immunomodulatory) activities described in FIGS. 8A, 8B, 9A, 9B, 10A, 10B, 10C, 10D, 10E, 10F, 10G, 11A, 11B, and 11C and in Example 6.

Like other members of TNF family, Neutrokinine-alpha exhibits activity on leukocytes including, for example, monocytes, lymphocytes (e.g., B cells) and neutrophils. For this reason Neutrokinine-alpha is active in directing the proliferation, differentiation and migration of these cell types. Such activity is useful for immune enhancement or suppression, myeloprotection, stem cell mobilization, acute and chronic inflammatory control and treatment of leukemia. Assays for measuring such activity are known in the art. For example, see Peters et al., *Immun. Today* 17:273 (1996); Young et al., *J. Exp. Med.* 182:1111 (1995); Caux et al., *Nature* 390:258 (1992); and Santiago-Schwarz et al., *Adv. Exp. Med. Biol.* 378:7 (1995).

Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequence contained in cDNA clone deposited in ATCC accession no. 97768, or the nucleic acid sequence shown in FIGS. 1A and 1B (SEQ ID NO:1), or fragments thereof, will encode a polypeptide "having Neutrokinine-alpha polypeptide functional activity" (e.g., biological activity). One of ordinary skill in the art will also immediately recognize that a large number of the nucleic acid molecules having a sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequence contained in cDNA clone deposited in ATCC accession no. 203518 or the nucleic acid sequence shown in FIGS. 5A and 5B (SEQ ID NO:18) will encode a polypeptide "having Neutrokinine-alphaSV polypeptide functional activity" (e.g., biological activity). In fact, since degenerate variants of these nucleotide sequences all encode the same polypeptide, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having Neutrokinine-alpha and/or Neutrokinine-alphaSV activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

Similarly, polynucleotides encoding polypeptides which contain all or some portion of the region V-142 through K-160 of SEQ ID NO:2 are likely to be valuable diagnostic and therapeutic polynucleotides with regard to detecting and/or altering expression of either Neutrokinine-alpha or Neutrokinine-alphaSV polynucleotides. In addition, polynucleotides which span the junction of amino acid residues T-141 and G-142 of the Neutrokinine-alphaSV polypeptide shown in SEQ ID NO:19 (in between which the V-142 through K-160 amino acid sequence of Neutrokinine-alpha is apparently inserted), are also likely to be useful both diagnostically and therapeutically. Such T-141/G-142 spanning polynucleotides will exhibit a much higher likelihood of hybridization with Neutrokinine-alphaSV polynucleotides than with Neutrokinine-alpha

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pha polynucleotides. A partial, non-limiting, non-exclusive list of such Neurokinine-alphaSV polypeptides which are encoded by polynucleotides of the invention includes polypeptides comprising, or alternatively consisting of, an amino acid sequence selected from the following: G-121 through E-163; E-122 through E-163; G-123 through E-163; N-124 through E-163; S-125 through E-163; S-126 through E-163; Q-127 through E-163; N-128 through E-163; S-129 through E-163; R-130 through E-163; N-131 through E-163; K-132 through E-163; R-133 through E-163; A-134 through E-163; V-135 through E-163; Q-136 through E-163; G-137 through E-163; P-138 through E-163; E-139 through E-163; E-140 through E-163; T-141 through E-163; G-142 through E-163; S-143 through E-163; Y-144 through E-163; T-145 through E-163; F-146 through E-163; V-147 through E-163; P-148 through E-163; W-149 through E-163; L-150 through E-163; L-151 through E-163; S-152 through E-163; F-153 through E-163; K-154 through E-163; R-155 through E-163; G-156 through E-163; S-157 through E-163; A-158 through E-163; L-159 through E-163; E-160 through E-163; E-161 through E-163; K-162 through E-163; G-121 through K-162; G-121 through E-161; G-121 through E-160; G-121 through L-159; G-121 through A-158; G-121 through S-157; G-121 through G-156; G-121 through R-155; G-121 through K-154; G-121 through F-153; G-121 through S-152; G-121 through L-151; G-121 through L-150; G-121 through W-149; G-121 through P-148; G-121 through V-147; G-121 through F-146; G-121 through T-145; G-121 through Y-144; G-121 through S-143; G-121 through G-142; G-121 through T-141; G-121 through E-140; G-121 through E-139; G-121 through P-138; G-121 through G-137; G-121 through Q-136; G-121 through V-135; G-121 through A-134; G-121 through R-133; G-121 through K-132; G-121 through N-131; G-121 through R-130; G-121 through S-129; G-121 through N-128; G-121 through Q-127; G-121 through S-126; G-121 through S-125; G-121 through N-124; G-121 through G-123; and G-121 through E-122 of SEQ ID NO:19. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

Vectors and Host Cells

The present invention also relates to vectors which include the isolated DNA molecules of the present invention, host cells which are genetically engineered with the recombinant vectors, or which are otherwise engineered to produce the polypeptides of the invention, and the production of Neurokinine-alpha and/or Neurokinine-alphaSV polypeptides, or fragments thereof, by recombinant or synthetic techniques.

In one embodiment, the polynucleotides of the invention are joined to a vector (e.g., a cloning or expression vector). The vector may be, for example, a phage, plasmid, viral or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells. The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Introduction of the vector construct into the host cell can be effected by techniques known in the art which include, but are not limited to, calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., *Basic Methods In Molecular Biology* (1986).

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be

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derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, for example, stabilization or simplified purification of expressed recombinant product.

In one embodiment, the DNA of the invention is operatively associated with an appropriate heterologous regulatory element (e.g., promoter or enhancer), such as, the phage lambda P1 promoter, the *E. coli* lac, trp, phoA, and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in *E. coli* and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as *E. coli*, *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells (e.g., *Saccharomyces cerevisiae* or *Pichia pastoris* (ATCC Accession No. 201178)); insect cells such as *Drosophila* S2 and *Spodoptera* S19 cells; animal cells such as CHO, COS, 293 and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

The host cell can be a higher eukaryotic cell, such as a mammalian cell (e.g., a human derived cell), or a lower eukaryotic cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. The host strain may be chosen which modulates the expression of the inserted gene sequences, or modifies and processes the gene product in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus expression of the genetically engineered polypeptide may be controlled. Furthermore, different host cells have characteristics and specific mechanisms for the translational and post-translational processing and modification (e.g., phosphorylation, cleavage) of proteins. Appropriate cell lines can be chosen to ensure the desired modifications and processing of the foreign protein expressed. Selection of appropriate vectors and promoters for expression in a host cell is a well-known procedure and the requisite techniques for expression vector construction, introduction of the vector into the host and expression in the host are routine skills in the art.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium*, and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice. As a representative, but nonlimiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well-

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known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM1 (Promega Biotec, Madison, Wis., USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Among vectors preferred for use in bacteria include pIE4-5 (ATCC Accession No. 209311; and variations thereof), pQE70, pQE60 and pQE-9, available from QIAGEN, Inc., supra; pBS vectors, Phagescript vectors, Bluescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene; and pirc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia. Preferred expression vectors for use in yeast systems include, but are not limited to, pYES2, pYDI1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalpha, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, pPIC9K, and PA0815 (all available from Invitrogen, Carlsbad, Calif.). Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL (available from Pharmacia). Other suitable vectors will be readily apparent to the skilled artisan.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents, such methods are well known to those skilled in the art.

In one embodiment, the yeast *Pichia pastoris* is used to express Neurokinine-alpha protein in a eukaryotic system. *Pichia pastoris* is a methylotrophic yeast which can metabolize methanol as its sole carbon source. A main step in the methanol metabolism pathway is the oxidation of methanol to formaldehyde using O₂. This reaction is catalyzed by the enzyme alcohol oxidase. In order to metabolize methanol as its sole carbon source, *Pichia pastoris* must generate high levels of alcohol oxidase due, in part, to the relatively low affinity of alcohol oxidase for O₂. Consequently, in a growth medium depending on methanol as a main carbon source, the promoter region of one of the two alcohol oxidase genes (AOX1) is highly active. In the presence of methanol, alcohol oxidase produced from the AOX1 gene comprises up to approximately 30% of the total soluble protein in *Pichia pastoris*. See, Ellis, S. B., et al., *Mol. Cell. Biol.* 5:1111-21 (1985); Koutz, P. J. et al., *Yeast* 5:167-77 (1989); Tschopp, J. F., et al., *Nucl. Acids Res.* 15:3859-76 (1987). Thus, a heterologous coding sequence, such as, for example, a Neurokinine-alpha or Neurokinine-alphaSV polynucleotide of the present invention, under the transcriptional regulation of all or part of the AOX1 regulatory sequence is expressed at exceptionally high levels in *Pichia* yeast grown in the presence of methanol.

In one example, the plasmid vector pPIC9K is used to express DNA encoding a Neurokinine-alpha or Neurokinine-alphaSV polypeptide of the invention, as set forth herein, in a *Pichia* yeast system essentially as described in "*Pichia* Protocols: Methods in Molecular Biology," D. R. Higgins and J. Cregg, eds. The Humana Press, Totowa, N.J., 1998. This expression vector allows expression and secretion of a Neurokinine-alpha or Neurokinine-alphaSV protein of the invention by virtue of the strong AOX1 promoter linked to the *Pichia pastoris* alkaline phosphatase (PHO) secretory signal peptide (i.e., leader) located upstream of a multiple cloning site.

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Many other yeast vectors could be used in place of pPIC9K, such as, pYES2, pYDI1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalpha, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, and PA0815, as one skilled in the art would readily appreciate, as long as the proposed expression construct provides appropriately located signals for transcription, translation, secretion (if desired), and the like, including an in-frame AUG as required.

In one embodiment, high-level expression of a heterologous coding sequence, such as, for example, a Neurokinine-alpha or Neurokinine-alphaSV polynucleotide of the present invention, may be achieved by cloning the heterologous polynucleotide of the invention into an expression vector such as, for example, pGAPZ or pGAPZalpha, and growing the yeast culture in the absence of methanol.

Transcription of the DNA encoding the polypeptides of the present invention by higher eukaryotes is increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp that act on a promoter to increase its transcription. Examples including the SV40 enhancer on the late side of the replication origin bp 100 to 270, a cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman (*Cell* 23:175 (1981)), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

In a specific embodiment, constructs designed to express a portion of the extracellular domain of the Neurokinine-alpha (e.g., amino acid residues Ala-134 through Leu-285) are preferred. One of skill in the art would be able to use the polynucleotide and polypeptide sequences provided as SEQ ID NO:1 and SEQ ID NO:2, respectively, or SEQ ID NO:18 and SEQ ID NO:19, respectively, to design polynucleotide primers to generate such an expression construct.

In another embodiment, constructs designed to express the entire predicted extracellular domain of the Neurokinine-alpha (i.e., amino acid residues Gln-73 through Leu-285) are preferred. One of skill in the art would be able to use the polynucleotide and polypeptide sequences provided as SEQ ID NO:1 and SEQ ID NO:2, respectively, or SEQ ID NO:18 and SEQ ID NO:19, respectively, to design polynucleotide primers to generate such an expression construct.

In addition to encompassing host cells containing the vector constructs discussed herein, the invention also encompasses primary, secondary, and immortalized host cells of vertebrate origin, particularly mammalian origin, that have been engineered to delete or replace endogenous genetic material (e.g., Neurokinine-alpha coding sequence), and/or to include genetic material (e.g., heterologous polynucleotide sequences) that is operably associated with Neurokinine-alpha polynucleotides of the invention, and which activates, alters, and/or amplifies endogenous Neurokinine-alpha polynucleotides. For example, techniques known in the art may be used to operably associate heterologous control regions (e.g., promoter and/or enhancer) and endogenous Neurokinine-alpha

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polynucleotide sequences via homologous recombination (see, e.g., U.S. Pat. No. 5,641,670, issued Jun. 24, 1997; International Publication No. WO 96/29411, published Sep. 26, 1996; International Publication No. WO 94/12650, published Aug. 4, 1994; Koller et al., *Proc. Natl. Acad. Sci. USA* 86:8932-8935 (1989); and Zijlstra et al., *Nature* 342:435-438 (1989), the disclosures of each of which are incorporated by reference in their entireties).

The host cells described *infra* can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Alternatively, cell-free translation systems can also be employed to produce the polypeptides of the invention using RNAs derived from the DNA constructs of the present invention.

The polypeptide of the invention may be expressed or synthesized in a modified form, such as a fusion protein (comprising the polypeptide joined via a peptide bond to a heterologous protein sequence (of a different protein)), and may include not only secretion signals, but also additional heterologous functional regions. Such a fusion protein can be made by ligating polynucleotides of the invention and the desired nucleic acid sequence encoding the desired amino acid sequence to each other, by methods known in the art, in the proper reading frame, and expressing the fusion protein product by methods known in the art. Alternatively, such a fusion protein can be made by protein synthetic techniques, e.g., by use of a peptide synthesizer. Thus, for instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence in the host cell, during purification, or during subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to polypeptides to engender secretion or excretion, to improve stability and to facilitate purification, among others, are familiar and routine techniques in the art.

In one embodiment, polynucleotides encoding Neurokinine-alpha and/or Neurokinine-alphaSV polypeptides of the invention may be fused to the polB pectate lyase signal sequence to increase the efficiency to expression and purification of such polypeptides in Gram-negative bacteria. See, U.S. Pat. Nos. 5,576,195 and 5,846,818, the contents of which are herein incorporated by reference in their entireties.

A preferred fusion protein comprises a heterologous region from immunoglobulin that is useful to stabilize and purify proteins. For example, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is thoroughly advantageous for use in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). On the other hand, for some uses it would be desirable to be able to delete the Fc part after the fusion protein has been expressed, detected and purified in the advantageous manner described. This is the case when Fc portion proves to be a hindrance to use in therapy and diagnosis, for example when the fusion protein is to be used as antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5 has been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. See, D. Bennett et al., *J. Molecular Recognition* 8:52-58 (1995) and K. Johanson et al., *J. Biol. Chem.* 270:9459-9471 (1995).

Polypeptides of the present invention include naturally purified products, products of chemical synthetic procedures,

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and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes.

Polypeptides of the invention can be chemically synthesized using techniques known in the art (e.g., see Creighton, 1983, *Proteins: Structures and Molecular Principles*, W.H. Freeman & Co., N.Y., and Hunkapiller, M., et al., 1984, *Nature* 310:105-111). For example, a peptide corresponding to a fragment of the complete Neurokinine-alpha or Neurokinine-alphaSV polypeptides of the invention can be synthesized by use of a peptide synthesizer. Furthermore, if desired, nonclassical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the Neurokinine-alpha or Neurokinine-alphaSV polynucleotide sequence. Non-classical amino acids include, but are not limited to, the D-isomers of the common amino acids, 2,4-diaminobutyric acid, α -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, β -Abu, ϵ -Ahu, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteine acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, β -alanine, fluoro-amino acids, designer amino acids such as β -methyl amino acids, Ca-methyl amino acids, Na-methyl amino acids, and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

The invention encompasses Neurokinine-alpha or Neurokinine-alphaSV polypeptides which are differentially modified during or after translation, e.g., by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications may be carried out by known techniques, including but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH_4 , acetylation, formylation, oxidation, reduction, metabolic synthesis in the presence of tunicamycin, etc.

Additional post-translational modifications encompassed by the invention include, for example, e.g., N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends, attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of prokaryotic host cell expression. The polypeptides may also be modified with a detectable label, such as an enzymatic, fluorescent, isotopic or affinity label to allow for detection and isolation of the protein. In addition, polypeptides of the invention may be modified by iodination.

In one embodiment, Neurokinine-alpha and/or Neurokinine-alphaSV polypeptides of the invention may also be labeled with biotin. In other related embodiments, biotinylated Neurokinine-alpha and/or Neurokinine-alphaSV polypeptides of the invention may be used, for example, as an imaging agent or as a means of identifying, one or more Neurokinine-alpha and/or Neurokinine-alphaSV receptor(s) or other coreceptor or

coligand molecules. Also provided by the invention are chemically modified derivatives of Neurokinine-alpha or Neurokinine-alphaSV

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which may provide additional advantages such as increased solubility, stability and in vivo or in vitro circulating time of the polypeptide, or decreased immunogenicity (see U.S. Pat. No. 4,179,337). The chemical moieties for derivatization may be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol and the like. The polypeptides may be modified at random positions within the molecule, or at predetermined positions within the molecule and may include one, two, three or more attached chemical moieties.

The polymer may be of any molecular weight, and may be branched or unbranched. For polyethylene glycol, the preferred molecular weight is between about 1 kDa and about 100 kDa (the term "about" indicating that in preparations of polyethylene glycol, some molecules will weigh more, some less, than the stated molecular weight) for ease in handling and manufacturing. Other sizes may be used, depending on the desired therapeutic profile (e.g., the duration of sustained release desired, the effects, if any on biological activity, the ease in handling, the degree or lack of antigenicity and other known effects of the polyethylene glycol to a therapeutic protein or analog). For example, the polyethylene glycol may have an average molecular weight of about 200, 500, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 8500, 9000, 9500, 10,000, 10,500, 11,000, 11,500, 12,000, 12,500, 13,000, 13,500, 14,000, 14,500, 15,000, 15,500, 16,000, 16,500, 17,000, 17,500, 18,000, 18,500, 19,000, 19,500, 20,000, 25,000, 30,000, 35,000, 40,000, 50,000, 55,000, 60,000, 65,000, 70,000, 75,000, 80,000, 85,000, 90,000, 95,000, or 100,000 kDa.

As noted above, the polyethylene glycol may have a branched structure. Branched polyethylene glycols are described, for example, in U.S. Pat. No. 5,643,575; Morpurgo et al., *Appl. Biochem. Biotechnol.* 56:59-72 (1996); Vorobjev et al., *Nucleosides Nucleotides* 18:2745-2750 (1999); and Caliceti et al., *Bioconjug. Chem.* 10:638-646 (1999), the disclosures of each of which are incorporated herein by reference.

The polyethylene glycol molecules (or other chemical moieties) should be attached to the protein with consideration of effects on functional or antigenic domains of the protein. There are a number of attachment methods available to those skilled in the art, e.g., EP 0 401 384, herein incorporated by reference (coupling PEG to G-CSF), see also Malik et al., *Exp. Hematol.* 20:1028-1035 (1992) (reporting pegylation of GM-CSF using tresyl chloride). For example, polyethylene glycol may be covalently bound through amino acid residues via a reactive group, such as, a free amino or carboxyl group. Reactive groups are those to which an activated polyethylene glycol molecule may be bound. The amino acid residues having a free amino group may include, for example, lysine residues and the N-terminal amino acid residues; those having a free carboxyl group may include aspartic acid residues, glutamic acid residues, and the C-terminal amino acid residue. Sulfhydryl groups may also be used as a reactive group for attaching the polyethylene glycol molecules. Preferred for therapeutic purposes is attachment at an amino group, such as attachment at the N-terminus or lysine group.

As suggested above, polyethylene glycol may be attached to proteins via linkage to any of a number of amino acid residues. For example, polyethylene glycol can be linked to a proteins via covalent bonds to lysine, histidine, aspartic acid, glutamic acid, or cysteine residues. One or more reaction chemistries may be employed to attach polyethylene glycol to specific amino acid residues (e.g., lysine, histidine, aspartic acid, glutamic acid, or cysteine) of the protein or to more than

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one type of amino acid residue (e.g., lysine, histidine, aspartic acid, glutamic acid, cysteine and combinations thereof) of the protein.

One may specifically desire proteins chemically modified at the N-terminus. Using polyethylene glycol as an illustration, one may select from a variety of polyethylene glycol molecules (by molecular weight, branching, etc.), the proportion of polyethylene glycol molecules to protein (or peptide) molecules in the reaction mix, the type of pegylation reaction to be performed, and the method of obtaining the selected N-terminally pegylated protein. The method of obtaining the N-terminally pegylated preparation (i.e., separating this moiety from other monopegylated moieties if necessary) may be by purification of the N-terminally pegylated material from a population of pegylated protein molecules. Selective proteins chemically modified at the N-terminus modification may be accomplished by reductive alkylation which exploits differential reactivity of different types of primary amino groups (lysine versus the N-terminal) available for derivatization in a particular protein. Under the appropriate reaction conditions, substantially selective derivatization of the protein at the N-terminus with a carbonyl group containing polymer is achieved.

As indicated above, pegylation of the proteins of the invention may be accomplished by any number of means. For example, polyethylene glycol may be attached to the protein either directly or by an intervening linker. Linkerless systems for attaching polyethylene glycol to proteins are described in Delgado et al., *Crit. Rev. Ther. Drug Carrier Sys.* 9:249-304 (1992); Francis et al., *Intern. J. of Hematol.* 68:1-18 (1998); U.S. Pat. No. 4,002,531; U.S. Pat. No. 5,349,052; WO 95/06058; and WO 98/32466, the disclosures of each of which are incorporated herein by reference.

One system for attaching polyethylene glycol directly to amino acid residues of proteins without an intervening linker employs tresylated MPEG, which is produced by the modification of monomethoxy polyethylene glycol (MPEG) using tresylchloride ($\text{ClSO}_2\text{CH}_2\text{CF}_3$). Upon reaction of protein with tresylated MPEG, polyethylene glycol is directly attached to amine groups of the protein. Thus, the invention includes protein-polyethylene glycol conjugates produced by reacting proteins of the invention with a polyethylene glycol molecule having a 2,2,2-trifluoroethane sulphonyl group.

Polyethylene glycol can also be attached to proteins using a number of different intervening linkers. For example, U.S. Pat. No. 5,612,460, the entire disclosure of which is incorporated herein by reference, discloses urethane linkers for connecting polyethylene glycol to proteins. Protein-polyethylene glycol conjugates wherein the polyethylene glycol is attached to the protein by a linker can also be produced by reaction of proteins with compounds such as MPEG-succinimidylsuccinate, MPEG activated with 1,1'-carbonyldiimidazole, MPEG-2,4,5-trichloropentylcarbonate, MPEG-p-nitrophenolcarbonate, and various MPEG-succinate derivatives. A number additional polyethylene glycol derivatives and reaction chemistries for attaching polyethylene glycol to proteins are described in WO 98/32466, the entire disclosure of which is incorporated herein by reference. Pegylated protein products produced using the reaction chemistries set out herein are included within the scope of the invention.

The number of polyethylene glycol moieties attached to each protein of the invention (i.e., the degree of substitution) may also vary. For example, the pegylated proteins of the invention may be linked, on average, to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, or more polyethylene glycol molecules. Similarly, the average degree of substitution within ranges such as 1-3, 2-4, 3-5, 4-6, 5-7, 6-8, 7-9, 8-10, 9-11, 10-12,

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11-13, 12-14, 13-15, 14-16, 15-17, 16-18, 17-19, or 18-20 polyethylene glycol moieties per protein molecule. Methods for determining the degree of substitution are discussed, for example, in Delgado et al., *Crit. Rev. Ther. Drug Carrier Sys.* 9:249-304 (1992).

The Neutrokin- α and/or Neutrokin- α SV polypeptides can be recovered and purified by known methods which include, but are not limited to, ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Neutrokin- α Polypeptides

The Neutrokin- α and/or Neutrokin- α SV polypeptides of the invention may be in monomers or multimers (i.e., dimers, trimers, tetramers and higher multimers). Accordingly, the present invention relates to monomers and multimers of the Neutrokin- α and/or Neutrokin- α SV polypeptides of the invention, their preparation, and compositions (preferably, pharmaceutical compositions) containing them. In specific embodiments, the polypeptides of the invention are monomers, dimers, trimers or tetramers. In additional embodiments, the multimers of the invention are at least dimers, at least trimers, or at least tetramers.

Multimers encompassed by the invention may be homomers or heteromers. As used herein, the term homomer refers to a multimer containing only Neutrokin- α and/or Neutrokin- α SV polypeptides of the invention (including Neutrokin- α and/or Neutrokin- α SV fragments, variants, and fusion proteins, as described herein). These homomers may contain Neutrokin- α and/or Neutrokin- α SV polypeptides having identical or different amino acid sequences. In a specific embodiment, a homomer of the invention is a multimer containing only Neutrokin- α and/or Neutrokin- α SV polypeptides having an identical amino acid sequence. In another specific embodiment, a homomer of the invention is a multimer containing Neutrokin- α and/or Neutrokin- α SV polypeptides having different amino acid sequences. In specific embodiments, the multimer of the invention is a homodimer (e.g., containing Neutrokin- α and/or Neutrokin- α SV polypeptides having identical or different amino acid sequences) or a homotrimer (e.g., containing Neutrokin- α and/or Neutrokin- α SV polypeptides having identical or different amino acid sequences). In a preferred embodiment, the multimer of the invention is a homotrimer. In additional embodiments, the homomeric multimer of the invention is at least a homodimer, at least a homotrimer, or at least a homotetramer.

As used herein, the term heteromer refers to a multimer containing heterologous polypeptides (i.e., polypeptides of a different protein) in addition to the Neutrokin- α and/or Neutrokin- α SV polypeptides of the invention. In a specific embodiment, the multimer of the invention is a heterodimer, a heterotrimer, or a heterotetramer. In additional embodiments, the heteromeric multimer of the invention is at least a heterodimer, at least a heterotrimer, or at least a heterotetramer. In a further nonexclusive embodiment, the heteromers of the invention contain CD40 ligand polypeptide sequence(s), or biologically active fragment(s) or variant(s) thereof.

Multimers of the invention may be the result of hydrophobic, hydrophilic, ionic and/or covalent associations and/or may be indirectly linked, by for example, liposome formation. Thus, in one embodiment, multimers of the invention,

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such as, for example, homodimers or homotrimers, are formed when polypeptides of the invention contact one another in solution. In another embodiment, heteromultimers of the invention, such as, for example, heterotrimers or heterotetramers, are formed when polypeptides of the invention contact antibodies to the polypeptides of the invention (including antibodies to the heterologous polypeptide sequence in a fusion protein of the invention) in solution. In other embodiments, multimers of the invention are formed by covalent associations with and/or between the Neutrokin- α and/or Neutrokin- α SV polypeptides of the invention. Such covalent associations may involve one or more amino acid residues contained in the polypeptide sequence (e.g., that recited in SEQ ID NO: 2 or SEQ ID NO: 19, or contained in the polypeptide encoded by the clones deposited in connection with this application). In one instance, the covalent associations are cross-linking between cysteine residues located within the polypeptide sequences which interact in the native (i.e., naturally occurring) polypeptide. In another instance, the covalent associations are the consequence of chemical or recombinant manipulation. Alternatively, such covalent associations may involve one or more amino acid residues contained in the heterologous polypeptide sequence in a Neutrokin- α and/or Neutrokin- α SV fusion protein. In one example, covalent associations are between the heterologous sequence contained in a fusion protein of the invention (see, e.g., U.S. Pat. No. 5,478,925). In a specific example, the covalent associations are between the heterologous sequence contained in a Neutrokin- α -Fc and/or Neutrokin- α -Fc fusion protein of the invention (as described herein). In another specific example, covalent associations of fusion proteins of the invention are between heterologous polypeptide sequence from another TNF family ligand/receptor member that is capable of forming covalently associated multimers, such as for example, osteoprotegerin (see, e.g., International Publication No. WO 98/49305, the contents of which are herein incorporated by reference in its entirety). In another specific example, covalent associations of fusion proteins of the invention are between heterologous polypeptide sequence from CD40L, or a soluble fragment thereof. In another embodiment, two or more Neutrokin- α and/or Neutrokin- α polypeptides of the invention are joined through synthetic linkers (e.g., peptide, carbohydrate or soluble polymer linkers). Examples include those peptide linkers described in U.S. Pat. No. 5,073,627 (hereby incorporated by reference). Proteins comprising multiple Neutrokin- α and/or Neutrokin- α SV polypeptides separated by peptide linkers may be produced using conventional recombinant DNA technology.

Another method for preparing multimer Neutrokin- α and/or Neutrokin- α SV polypeptides of the invention involves use of Neutrokin- α and/or Neutrokin- α SV polypeptides fused to a leucine zipper or isoleucine zipper polypeptide sequence. Leucine zipper or isoleucine zipper domains are polypeptides that promote multimerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz et al., *Science* 240:1759, (1988)), and have since been found in a variety of different proteins. Among the known leucine zippers or isoleucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble multimeric Neutrokin- α and/or Neutrokin- α SV proteins are those described in PCT application WO 94/10308, hereby incorporated by reference. Recombinant fusion proteins comprising a soluble Neutrokin- α and/or Neutrokin- α SV polypeptide fused

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to a peptide that dimerizes or trimerizes in solution are expressed in suitable host cells, and the resulting soluble multimeric Neurokinine-alpha and/or Neurokinine-alphaSV is recovered from the culture supernatant using techniques known in the art.

Certain members of the TNF family of proteins are believed to exist in trimeric form (Beutler and Hufnagel, *Science* 264:667, 1994; Banner et al., *Cell* 73:431, 1993). Thus, trimeric Neurokinine-alpha and/or Neurokinine-alphaSV may offer the advantage of enhanced biological activity. Preferred leucine zipper moieties are those that preferentially form trimers. One example is a leucine zipper derived from lung surfactant protein D (SPD), as described in Hoppe et al. (*FEBS Letters* 344:191, (1994)) and in U.S. patent application Ser. No. 08/446,922, hereby incorporated by reference. Other peptides derived from naturally occurring trimeric proteins may be employed in preparing trimeric Neurokinine-alpha and/or Neurokinine-alphaSV.

In another example, proteins of the invention are associated by interactions between the Flag® polypeptide sequence contained in Flag®-Neurokinine-alpha or Flag®-Neurokinine-alphaSV fusion proteins of the invention. In a further embodiment, proteins of the invention are associated by interactions between the heterologous polypeptide sequence contained in Flag®-Neurokinine-alpha or Flag®-Neurokinine-alphaSV fusion proteins of the invention and anti-Flag® antibody.

The multimers of the invention may be generated using chemical techniques known in the art. For example, polypeptides desired to be contained in the multimers of the invention may be chemically cross-linked using linker molecules and linker molecule length optimization techniques known in the art (see, e.g., U.S. Pat. No. 5,478,925, which is herein incorporated by reference in its entirety). Additionally, multimers of the invention may be generated using techniques known in the art to form one or more inter-molecule cross-links between the cysteine residues located within the sequence of the polypeptides desired to be contained in the multimer (see, e.g., U.S. Pat. No. 5,478,925, which is herein incorporated by reference in its entirety). Further, polypeptides of the invention may be routinely modified by the addition of cysteine or biotin to the C terminus or N-terminus of the polypeptide and techniques known in the art may be applied to generate multimers containing one or more of these modified polypeptides (see, e.g., U.S. Pat. No. 5,478,925, which is herein incorporated by reference in its entirety). Additionally, techniques known in the art may be applied to generate liposomes containing the polypeptide components desired to be contained in the multimer of the invention (see, e.g., U.S. Pat. No. 5,478,925, which is herein incorporated by reference in its entirety).

Alternatively, multimers of the invention may be generated using genetic engineering techniques known in the art. In one embodiment, polypeptides contained in multimers of the invention are produced recombinantly using fusion protein technology described herein or otherwise known in the art (see, e.g., U.S. Pat. No. 5,478,925, which is herein incorporated by reference in its entirety). In a specific embodiment, polynucleotides coding for a homodimer of the invention are generated by ligating a polynucleotide sequence encoding a polypeptide of the invention to a sequence encoding a linker polypeptide and then further to a synthetic polynucleotide encoding the translated product of the polypeptide in the reverse orientation from the original C-terminus to the N-terminus (lacking the leader sequence) (see, e.g., U.S. Pat. No. 5,478,925, which is herein incorporated by reference in its entirety). In another embodiment, recombinant techniques described herein or otherwise known in the art are applied to

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generate recombinant polypeptides of the invention which contain a transmembrane domain and which can be incorporated by membrane reconstitution techniques into liposomes (see, e.g., U.S. Pat. No. 5,478,925, which is herein incorporated by reference in its entirety).

In one embodiment, the invention provides an isolated Neurokinine-alpha polypeptide having the amino acid sequence encoded by the cDNA clone contained in ATCC No. 97768, or the amino acid sequence in FIGS. 1A and 1B (SEQ ID NO:2), or a polypeptide comprising a portion (i.e., a fragment) of the above polypeptides. In another embodiment, the invention provides an isolated Neurokinine-alphaSV polypeptide having the amino acid encoded by the cDNA clone contained in ATCC No. 203518, or the amino acid sequence in FIGS. 5A and 5B (SEQ ID NO:19), or a polypeptide comprising a portion (i.e., fragment) of the above polypeptides.

Polypeptide fragments of the present invention include polypeptides comprising or alternatively, consisting of, an amino acid sequence contained in SEQ ID NO:2, encoded by the cDNA contained in the plasmid having ATCC accession number 97768, or encoded by nucleic acids which hybridize (e.g., under stringent hybridization conditions) to the nucleotide sequence contained in the deposited clone, or the complementary strand of the nucleotide sequence shown in FIGS. 1A-B (SEQ ID NO:1).

Additionally, polypeptide fragments of the present invention include polypeptides comprising or alternatively, consisting of, an amino acid sequence contained in SEQ ID NO:19, encoded by the cDNA contained in the plasmid having ATCC accession number 203518, or encoded by nucleic acids which hybridize (e.g., under stringent hybridization conditions) to the nucleotide sequence contained in the deposited clone, or the complementary strand of the nucleotide sequence shown in FIGS. 5A-B (SEQ ID NO:18).

Additionally, polypeptide fragments of the present invention include polypeptides comprising or alternatively, consisting of, an amino acid sequence encoded by nucleic acids which hybridize (e.g., under hybridization conditions described herein) to the complementary strand of the nucleotide sequence shown in SEQ ID NO:21.

Polypeptide fragments of the present invention also include polypeptides comprising or alternatively, consisting of, an amino acid sequence contained in SEQ ID NO:23, or encoded by nucleic acids which hybridize (e.g., under hybridization conditions described herein) to the complementary strand of the nucleotide sequence shown in SEQ ID NO:22.

In addition, polypeptide fragments of the present invention include polypeptides comprising or alternatively, consisting of, an amino acid sequence contained in SEQ ID NO:28, or encoded by nucleic acids which hybridize (e.g., under hybridization conditions described herein) to the complementary strand of the nucleotide sequence shown in SEQ ID NO:27.

Additionally, polypeptide fragments of the present invention include polypeptides comprising or alternatively, consisting of, an amino acid sequence contained in SEQ ID NO:30, or encoded by nucleic acids which hybridize (e.g., under hybridization conditions described herein) to the complementary strand of the nucleotide sequence shown in SEQ ID NO:29.

Polypeptide fragments of the present invention include polypeptides comprising or alternatively, consisting of, an amino acid sequence contained in SEQ ID NO:2, encoded by the cDNA contained in the deposited clone, or encoded by nucleic acids which hybridize (e.g., under stringent hybridization conditions) to the nucleotide sequence contained in the deposited clone, or shown in FIGS. 1A and 1B (SEQ ID NO:1) or the complementary strand thereto. Protein frag-

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ments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments that comprise or alternatively, consist of from about amino acid residues: 1 to 50, 51 to 100, 101 to 150, 151 to 200, 201 to 250, and/or 251 to 285 of SEQ ID NO:2. Moreover, polypeptide fragments can be at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 175 or 200 amino acids in length.

In specific embodiments, polypeptide fragments of the invention comprise, or alternatively consist of, amino acid residues: 1-46, 31-44, 47-72, 73-285, 73-83, 94-102, 148-152, 166-181, 185-209, 210-221, 226-237, 244-249, 253-265, and/or 277-284, as depicted in FIGS. 1A and 1B (SEQ ID NO:2). Polynucleotides encoding these polypeptides are also encompassed by the invention.

It will be recognized by one of ordinary skill in the art that mutations targeted to regions of a Neutrokin-alpha polypeptide of the invention which encompass the nineteen amino acid residue insertion which is not found in the Neutrokin-alphaSV polypeptide sequence (i.e., amino acid residues Val-142 through Lys-160 of the sequence presented in FIGS. 1A and 1B and in SEQ ID NO:2) may affect the observed biological activities of the Neutrokin-alpha polypeptide. More specifically, a partial, non-limiting and non-exclusive list of such residues of the Neutrokin-alpha polypeptide sequence which may be targeted for mutation includes the following amino acid residues of the Neutrokin-alpha polypeptide sequence as shown in SEQ ID NO:2: V-142; T-143; Q-144; D-145; C-146; L-147; Q-148; L-149; I-150; A-151; D-152; S-153; E-154; T-155; P-156; T-157; I-158; Q-159; and K-160. Polynucleotides encoding Neutrokin-alpha polypeptides which have one or more mutations in the region from V-142 through K-160 of SEQ ID NO:2 are contemplated. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

Polypeptide fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments that comprise or alternatively, consist of from about amino acid residues: 1 to 15, 16-30, 31-46, 47-55, 56-72, 73-104, 105-163, 163-188, 186-210 and 210-284 of the amino acid sequence disclosed in SEQ ID NO:2. Additional representative examples of polypeptide fragments of the invention, include, for example, fragments that comprise or alternatively, consist of from about amino acid residues: 1 to 143, 1-150, 47-143, 47-150, 73-143, 73-150, 100-150, 140-145, 142-148, 140-150, 140-200, 140-225, and 140-266 of the amino acid sequence disclosed in SEQ ID NO:19. Moreover, polypeptide fragments can be at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 175 or 200 amino acids in length. In this context, "about" means the particularly recited ranges and ranges larger or smaller by several, a few, 5, 4, 3, 2 or 1 amino acid residues at either or both the amino- and carboxy-termini. Polynucleotides encoding these polypeptide fragments are also encompassed by the invention.

Additional preferred embodiments encompass polypeptide fragments comprising, or alternatively consisting of, the predicted intracellular domain of Neutrokin-alpha (amino acid residues 1-46 of SEQ ID NO:2), the predicted transmembrane domain of Neutrokin-alpha (amino acid residues 47-72 of SEQ ID NO:2), the predicted extracellular domain of Neutrokin-alpha (amino acid residues 73-285 of SEQ ID NO:2), the predicted TNF conserved domain of Neutrokin-

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alpha (amino acids 191 to 284 of SEQ ID NO:2), and a polypeptide comprising, or alternatively, consisting of the predicted intracellular domain fused to the predicted extracellular domain of Neutrokin-alpha (amino acid residues 1-46 fused to amino acid residues 73-285 of SEQ ID NO:2). Polynucleotides encoding these polypeptides are also encompassed by the invention.

Further additional preferred embodiments encompass polypeptide fragments comprising, or alternatively consisting of, the predicted intracellular domain of Neutrokin-alphaSV (amino acid residues 1-46 of SEQ ID NO:19), the predicted transmembrane domain of Neutrokin-alphaSV (amino acid residues 47-72 of SEQ ID NO:19), the predicted extracellular domain of Neutrokin-alphaSV (amino acid residues 73-266 of SEQ ID NO:19), the predicted TNF conserved domain of Neutrokin-alphaSV (amino acids 172 to 265 of SEQ ID NO:19), and a polypeptide comprising, or alternatively, consisting of the predicted intracellular domain fused to the predicted extracellular domain of Neutrokin-alphaSV (amino acid residues 1-46 fused to amino acid residues 73-266 of SEQ ID NO:19). Polynucleotides encoding these polypeptides are also encompassed by the invention.

Certain additional embodiments of the invention encompass polypeptide fragments comprising, or alternatively consisting of, the predicted beta-pleated sheet regions identified in FIGS. 7A-1 and 7A-2. These polypeptide fragments of the invention comprise, or alternatively consist of, amino acid residues Gln-144 to Ala-151, Phe-172 to Lys-173, Ala-177 to Glu-179, Asn-183 to Ile-185, Gly-191 to Lys-204, His-210 to Val-219, Leu-226 to Pro-237, Asn-242 to Ala-251, Gly-256 to Ile-263 and/or Val-276 to Leu-284 of SEQ ID NO:2. In another, nonexclusive embodiment, these polypeptide fragments of the invention also comprise, or alternatively consist of, amino acid residues Phe-153 to Lys-154, Ala-158 to Glu-160, Asn-164 to Ile-166, Gly-172 to Lys-185, His-191 to Val-200, Leu-207 to Pro-218, Asn-223 to Ala-232, Gly-237 to Ile-244 and/or Val-257 to Leu-265 of SEQ ID NO:19; and amino acid residues Phe-42 to Lys-43, Ala-47 to Glu-49, Asn-53 to Ile-55, Gly-61 to Pro-74, His-80 to Val-89, Leu-96 to Pro-107, Asn-112 to Ala-121, Gly-126 to Ile-133 and/or Asp-146 to Leu-154 of SEQ ID NO:23. In further nonexclusive embodiments, these polypeptide fragments of the invention also comprise, or alternatively consist of, amino acid residues Gln-78 to Ala-85; Phe-106 to Lys-107, Ala-111 to Glu-113, Asn-117 to Ile-119, Gly-125 to Lys-138, His-144 to Val-153, Leu-160 to Pro-171, Asn-176 to Ala-185, Gly-190 to Ile-197 and/or Val-210 to Leu-218 of SEQ ID NO:28; and amino acid residues Gln-78 to Ala-85; Phe-106 to Lys-107, Ala-111 to Glu-113, Asn-117 to Ile-119, Gly-125 to Lys-138, His-144 to Val-153, Leu-160 to Pro-171, Asn-176 to Ala-185, Gly-190 to Ile-197 and/or Val-210 to Leu-218 of SEQ ID NO:30. Polynucleotides encoding these polypeptide fragments are also provided.

A partial, non-limiting, and exemplary list of polypeptides of the invention which comprise, or alternatively consist of, combinations of amino acid sequences of the invention includes, for example, [Met-1 to Lys-113] fused to [Leu-114 to Thr-141] fused to [Ile-142 to Lys-160] fused to [Gly-161 to Gln-198] fused to [Val-199 to Ala-248] fused to [Gly-250 to Leu-285] of SEQ ID NO:2; [Met-1 to Lys-113] fused to [Ile-142 to Lys-160] fused to [Gly-161 to Gln-198] fused to [Val-199 to Ala-248] fused to [Gly-250 to Leu-285] of SEQ ID NO:2; or [Met-1 to Lys-113] fused to [Leu-114 to Thr-141] fused to [Ile-142 to Lys-160] fused to [Gly-161 to Gln-198] fused to [Gly-250 to Leu-285] of SEQ ID NO:2. Other combinations may include the polypeptide fragments in an order other than that recited above (e.g., [Leu-114 to Thr-141]

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fused to [Val-199 to Ala-248] fused to [Gly-250 to Leu-285] fused to [Ile-142 to Lys-160] of SEQ ID NO:2). Other combinations may also include heterologous polypeptide fragments as described herein and/or other polypeptides or polypeptide fragments of the present invention (e.g., [Met-1 to Lys-113] fused to [Leu-114 to Thr-141] fused to [Ile-142 to Lys-160] fused to [Gly-161 to Gln-198] fused to [Gly-250 to Leu-285] of SEQ ID NO:2 fused to a FLAG tag). Polynucleotides encoding any of these polypeptides are encompassed by the invention.

An additional partial, non-limiting, and exemplary list of polypeptides of the invention which comprise, or alternatively consist of, combinations of amino acid sequences includes, for example, [Met-1 to Lys-113] fused to [Leu-114 to Thr-141] fused to [Gly-142 to Gln-179] fused to [Val-180 to Ala-229] fused to [Gly-230 to Leu-266] of SEQ ID NO:19; [Met-1 to Lys-113] fused to [Gly-142 to Gln-179] fused to [Val-180 to Ala-229] fused to [Gly-230 to Leu-266] of SEQ ID NO:19; or [Met-1 to Lys-113] fused to [Leu-114 to Thr-141] fused to [Gly-142 to Gln-179] fused to [Gly-230 to Leu-266] of SEQ ID NO:19. Other combinations may include the polypeptide fragments in an order other than that recited above (e.g., [Leu-114 to Thr-141] fused to [Val-180 to Ala-229] fused to [Gly-230 to Leu-266] fused to [Gly-142 to Gln-179] of SEQ ID NO:19). Other combinations may also include heterologous polypeptide fragments as described herein and/or other polypeptides or polypeptide fragments of the present invention (e.g., [Met-1 to Lys-113] fused to [Leu-114 to Thr-141] fused to [Gly-142 to Gln-179] fused to [Gly-230 to Leu-266] of SEQ ID NO:19 fused to a FLAG tag). Polynucleotides encoding any of these polypeptides are encompassed by the invention.

A further partial, non-limiting, and exemplary list of polypeptides of the invention which comprise, or alternatively consist of, combinations of amino acid sequences includes, for example, [Met-1 to Lys-106] fused to [Leu-107 to Thr-134] fused to [Ile-167 to Lys-184] fused to [Gly-185 to Gln-224] fused to [Val-225 to Ala-272] fused to [Gly-273 to Leu-309] of SEQ ID NO:23; [Met-1 to Lys-106] fused to [Glu-135 to Asn-165] fused to [Ile-167 to Lys-184] fused to [Gly-185 to Gln-224] fused to [Val-225 to Ala-272] fused to [Gly-273 to Leu-309] of SEQ ID NO:23; or [Met-1 to Lys-106] fused to [Leu-107 to Thr-134] fused to [Glu-135 to Asn-165] fused to [Ile-167 to Lys-184] fused to [Gly-185 to Gln-224] fused to [Gly-273 to Leu-309] of SEQ ID NO:23. Other combinations may include the polypeptide fragments in an order other than that recited above (e.g., [Met-1 to Lys-106] fused to [Gly-185 to Gln-224] fused to [Ile-167 to Lys-184] fused to [Val-225 to Ala-272] fused to [Leu-107 to Thr-134] fused to [Gly-273 to Leu-309] of SEQ ID NO:23). Other combinations may also include heterologous polypeptide fragments as described herein and/or other polypeptides or polypeptide fragments of the present invention (e.g., [Met-1 to Lys-106] fused to [Glu-135 to Asn-165] fused to [Ile-167 to Lys-184] fused to [Gly-185 to Gln-224] fused to [Val-225 to Ala-272] fused to [Gly-273 to Leu-309] of SEQ ID NO:39 fused to a FLAG tag). Polynucleotides encoding any of these polypeptides are encompassed by the invention.

A further partial, non-limiting, and exemplary list of polypeptides of the invention which comprise, or alternatively consist of, combinations of amino acid sequences includes, for example, [Tyr-1 to Lys-47] fused to [Leu-48 to Thr-75] fused to [Ile-76 to Lys-94] fused to [Gly-95 to Gln-132] fused to [Val-133 to Ala-182] fused to [Gly-183 to Ala-219] of SEQ ID NO:28; [Tyr-1 to Lys-47] fused to [Leu-48 to Thr-75] fused to [Ile-76 to Lys-94] fused to [Val-133 to Ala-182] of SEQ ID NO:28; or [Tyr-1 to Lys-47] fused to

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[Ile-76 to Lys-94] fused to [Val-133 to Ala-182] fused to [Gly-183 to Ala-219] of SEQ ID NO:28. Other combinations may include the polypeptide fragments in an order other than that recited above (e.g., [Tyr-1 to Lys-47] fused to [Gly-183 to Ala-219] fused to [Val-133 to Ala-182] fused to [Leu-48 to Thr-75] of SEQ ID NO:28). Other combinations may also include heterologous polypeptide fragments as described herein and/or other polypeptides or polypeptide fragments of the present invention (e.g., [Leu-48 to Thr-75] fused to [Ile-76 to Lys-94] fused to [Gly-95 to Gln-132] fused to [Val-133 to Ala-182] of SEQ ID NO:28 fused to an Fc receptor tag). Polynucleotides encoding any of these polypeptides are encompassed by the invention.

A further partial, non-limiting, and exemplary list of polypeptides of the invention which comprise, or alternatively consist of, combinations of amino acid sequences includes, for example, [Tyr-1 to Lys-47] fused to [Leu-48 to Thr-75] fused to [Ile-76 to Lys-94] fused to [Gly-95 to Gln-132] fused to [Val-133 to Ala-182] fused to [Gly-183 to Ala-219] of SEQ ID NO:30; [Tyr-1 to Lys-47] fused to [Leu-48 to Thr-75] fused to [Ile-76 to Lys-94] fused to [Val-133 to Ala-182] of SEQ ID NO:30; or [Tyr-1 to Lys-47] fused to [Ile-76 to Lys-94] fused to [Val-133 to Ala-182] fused to [Gly-183 to Ala-219] of SEQ ID NO:30. Other combinations may include the polypeptide fragments in an order other than that recited above (e.g., [Tyr-1 to Lys-47] fused to [Gly-183 to Ala-219] fused to [Val-133 to Ala-182] fused to [Leu-48 to Thr-75] of SEQ ID NO:30). Other combinations may also include heterologous polypeptide fragments as described herein and/or other polypeptides or polypeptide fragments of the present invention (e.g., [Leu-48 to Thr-75] fused to [Ile-76 to Lys-94] fused to [Gly-95 to Gln-132] fused to [Val-133 to Ala-182] of SEQ ID NO:30 fused to an Fc receptor tag). Polynucleotides encoding any of these polypeptides are encompassed by the invention.

Additional embodiments of the invention encompass Neutrokin- α and/or Neutrokin- α SV polypeptide fragments comprising, or alternatively consisting of, functional regions of polypeptides of the invention, such as the Garnier-Robson α -regions, β -regions, turn-regions, and coil-regions, Chou-Fasman α -regions, β -regions, and coil-regions, Kyte-Doolittle hydrophilic regions and hydrophobic regions, Eisenberg α - and β -amphipathic regions, Karplus-Schulz flexible regions, Emini surface-forming regions and Jameson-Wolf regions of high antigenic index set out in FIGS. 3 and 6 and in Table I and as described herein. In a preferred embodiment, the polypeptide fragments of the invention are antigenic. The data presented in columns VIII, IX, XIII, and XIV of Table I can be used to routinely determine regions of Neutrokin- α which exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from the data presented in columns VIII, IX, XIII, and/or IV by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response. Among highly preferred fragments of the invention are those that comprise regions of Neutrokin- α and/or Neutrokin- α SV that combine several structural features, such as several (e.g., 1, 2, 3 or 4) of the features set out above. Polynucleotides encoding these polypeptides are also encompassed by the invention.

In another embodiment, the invention provides a polypeptide comprising, or alternatively consisting of, an epitope-bearing portion of a polypeptide of the invention. Polynucleotides encoding these polypeptides are also encompassed by the invention. The epitope of this polypeptide portion is an

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immunogenic or antigenic epitope of a polypeptide of the invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein is the immunogen. (On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. See, for instance, Geysen et al., *Proc. Natl. Acad. Sci. USA* 81:3998-4002 (1983).

As to the selection of polypeptides bearing an antigenic epitope (i.e., that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, for instance, Sutcliffe, J. G., Shinnick, T. M., Green, N. and Leamer, R. A. (1983) "Antibodies that react with predetermined sites on proteins", *Science*, 219:660-666. Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (i.e., immunogenic epitopes) nor to the amino or carboxyl terminals. Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind specifically to a polypeptide of the invention. See, for instance, Wilson et al., *Cell* 37:767-778 (1984) at 777.

Antigenic epitope-bearing peptides and polypeptides of the invention preferably contain a sequence of at least 4, at least 5, at least 6, at least 7, more preferably at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 20, at least 25, at least 30, at least 40, at least 50, and, most preferably, between about 15 to about 30 amino acids contained within the amino acid sequence of a polypeptide of the invention. Preferred polypeptides comprising immunogenic or antigenic epitopes are at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 amino acid residues in length. Additional non-exclusive preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as portions thereof.

Non-limiting examples of antigenic polypeptides or peptides that can be used to generate Neurokinine- α - and/or Neurokinine- α SV-specific antibodies include: a polypeptide comprising, or alternatively consisting of, amino acid residues from about Phe-115 to about Leu-147 in FIGS. 1A and 1B (SEQ ID NO:2); a polypeptide comprising, or alternatively consisting of, amino acid residues from about Ile-150 to about Tyr-163 in FIGS. 1A and 1B (SEQ ID NO:2); a polypeptide comprising, or alternatively consisting of, amino acid residues from about Ser-171 to about Phe-194 in FIGS. 1A and 1B (SEQ ID NO:2); a polypeptide comprising, or alternatively consisting of, amino acid residues from about Glu-223 to about Tyr-246 in FIGS. 1A and 1B (SEQ ID NO:2); and a polypeptide comprising, or alternatively consisting of, amino acid residues from about Ser-271 to about Phe-278 in FIGS. 1A and 1B (SEQ ID NO:2). In this context, "about" means the particularly recited ranges and ranges larger or smaller by several, a few, 5, 4, 3, 2 or 1 amino acid residues at either or both the amino- and carboxy-terminals. These polypeptide fragments have been determined to bear antigenic epitopes of the Neurokinine- α polypeptide by the analysis of the Jameson-Wolf antigenic index, as shown in FIG. 3 and Table I, above.

Non-limiting examples of antigenic polypeptides or peptides that can be used to generate Neurokinine- α - and/or Neurokinine- α SV-specific antibodies include: a polypep-

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ptide comprising, or alternatively consisting of, amino acid residues from about Pro-32 to about Leu-47 in FIGS. 5A and 5B (SEQ ID NO:19); a polypeptide comprising, or alternatively consisting of, amino acid residues from about Glu-116 to about Ser-143 in FIGS. 5A and 5B (SEQ ID NO:19); a polypeptide comprising, or alternatively consisting of, amino acid residues from about Phe-153 to about Tyr-173 in FIGS. 5A and 5B (SEQ ID NO:19); a polypeptide comprising, or alternatively consisting of, amino acid residues from about Pro-218 to about Tyr-227 in FIGS. 5A and 5B (SEQ ID NO:19); a polypeptide comprising, or alternatively consisting of, amino acid residues from about Ala-232 to about Glu-241 in FIGS. 5A and 5B (SEQ ID NO:19); a polypeptide comprising, or alternatively consisting of, amino acid residues from about Ile-244 to about Ala-249 in FIGS. 5A and 5B (SEQ ID NO:19); and a polypeptide comprising, or alternatively consisting of, amino acid residues from about Ser-252 to about Val-257 in FIGS. 5A and 5B (SEQ ID NO:19). In this context, "about" means the particularly recited ranges and ranges larger or smaller by several, a few, 5, 4, 3, 2 or 1 amino acid residues at either or both the amino- and carboxy-terminals. Polynucleotides encoding these polypeptides are also encompassed by the invention. These polypeptide fragments have been determined to bear antigenic epitopes of the Neurokinine- α SV polypeptide by the analysis of the Jameson-Wolf antigenic index, as shown in FIG. 6 and a tabular representation of the data presented in FIG. 6 generated by the Protean component of the DNA*STAR computer program (as set forth above).

The epitope-bearing peptides and polypeptides of the invention may be produced by any conventional means. See, e.g., Houghten, R. A. (1985) General method for the rapid solid-phase synthesis of large numbers of peptides: specificity of antigen-antibody interaction at the level of individual amino acids. *Proc. Natl. Acad. Sci. USA* 82:5131-5135; this "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Pat. No. 4,631,211 to Houghten et al. (1986).

Epitope-bearing peptides and polypeptides of the invention have uses that include, but are not limited to, to induce antibodies according to methods well known in the art. See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow, M. et al., *Proc. Natl. Acad. Sci. USA* 82:910-914; and Bittile, F. J. et al., *J. Gen. Virol.* 66:2347-2354 (1985). Immunogenic epitope-bearing peptides of the invention, i.e., those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. See, for instance, Geysen et al., supra. Further still, U.S. Pat. No. 5,194,392 to Geysen (1990) describes a general method of detecting or determining the sequence of monomers (amino acids or other compounds) which is a topological equivalent of the epitope (i.e., a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Pat. No. 4,433,092 to Geysen (1989) describes a method of detecting or determining a sequence of monomers which is a topographical equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Pat. No. 5,480,971 to Houghten, R. A. et al. (1996) on Peralkylated Oligopeptide Mixtures discloses linear C1-C7-alkyl peralkylated oligopeptides and sets and libraries of such peptides, as well as methods for using such oligopeptide sets and libraries for determining the sequence of a peralkylated oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods.

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The present invention encompasses polypeptides comprising, or alternatively consisting of, an epitope of the polypeptide having an amino acid sequence of SEQ ID NO:2, or an epitope of the polypeptide sequence encoded by a polynucleotide sequence contained in ATCC deposit No. 97768, or encoded by a polynucleotide that hybridizes to the complement of the sequence of SEQ ID NO:1 or the cDNA sequence contained in ATCC deposit No. 97768 (e.g., under hybridization conditions described herein). The present invention further encompasses polynucleotide sequences comprising, or alternatively consisting of, a sequence encoding an epitope of a polypeptide sequence of the invention (such as, for example, the sequence disclosed in SEQ ID NO:1), polynucleotide sequences of the complementary strand of a polynucleotide sequence encoding an epitope of the invention, and polynucleotide sequences which hybridize to the complementary strand (e.g., under hybridization conditions described herein).

The present invention also encompasses polypeptides comprising, or alternatively consisting of, an epitope of the polypeptide having an amino acid sequence of SEQ ID NO:19, or an epitope of the polypeptide sequence encoded by a polynucleotide sequence contained in ATCC deposit No. 203518, or encoded by a polynucleotide that hybridizes to the complement of the sequence of SEQ ID NO:18 or the cDNA sequence contained in ATCC deposit No. 203518 (e.g., under hybridization conditions described herein). The present invention further encompasses polynucleotide sequences comprising, or alternatively consisting of, a sequence encoding an epitope of a polypeptide sequence of the invention (such as, for example, the sequence disclosed in SEQ ID NO:18), polynucleotide sequences of the complementary strand of a polynucleotide sequence encoding an epitope of the invention, and polynucleotide sequences which hybridize to the complementary strand (e.g., under hybridization conditions described herein).

The term "epitopes," as used herein, refers to portions of a polypeptide having antigenic or immunogenic activity in an animal, preferably a mammal, and most preferably in a human. In a preferred embodiment, the present invention encompasses a polypeptide comprising an epitope, as well as the polynucleotide encoding this polypeptide. An "immunogenic epitope," as used herein, is defined as a portion of a protein that elicits an antibody response in an animal, as determined by any method known in the art, for example, by the methods for generating antibodies described *infra*. (See, for example, Geysen et al., *Proc. Natl. Acad. Sci. USA* 81:3998-4002 (1983)). The term "antigenic epitope," as used herein, is defined as a portion of a protein to which an antibody can immunospecifically bind its antigen as determined by any method well known in the art, for example, by the immunoassays described herein. Immunospecific binding excludes non-specific binding but does not necessarily exclude cross-reactivity with other antigens. Antigenic epitopes need not necessarily be immunogenic.

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, *Proc. Natl. Acad. Sci. USA* 82:5131-5135 (1985), further described in U.S. Pat. No. 4,631,211).

In the present invention, antigenic epitopes preferably contain a sequence of at least 4, at least 5, at least 6, at least 7, more preferably at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 20, at least 25, at least 30, at least 40, at least 50, and, most preferably, between about 15 to about 30 amino acids. Preferred polypeptides comprising immunogenic or antigenic epitopes are at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80,

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85, 90, 95, or 100 amino acid residues in length. Additional non-exclusive preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as portions thereof. Antigenic epitopes are useful, for example, to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. Preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these antigenic epitopes. Antigenic epitopes can be used as the target molecules in immunoassays. (See, for instance, Wilson et al., *Cell* 37:767-778 (1984); Sutcliffe et al., *Science* 219:660-666 (1983)).

Similarly, immunogenic epitopes can be used, for example, to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., *supra*; Wilson et al., *supra*; Chow et al., *Proc. Natl. Acad. Sci. USA* 82:910-914; and Bittle et al., *J. Gen. Virol.* 66:2347-2354 (1985)). Preferred immunogenic epitopes include the immunogenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these immunogenic epitopes. The polypeptides comprising one or more immunogenic epitopes may be presented for eliciting an antibody response together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse), or, if the polypeptide is of sufficient length (at least about 25 amino acids), the polypeptide may be presented without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting).

Epitope-bearing polypeptides of the present invention may be used to induce antibodies according to methods well known in the art including, but not limited to, *in vivo* immunization, *in vitro* immunization, and phage display methods. See, e.g., Sutcliffe et al., *supra*; Wilson et al., *supra*, and Bittle et al., *J. Gen. Virol.* 66:2347-2354 (1985). If *in vivo* immunization is used, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine residues may be coupled to a carrier using a linker such as maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carriers using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier-coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 micrograms of peptide or carrier protein and Freund's adjuvant or any other adjuvant known for stimulating an immune response. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

As one of skill in the art will appreciate, and as discussed above, the polypeptides of the present invention comprising an immunogenic or antigenic epitope can be fused to other polypeptide sequences. For example, the polypeptides of the present invention may be fused with the constant domain of immunoglobulins (IgA, IgE, IgG, IgM), or portions thereof (CH1, CH2, CH3, or any combination thereof and portions thereof) resulting in chimeric polypeptides. Such fusion proteins may facilitate purification and may increase half-life in

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vivo. This has been shown for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. See, e.g., EP 394,827; Trautnecker et al., *Nature*, 331:84-86 (1988). Enhanced delivery of an antigen across the epithelial barrier to the immune system has been demonstrated for antigens (e.g., insulin) conjugated to an FcRn binding partner such as IgG or Fc fragments (see, e.g., PCT Publications WO 96/22024 and WO 99/04813). IgG Fusion proteins that have a disulfide-linked dimeric structure due to the IgG portion disulfide bonds have also been found to be more efficient in binding and neutralizing other molecules than monomeric polypeptides or fragments thereof alone. See, e.g., Fountoulakis et al., *J. Biochem.*, 270:3958-3964 (1995). Nucleic acids encoding the above epitopes can also be recombined with a gene of interest as an epitope tag (e.g., the hemagglutinin ("HA") tag or flag tag) to aid in detection and purification of the expressed polypeptide. For example, a system described by Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht et al., 1991, *Proc. Natl. Acad. Sci. USA* 88:8972-8977). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the open reading frame of the gene is translationally fused to an amino-terminal tag consisting of six histidine residues. The tag serves as a matrix-binding domain for the fusion protein. Extracts from cells infected with the recombinant vaccinia virus are loaded onto Ni²⁺ nitrilotriacetic acid-agarose column and histidine-tagged proteins can be selectively eluted with imidazole-containing buffers.

In another embodiment, the Neurokinine-alpha and/or Neurokinine-alphaSV polypeptides of the present invention and the epitope-bearing fragments thereof are fused with a heterologous antigen (e.g., polypeptide, carbohydrate, phospholipid, or nucleic acid). In specific embodiments, the heterologous antigen is an immunogen.

In a more specific embodiment, the heterologous antigen is the gp120 protein of HIV, or a fragment thereof. Polynucleotides encoding these polypeptides are also encompassed by the invention.

In another embodiment, the Neurokinine-alpha and/or Neurokinine-alphaSV polypeptides of the present invention and the epitope-bearing fragments thereof are fused with polypeptide sequences of another TNF ligand family member (or biologically active fragments or variants thereof). In a specific embodiment, the Neurokinine-alpha and/or Neurokinine-alphaSV polypeptides of the present invention are fused with a CD40L polypeptide sequence. In a preferred embodiment, the CD40L polypeptide sequence is soluble.

The techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling") may be employed to modulate the activities of Neurokinine-alpha and/or Neurokinine-alphaSV thereby effectively generating agonists and antagonists of Neurokinine-alpha and/or Neurokinine-alphaSV. See generally, U.S. Pat. Nos. 5,605,793, 5,811,238, 5,830,721, 5,834,252, and 5,837,458, and Patten, P. A., et al., *Curr. Opinion Biotechnol.* 8:724-33 (1997); Hamayama, S. *Trends Biotechnol.* 16(2):76-82 (1998); Hansson, L. O., et al., *J. Mol. Biol.* 287: 265-76 (1999); and Lorenzo, M. M. and Blasco, R. *Biotechniques* 24(2):308-13 (1998) (each of these patents and publications are hereby incorporated by reference). In one embodiment, alteration of Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides and corresponding polypeptides may be achieved by DNA shuffling. DNA shuffling involves the assembly of two or more DNA segments

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into a desired Neurokinine-alpha and/or Neurokinine-alphaSV molecule by homologous, or site-specific, recombination. In another embodiment, Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides and corresponding polypeptides may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of Neurokinine-alpha and/or Neurokinine-alphaSV may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc., of one or more heterologous molecules. In preferred embodiments, the heterologous molecules are, for example, TNF-alpha, lymphotoxin-alpha (LT-alpha, also known as TNF-beta), LT-beta (found in complex heterotrimer LT-alpha2-beta), OPG, FasL, CD27L, CD30L, CD40L, 4-1BBL, DcR3, OX40L, TNF-gamma (International Publication No. WO 96/14328), AIM-I (International Publication No. WO 97/33899), AIM-II (International Publication No. WO 97/34911), APRIL, (J. Exp. Med. 188(6):1185-1190), endokine-alpha (International Publication No. WO 98/07880), OPG, OX40, and nerve growth factor (NGF), and soluble forms of Fas, CD30, CD27, CD40 and 4-1BB, TR2 (International Publication No. WO 96/34095), DR3 (International Publication No. WO 97/33904), DR4 (International Publication No. WO 98/32856), TR5 (International Publication No. WO 98/30693), TR6 (International Publication No. WO 98/30694), TR7 (International Publication No. WO 98/41629), TRANK, TR9 (International Publication No. WO 98/56892), TR10 (International Publication No. WO 98/54202), 312C2 (International Publication No. WO 98/06842), TR12, CAD, and v-FLIP. In further embodiments, the heterologous molecules are any member of the TNF family.

In a preferred embodiments, Neurokinine-alpha and/or Neurokinine-alphaSV polypeptides of the invention (including biologically active fragments or variants thereof), are fused with soluble CD40L polypeptides, or biologically active fragments or variants thereof.

To improve or alter the characteristics of Neurokinine-alpha and/or Neurokinine-alphaSV polypeptides, protein engineering may be employed. Recombinant DNA technology known to those skilled in the art can be used to create novel mutant proteins or "mutants" including single or multiple amino acid substitutions, deletions, additions or fusion proteins. Such modified polypeptides can show, e.g., enhanced activity or increased stability. In addition, they may be purified in higher yields and show better solubility than the corresponding natural polypeptide, at least under certain purification and storage conditions. For instance, for many proteins, including the extracellular domain or the mature form(s) of a secreted protein, it is known in the art that one or more amino acids may be deleted from the N-terminus or C-terminus without substantial loss of biological function. For instance, Ron et al., *J. Biol. Chem.*, 268:2984-2988 (1993) reported modified KGF proteins that had heparin binding activity even if 3, 8, or 27 amino-terminal amino acid residues were missing.

In the present case, since the protein of the invention is a member of the TNF polypeptide family, deletions of N-terminal amino acids up to the Gly (G) residue at position 191 in FIGS. 1A and 1B (SEQ ID NO:2) may retain some biological activity such as, for example, the ability to stimulate lymphocyte (e.g., B cell) proliferation, differentiation, and/or activation, and cytotoxicity to appropriate target cells. Polypeptides having further N-terminal deletions including the Gly (G) residue would not be expected to retain biological activities because it is known that this residue in TNF-related polypep-

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tides is in the beginning of the conserved domain required for biological activities. However, even if deletion of one or more amino acids from the N-terminus of a protein results in modification or loss of one or more biological functions of the protein, other functional activities may still be retained. Thus, the ability of the shortened protein to induce and/or bind to antibodies which recognize the complete or extracellular domain of the protein generally will be retained when less than the majority of the residues of the complete or extracellular domain of the protein are removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete protein retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence of the Neutrokin-alpha shown in FIGS. 1A and 1B (SEQ ID NO:2), up to the glycine residue at position 191 (Gly-191 residue from the amino terminus), and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising, or alternatively consisting of, the amino acid sequence of residues n'-285 of SEQ ID NO:2, where n' is an integer in the range of the amino acid position of amino acid residues 2-190 of the amino acid sequence in SEQ ID NO:2. Polynucleotides encoding these polypeptides are also encompassed by the invention. More in particular, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, an amino acid sequence selected from the group consisting of residues 2-285, 3-285, 4-285, 5-285, 6-285, 7-285, 8-285, 9-285, 10-285, 11-285, 12-285, 13-285, 14-285, 15-285, 16-285, 17-285, 18-285, 19-285, 20-285, 21-285, 22-285, 23-285, 24-285, 25-285, 26-285, 27-285, 28-285, 29-285, 30-285, 31-285, 32-285, 33-285, 34-285, 35-285, 36-285, 37-285, 38-285, 39-285, 40-285, 41-285, 42-285, 43-285, 44-285, 45-285, 46-285, 47-285, 48-285, 49-285, 50-285, 51-285, 52-285, 53-285, 54-285, 55-285, 56-285, 57-285, 58-285, 59-285, 60-285, 61-285, 62-285, 63-285, 64-285, 65-285, 66-285, 67-285, 68-285, 69-285, 70-285, 71-285, 72-285, 73-285, 74-285, 75-285, 76-285, 77-285, 78-285, 79-285, 80-285, 81-285, 82-285, 83-285, 84-285, 85-285, 86-285, 87-285, 88-285, 89-285, 90-285, 91-285, 92-285, 93-285, 94-285, 95-285, 96-285, 97-285, 98-285, 99-285, 100-285, 101-285, 102-285, 103-285, 104-285, 105-285, 106-285, 107-285, 108-285, 109-285, 110-285, 111-285, 112-285, 113-285, 114-285, 115-285, 116-285, 117-285, 118-285, 119-285, 120-285, 121-285, 122-285, 123-285, 124-285, 125-285, 126-285, 127-285, 128-285, 129-285, 130-285, 131-285, 132-285, 133-285, 134-285, 135-285, 136-285, 137-285, 138-285, 139-285, 140-285, 141-285, 142-285, 143-285, 144-285, 145-285, 146-285, 147-285, 148-285, 149-285, 150-285, 151-285, 152-285, 153-285, 154-285, 155-285, 156-285, 157-285, 158-285, 159-285, 160-285, 161-285, 162-285, 163-285, 164-285, 165-285, 166-285, 167-285, 168-285, 169-285, 170-285, 171-285, 172-285, 173-285, 174-285, 175-285, 176-285, 177-285, 178-285, 179-285, 180-285, 181-285, 182-285, 183-285, 184-285, 185-285, 186-285, 187-285, 188-285, 189-285, and 190-285 of SEQ ID NO:2. Polypeptides encoded by these polynucleotides are also encompassed by the invention. The present invention is also directed to nucleic acid molecules comprising, or alternatively, consisting of, a polynucleotide sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the polynucleotide sequence encoding the Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides described above. The present invention also encompasses the

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above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these nucleic acids and/or polynucleotide sequences are also encompassed by the invention, as are polypeptides comprising, or alternatively consisting of, an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the amino acid sequence described above, and polynucleotides that encode such polypeptides.

Furthermore, since the predicted extracellular domain of the Neutrokin-alpha polypeptides of the invention may itself elicit biological activity, deletions of N- and C-terminal amino acid residues from the predicted extracellular region of the polypeptide (spanning positions Gln-73 to Leu-285 of SEQ ID NO:2) may retain some biological activity such as, for example, ligand binding, stimulation of lymphocyte (e.g., B cell) proliferation, differentiation, and/or activation, and modulation of cell replication or modulation of target cell activities. However, even if deletion of one or more amino acids from the N-terminus of the predicted extracellular domain of a Neutrokin-alpha polypeptide results in modification or loss of one or more biological functions of the polypeptide, other functional activities may still be retained. Thus, the ability of the shortened polypeptides to induce and/or bind to antibodies which recognize the complete or mature or extracellular domains of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature or extracellular domains of the polypeptides are removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence of Neutrokin-alpha shown in SEQ ID NO:2, up to the glycine residue at position number 280, and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising, or alternatively consisting of, the amino acid sequence of residues n'-285 of SEQ ID NO:2, where n' is an integer in the range of the amino acid position of amino acid residues 73-280 in SEQ ID NO:2, and 73 is the position of the first residue from the N-terminus of the predicted extracellular domain of the Neutrokin-alpha polypeptide (disclosed in SEQ ID NO:2). Polynucleotides encoding these polypeptides are also encompassed by the invention. More in particular, in certain embodiments, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, an amino acid sequence selected from the group consisting of residues of Q-73 to L-285; G-74 to L-285; D-75 to L-285; L-76 to L-285; A-77 to L-285; S-78 to L-285; L-79 to L-285; R-80 to L-285; A-81 to L-285; E-82 to L-285; L-83 to L-285; Q-84 to L-285; G-85 to L-285; H-86 to L-285; H-87 to L-285; A-88 to L-285; E-89 to L-285; K-90 to L-285; L-91 to L-285; P-92 to L-285; A-93 to L-285; G-94 to L-285; A-95 to L-285; G-96 to L-285; A-97 to L-285; P-98 to L-285; K-99 to L-285; A-100 to L-285; G-101 to L-285; L-102 to L-285; F-103 to L-285; F-104 to L-285; A-105 to L-285; P-106 to L-285; A-107 to L-285; V-108 to L-285; T-109 to L-285; A-111 to L-285; G-111 to L-285; L-112 to L-285; K-113 to L-285; I-114 to L-285; F-115 to L-285; E-116 to L-285; P-117 to L-285; P-118 to L-285; A-119 to L-285; P-120 to L-285; G-121 to L-285; E-122 to L-285; G-123 to L-285; N-124 to L-285; S-125 to L-285; S-126 to L-285; Q-127 to L-285; N-128 to L-285; S-129 to L-285; R-130 to L-285; N-131 to L-285; K-132 to L-285; R-133 to L-285; A-134 to L-285; V-135 to L-285; Q-136 to

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L-285; G-137 to L-285; P-138 to L-285; E-139 to L-285; E-140 to L-285; T-141 to L-285; V-142 to L-285; T-143 to L-285; Q-144 to L-285; D-145 to L-285; C-146 to L-285; L-147 to L-285; Q-148 to L-285; L-149 to L-285; I-150 to L-285; A-151 to L-285; D-152 to L-285; S-153 to L-285; E-154 to L-285; T-155 to L-285; P-156 to L-285; T-157 to L-285; I-158 to L-285; Q-159 to L-285; K-160 to L-285; G-161 to L-285; S-162 to L-285; Y-163 to L-285; T-164 to L-285; F-165 to L-285; V-166 to L-285; P-167 to L-285; W-168 to L-285; L-169 to L-285; L-170 to L-285; S-171 to L-285; F-172 to L-285; K-173 to L-285; R-174 to L-285; G-175 to L-285; S-176 to L-285; A-177 to L-285; L-178 to L-285; E-179 to L-285; E-180 to L-285; K-181 to L-285; E-182 to L-285; N-183 to L-285; K-184 to L-285; I-185 to L-285; L-186 to L-285; V-187 to L-285; K-188 to L-285; E-189 to L-285; T-190 to L-285; G-191 to L-285; Y-192 to L-285; F-193 to L-285; F-194 to L-285; I-195 to L-285; Y-196 to L-285; G-197 to L-285; Q-198 to L-285; V-199 to L-285; I-200 to L-285; Y-201 to L-285; I-202 to L-285; D-203 to L-285; K-204 to L-285; T-205 to L-285; Y-206 to L-285; A-207 to L-285; M-208 to L-285; G-209 to L-285; H-210 to L-285; L-211 to L-285; I-212 to L-285; Q-213 to L-285; R-214 to L-285; K-215 to L-285; K-216 to L-285; V-217 to L-285; H-218 to L-285; V-219 to L-285; F-220 to L-285; G-221 to L-285; D-222 to L-285; E-223 to L-285; L-224 to L-285; S-225 to L-285; L-226 to L-285; V-227 to L-285; T-228 to L-285; L-229 to L-285; F-230 to L-285; R-231 to L-285; C-232 to L-285; I-233 to L-285; Q-234 to L-285; N-235 to L-285; M-236 to L-285; P-237 to L-285; E-238 to L-285; I-239 to L-285; L-240 to L-285; P-241 to L-285; N-242 to L-285; N-243 to L-285; S-244 to L-285; C-245 to L-285; Y-246 to L-285; S-247 to L-285; A-248 to L-285; G-249 to L-285; I-250 to L-285; A-251 to L-285; K-252 to L-285; I-253 to L-285; E-254 to L-285; E-255 to L-285; G-256 to L-285; D-257 to L-285; E-258 to L-285; R-259 to L-285; Q-260 to L-285; L-261 to L-285; A-262 to L-285; I-263 to L-285; P-264 to L-285; R-265 to L-285; E-266 to L-285; N-267 to L-285; A-268 to L-285; Q-269 to L-285; I-270 to L-285; S-271 to L-285; L-272 to L-285; D-273 to L-285; G-274 to L-285; D-275 to L-285; V-276 to L-285; T-277 to L-285; F-278 to L-285; I-279 to L-285; and G-280 to L-285 of SEQ ID NO:2. Polypeptides encoded by these polynucleotides are also encompassed by the invention. The present invention is also directed to nucleic acid molecules comprising, or alternatively, consisting of, a polynucleotide sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the polynucleotide sequence encoding the Neutrokin- α and/or Neutrokin- α SV polypeptides described above. The present invention also encompasses the above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these nucleic acids and/or polynucleotide sequences are also encompassed by the invention, as are polypeptides comprising, or alternatively consisting of, an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the amino acid sequence described above, and polynucleotides that encode such polypeptides.

Highly preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of, a polynucleotide having a nucleotide sequence at least 80%, 85%, 90% identical and more preferably at least 95%, 96%, 97%, 98%, 99% or 100% identical to a polynucleotide sequence encoding the Neutrokin- α polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2). Preferred embodiments of the invention are directed to nucleic acid molecules

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comprising, or alternatively consisting of, a polynucleotide having a nucleotide sequence at least 90% identical to a polynucleotide sequence encoding the Neutrokin- α polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2). More preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of, a polynucleotide having a nucleotide sequence at least 95% identical to a polynucleotide sequence encoding the Neutrokin- α polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2). More preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of, a polynucleotide having a nucleotide sequence at least 96% identical to a polynucleotide sequence encoding the Neutrokin- α polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2).

Additionally, more preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of, a polynucleotide having a nucleotide sequence at least 97% to a polynucleotide sequence encoding the Neutrokin- α polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2). Additionally, more preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of, a polynucleotide having a nucleotide sequence at least 98% to a polynucleotide sequence encoding the Neutrokin- α polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2). Additionally, more preferred embodiments of the invention are directed to nucleic acid molecules comprising, or alternatively consisting of, a polynucleotide having a nucleotide sequence at least 99% identical to a polynucleotide sequence encoding the Neutrokin- α polypeptide having the amino acid sequence at positions 134-285 in FIGS. 1A and 1B (SEQ ID NO:2).

In specific embodiments, a polypeptide comprising, or alternatively consisting of, one of the following N-terminally deleted polypeptide fragments of Neutrokin- α and/or Neutrokin- α SV are preferred: amino acid residues Ala-71 through Leu-285, amino acid residues Ala-81 through Leu-285, amino acid residues Leu-112 through Leu-285, amino acid residues Ala-134 through Leu-285, amino acid residues Leu-147 through Leu-285, and amino acid residues Gly-161 through Leu-285 of SEQ ID NO:2. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Similarly, many examples of biologically functional C-terminal deletion mutants are known. For instance, Interferon gamma shows up to ten times higher activities by deleting 8-10 amino acid residues from the carboxy terminus of the protein (Döheli et al., *J. Biotechnology* 7:199-216 (1988)). Since the present protein is a member of the TNF polypeptide family, deletions of C-terminal amino acids up to the leucine residue at position 284 are expected to retain most if not all biological activity such as, for example, ligand binding, the ability to stimulate lymphocyte (e.g., B cell) proliferation, differentiation, and/or activation, and modulation of cell replication. Polypeptides having deletions of up to about 10 additional C-terminal residues (i.e., up to the glycine residue at position 274) also may retain some activity such as receptor binding, although such polypeptides would lack a portion of the conserved TNF domain which extends to about Leu-284 of SEQ ID NO:2. However, even if deletion of one or more amino acids from the C-terminus of a protein results in modification or loss of one or more biological functions of the

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protein, other functional activities may still be retained. Thus, the ability of the shortened protein to induce and/or bind to antibodies which recognize the complete or mature protein generally will be retained when less than the majority of the residues of the complete or mature protein are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete protein retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the carboxy terminus of the amino acid sequence of the Neurotrophin- α polypeptide shown in FIGS. 1A and 1B (SEQ ID NO:2), up to the glycine residue at position 274 (Gly-274) and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising, or alternatively consisting of, the amino acid sequence of residues 1-m¹ of the amino acid sequence in SEQ ID NO:2, where m¹ is any integer in the range of the amino acid position of amino acid residues 274-284 in SEQ ID NO:2. Polynucleotides encoding these polypeptides are also encompassed by the invention. More in particular, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, an amino acid sequence selected from the group consisting of residues 1-274, 1-275, 1-276, 1-277, 1-278, 1-279, 1-280, 1-281, 1-282, 1-283 and 1-284 of SEQ ID NO:2. Polypeptides encoded by these polynucleotides are also encompassed by the invention. The present invention is also directed to nucleic acid molecules comprising, or alternatively, consisting of, a polynucleotide sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the polynucleotide sequence encoding the Neurotrophin- α and/or Neurotrophin- α SV polypeptides described above. The present invention also encompasses the above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these nucleic acids and/or polynucleotide sequences are also encompassed by the invention, as are polypeptides comprising, or alternatively consisting of, an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the amino acid sequence described above, and polynucleotides that encode such polypeptides.

Also provided are polypeptides comprising, or alternatively consisting of, one or more amino acids deleted from both the amino and the carboxyl termini, which may be described generally as having residues n'-m¹ of SEQ ID NO:2, where n¹ and m¹ are integers as defined above. Also included are a nucleotide sequence encoding a polypeptide comprising, or alternatively consisting of, a portion of the complete Neurotrophin- α amino acid sequence encoded by the deposited cDNA clone contained in ATCC Accession No. 97768 where this portion excludes from 1 to 190 amino acids from the amino terminus or from 1 to 11 amino acids from the C-terminus of the complete amino acid sequence (or any combination of these N-terminal and C-terminal deletions) encoded by the cDNA clone in the deposited plasmid. Polynucleotides encoding all of the above deletion polypeptides are encompassed by the invention.

Similarly, deletions of C-terminal amino acid residues of the predicted extracellular domain of Neurotrophin- α up to the leucine residue at position 79 of SEQ ID NO:2 may retain some biological activity, such as, for example, ligand binding, stimulation of lymphocyte (e.g., B cell) proliferation, differentiation, and/or activation, and modulation of cell replication or modulation of target cell activities. Polypeptides having further C-terminal deletions including Leu-79 of SEQ ID NO:2 would not be expected to retain biological activities.

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However, even if deletion of one or more amino acids from the C-terminus of a polypeptide results in modification or loss of one or more biological functions of the polypeptide, other functional activities may still be retained. Thus, the ability of the shortened polypeptide to induce and/or bind to antibodies which recognize the complete, mature or extracellular forms of the polypeptide generally will be retained when less than the majority of the residues of the complete, mature or extracellular forms of the polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of the predicted extracellular domain retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the carboxy terminus of the amino acid sequence of the predicted extracellular domain of Neurotrophin- α polypeptide shown in SEQ ID NO:2, up to the leucine residue at position 79 of SEQ ID NO:2, and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising, or alternatively consisting of, the amino acid sequence of residues 73-m² of the amino acid sequence in SEQ ID NO:2, where m² is any integer in the range of the amino acid position of amino acid residues 79 to 285 in the amino acid sequence in SEQ ID NO:2, and residue 78 is the position of the first residue at the C-terminus of the predicted extracellular domain of the Neurotrophin- α polypeptide (disclosed in SEQ ID NO:2). Polypeptides encoded by these polynucleotides are also encompassed by the invention. More in particular, in certain embodiments, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, an amino acid sequence selected from the group consisting of residues Q-73 to Leu-285; Q-73 to L-284; Q-73 to K-283; Q-73 to L-282; Q-73 to A-281; Q-73 to G-280; Q-73 to F-279; Q-73 to F-278; Q-73 to T-277; Q-73 to V-276; Q-73 to D-275; Q-73 to G-274; Q-73 to D-273; Q-73 to L-272; Q-73 to S-271; Q-73 to I-270; Q-73 to Q-269; Q-73 to A-268; Q-73 to N-267; Q-73 to E-266; Q-73 to R-265; Q-73 to P-264; Q-73 to I-263; Q-73 to A-262; Q-73 to L-261; Q-73 to Q-260; Q-73 to L-259; Q-73 to E-258; Q-73 to D-257; Q-73 to G-256; Q-73 to E-255; Q-73 to E-254; Q-73 to I-253; Q-73 to K-252; Q-73 to A-251; Q-73 to I-250; Q-73 to G-249; Q-73 to A-248; Q-73 to S-247; Q-73 to Y-246; Q-73 to C-245; Q-73 to S-244; Q-73 to N-243; Q-73 to N-242; Q-73 to P-241; Q-73 to L-240; Q-73 to T-239; Q-73 to E-238; Q-73 to P-237; Q-73 to M-236; Q-73 to N-235; Q-73 to Q-234; Q-73 to I-233; Q-73 to C-232; Q-73 to R-231; Q-73 to F-230; Q-73 to L-229; Q-73 to T-228; Q-73 to V-227; Q-73 to I-226; Q-73 to S-225; Q-73 to I-224; Q-73 to F-223; Q-73 to D-222; Q-73 to G-221; Q-73 to F-220; Q-73 to V-219; Q-73 to H-218; Q-73 to V-217; Q-73 to K-216; Q-73 to K-215; Q-73 to R-214; Q-73 to Q-213; Q-73 to I-212; Q-73 to L-211; Q-73 to H-210; Q-73 to G-209; Q-73 to M-208; Q-73 to A-207; Q-73 to Y-206; Q-73 to T-205; Q-73 to K-204; Q-73 to D-203; Q-73 to T-202; Q-73 to Y-201; Q-73 to L-200; Q-73 to V-199; Q-73 to Q-198; Q-73 to G-197; Q-73 to Y-196; Q-73 to I-195; Q-73 to F-194; Q-73 to F-193; Q-73 to Y-192; Q-73 to G-191; Q-73 to T-190; Q-73 to F-189; Q-73 to K-188; Q-73 to V-187; Q-73 to L-186; Q-73 to I-185; Q-73 to K-184; Q-73 to N-183; Q-73 to E-182; Q-73 to K-181; Q-73 to E-180; Q-73 to E-179; Q-73 to L-178; Q-73 to A-177; Q-73 to S-176; Q-73 to G-175; Q-73 to R-174; Q-73 to K-173; Q-73 to F-172; Q-73 to S-171; Q-73 to L-170; Q-73 to L-169; Q-73 to W-168; Q-73 to P-167; Q-73 to V-166; Q-73 to F-165; Q-73 to T-164; Q-73 to Y-163; Q-73 to S-162; Q-73 to G-161; Q-73 to K-160; Q-73 to Q-159; Q-73 to I-158; Q-73 to T-157; Q-73 to P-156; Q-73 to T-155; Q-73 to E-154; Q-73 to S-153; Q-73

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to D-152; Q-73 to A-151; Q-73 to I-150; Q-73 to L-149; Q-73 to Q-148; Q-73 to L-147; Q-73 to C-146; Q-73 to D-145; Q-73 to Q-144; Q-73 to T-143; Q-73 to V-142; Q-73 to T-141; Q-73 to E-140; Q-73 to F-139; Q-73 to P-138; Q-73 to G-137; Q-73 to Q-136; Q-73 to V-135; Q-73 to A-134; Q-73 to R-133; Q-73 to K-132; Q-73 to N-131; Q-73 to R-130; Q-73 to S-129; Q-73 to N-128; Q-73 to Q-127; Q-73 to S-126; Q-73 to S-125; Q-73 to N-124; Q-73 to G-123; Q-73 to E-122; Q-73 to G-121; Q-73 to P-120; Q-73 to A-119; Q-73 to P-118; Q-73 to P-117; Q-73 to E-116; Q-73 to F-115; Q-73 to I-114; Q-73 to K-113; Q-73 to L-112; Q-73 to G-111; Q-73 to A-110; Q-73 to T-109; Q-73 to V-108; Q-73 to A-107; Q-73 to P-106; Q-73 to A-105; Q-73 to E-104; Q-73 to E-103; Q-73 to L-102; Q-73 to G-101; Q-73 to A-100; Q-73 to K-99; Q-73 to P-98; Q-73 to A-97; Q-73 to G-96; Q-73 to A-95; Q-73 to G-94; Q-73 to A-93; Q-73 to P-92; Q-73 to L-91; Q-73 to K-90; Q-73 to E-89; Q-73 to A-88; Q-73 to H-87; Q-73 to H-86; Q-73 to G-85; Q-73 to Q-84; Q-73 to L-83; Q-73 to E-82; Q-73 to A-81; Q-73 to R-80; and Q-73 to I-79 of SEQ ID NO:2. Polypeptides encoded by these polynucleotides are also encompassed by the invention. The present invention is also directed to nucleic acid molecules comprising, or alternatively, consisting of, a polynucleotide sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the polynucleotide sequence encoding the Neurokinine-alpha and/or Neurokinine-alphaSV polypeptides described above. The present invention also encompasses the above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these nucleic acids and/or polynucleotide sequences are also encompassed by the invention, as are polypeptides comprising, or alternatively consisting of, an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the amino acid sequence described above, and polynucleotides that encode such polypeptides.

The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini of the predicted extracellular domain of Neurokinine-alpha, which may be described generally as having residues n^2 - m^2 of SEQ ID NO:2 where n^2 and m^2 are integers as defined above.

In another embodiment, a nucleotide sequence encoding a polypeptide consisting of a portion of the extracellular domain of the Neurokinine-alpha amino acid sequence encoded by the cDNA plasmid contained in the deposit having ATCC accession no. 97768, where this portion excludes from 1 to about 206 amino acids from the amino terminus of the extracellular domain of the amino acid sequence encoded by the cDNA plasmid contained in the deposit having ATCC accession no. 97768, or from 1 to about 206 amino acids from the carboxy terminus of the extracellular domain of the amino acid sequence encoded by the cDNA plasmid contained in the deposit having ATCC accession no. 97768, or any combination of the above amino terminal and carboxy terminal deletions, of the entire extracellular domain of the amino acid sequence encoded by the cDNA plasmid contained in the deposit having ATCC accession no. 97768.

As mentioned above, even if deletion of one or more amino acids from the N-terminus of a polypeptide results in modification or loss of one or more functional activities (e.g., biological activity) of the polypeptide, other functions or biological activities may still be retained. Thus, the ability of a shortened Neurokinine-alpha mutein to induce and/or bind to antibodies which recognize the full-length or mature forms or the extracellular domain of the polypeptide generally will be retained when less than the majority of the residues of the full-length or mature or extracellular domain of the polypep-

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ptide are removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a Neurokinine-alpha mutein with a large number of deleted N-terminal amino acid residues may retain some functional (e.g., biological or immunogenic) activities. In fact, peptides composed of as few as six Neurokinine-alpha amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the amino terminus of the predicted full-length amino acid sequence of the Neurokinine-alpha shown in SEQ ID NO:2, up to the glycine residue at position number 280 of the sequence shown SEQ ID NO:2 and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues n^3 -285 of the sequence shown in SEQ ID NO:2, where n^3 is an integer in the range of the amino acid position of amino acid residues 1 to 280 of the amino acid sequence in SEQ ID NO:2.

More in particular, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, an amino acid sequence selected from the group consisting of residues of D-2 to L-285; D-3 to L-285; S-4 to L-285; T-5 to L-285; E-6 to L-285; R-7 to L-285; E-8 to L-285; Q-9 to L-285; S-10 to L-285; R-11 to L-285; L-12 to L-285; T-13 to L-285; S-14 to L-285; C-15 to L-285; L-16 to L-285; K-17 to L-285; K-18 to L-285; R-19 to L-285; F-20 to L-285; E-21 to L-285; M-22 to L-285; K-23 to L-285; L-24 to L-285; K-25 to L-285; E-26 to L-285; C-27 to L-285; V-28 to L-285; S-29 to L-285; I-30 to L-285; L-31 to L-285; P-32 to L-285; R-33 to L-285; K-34 to L-285; E-35 to L-285; S-36 to L-285; P-37 to L-285; S-38 to L-285; V-39 to L-285; R-40 to L-285; S-41 to L-285; S-42 to L-285; K-43 to L-285; D-44 to L-285; G-45 to L-285; K-46 to L-285; L-47 to L-285; L-48 to L-285; A-49 to L-285; A-50 to L-285; T-51 to L-285; L-52 to L-285; L-53 to L-285; L-54 to L-285; A-55 to L-285; L-56 to L-285; L-57 to L-285; S-58 to L-285; C-59 to L-285; C-60 to L-285; L-61 to L-285; T-62 to L-285; V-63 to L-285; V-64 to L-285; S-65 to L-285; F-66 to L-285; Y-67 to L-285; Q-68 to L-285; V-69 to L-285; A-70 to L-285; A-71 to L-285; L-72 to L-285; Q-73 to L-285; G-74 to L-285; D-75 to L-285; L-76 to L-285; A-77 to L-285; S-78 to L-285; L-79 to L-285; R-80 to L-285; A-81 to L-285; E-82 to L-285; L-83 to L-285; Q-84 to L-285; G-85 to L-285; I-86 to L-285; I-87 to L-285; A-88 to L-285; E-89 to L-285; K-90 to L-285; L-91 to L-285; P-92 to L-285; A-93 to L-285; G-94 to L-285; A-95 to L-285; G-96 to L-285; A-97 to L-285; P-98 to L-285; K-99 to L-285; A-100 to L-285; G-101 to L-285; L-102 to L-285; E-103 to L-285; E-104 to L-285; A-105 to L-285; P-106 to L-285; A-107 to L-285; V-108 to L-285; T-109 to L-285; A-110 to L-285; G-111 to L-285; L-112 to L-285; K-113 to L-285; L-114 to L-285; F-115 to L-285; E-116 to L-285; P-117 to L-285; P-118 to L-285; A-119 to L-285; P-120 to L-285; G-121 to L-285; E-122 to L-285; G-123 to L-285; N-124 to L-285; S-125 to L-285; S-126 to L-285; Q-127 to L-285; N-128 to L-285; S-129 to L-285; R-130 to L-285; N-131 to L-285; K-132 to L-285; R-133 to L-285; A-134 to L-285; V-135 to L-285; Q-136 to L-285; G-137 to L-285; P-138 to L-285; E-139 to L-285; E-140 to L-285; T-141 to L-285; V-142 to L-285; T-143 to L-285; Q-144 to L-285; D-145 to L-285; C-146 to L-285; L-147 to L-285; Q-148 to L-285; L-149 to L-285; I-150 to L-285; A-151 to L-285; D-152 to L-285; S-153 to L-285; E-154 to L-285; T-155 to L-285; P-156 to L-285; T-157 to L-285; I-158 to L-285; Q-159 to L-285; K-160 to L-285; G-161 to L-285; S-162 to L-285; Y-163 to

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L-285; T-164 to L-285; F-165 to L-285; V-166 to L-285; P-167 to L-285; W-168 to L-285; L-169 to L-285; L-170 to L-285; S-171 to L-285; F-172 to L-285; K-173 to L-285; R-174 to L-285; G-175 to L-285; S-176 to L-285; A-177 to L-285; L-178 to L-285; F-179 to L-285; E-180 to L-285; K-181 to L-285; E-182 to L-285; N-183 to L-285; K-184 to L-285; I-185 to L-285; L-186 to L-285; V-187 to L-285; K-188 to L-285; E-189 to L-285; T-190 to L-285; G-191 to L-285; Y-192 to L-285; F-193 to L-285; F-194 to L-285; I-195 to L-285; Y-196 to L-285; G-197 to L-285; Q-198 to L-285; V-199 to L-285; L-200 to L-285; Y-201 to L-285; T-202 to L-285; D-203 to L-285; K-204 to L-285; T-205 to L-285; Y-206 to L-285; A-207 to L-285; M-208 to L-285; G-209 to L-285; H-210 to L-285; L-211 to L-285; I-212 to L-285; Q-213 to L-285; R-214 to L-285; K-215 to L-285; K-216 to L-285; V-217 to L-285; H-218 to L-285; V-219 to L-285; F-220 to L-285; G-221 to L-285; D-222 to L-285; E-223 to L-285; L-224 to L-285; S-225 to L-285; L-226 to L-285; V-227 to L-285; T-228 to L-285; L-229 to L-285; F-230 to L-285; R-231 to L-285; C-232 to L-285; I-233 to L-285; Q-234 to L-285; N-235 to L-285; M-236 to L-285; P-237 to L-285; E-238 to L-285; T-239 to L-285; L-240 to L-285; P-241 to L-285; N-242 to L-285; N-243 to L-285; S-244 to L-285; C-245 to L-285; Y-246 to L-285; S-247 to L-285; A-248 to L-285; G-249 to L-285; I-250 to L-285; A-251 to L-285; K-252 to L-285; L-253 to L-285; E-254 to L-285; E-255 to L-285; G-256 to L-285; D-257 to L-285; E-258 to L-285; L-259 to L-285; Q-260 to L-285; L-261 to L-285; A-262 to L-285; I-263 to L-285; P-264 to L-285; R-265 to L-285; E-266 to L-285; N-267 to L-285; A-268 to L-285; Q-269 to L-285; I-270 to L-285; S-271 to L-285; L-272 to L-285; D-273 to L-285; G-274 to L-285; D-275 to L-285; V-276 to L-285; T-277 to L-285; F-278 to L-285; F-279 to L-285; and G-280 to L-285 of SEQ ID NO:2. The present application is also directed to nucleic acid molecules comprising, or alternatively, consisting of, a polynucleotide sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the polynucleotide sequence encoding the Neurokinine-alpha and/or Neurokinine-alphaSV polypeptides described above. The present invention also encompasses the above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these nucleic acids and/or polynucleotide sequences are also encompassed by the invention, as are polypeptides comprising an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the amino acid sequence described above, and polynucleotides that encode such polypeptides.

Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification or loss of one or more functional activities (e.g., biological activity) of the protein, other functional activities may still be retained. Thus, the ability of a shortened Neurokinine-alpha mutein to induce and/or bind to antibodies which recognize the complete or mature form or the extracellular domain of the polypeptide generally will be retained when less than the majority of the residues of the complete or mature form or the extracellular domain of the polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a Neurokinine-alpha mutein with a large number of deleted C-terminal amino acid residues may retain some functional (e.g., biological or immunogenic) activities. In fact, peptides com-

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posed of as few as six Neurokinine-alpha amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides in another embodiment, polypeptides having one or more residues deleted from the carboxy terminus of the amino acid sequence of the Neurokinine-alpha shown in SEQ ID NO:2, up to the glutamic acid residue at position number 6, and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues 1-m³ of SEQ ID NO:2, where m³ is an integer in the range of the amino acid position of amino acid residues 6-284 of the amino acid sequence in SEQ ID NO:2.

More in particular, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, an amino acid sequence selected from the group consisting of residues M-1 to L-284; M-1 to K-283; M-1 to L-282; M-1 to A-281; M-1 to G-280; M-1 to F-279; M-1 to F-278; M-1 to T-277; M-1 to V-276; M-1 to D-275; M-1 to G-274; M-1 to D-273; M-1 to L-272; M-1 to S-271; M-1 to I-270; M-1 to Q-269; M-1 to A-268; M-1 to N-267; M-1 to E-266; M-1 to R-265; M-1 to P-264; M-1 to I-263; M-1 to A-262; M-1 to L-261; M-1 to Q-260; M-1 to L-259; M-1 to E-258; M-1 to D-257; M-1 to G-256; M-1 to E-255; M-1 to E-254; M-1 to L-253; M-1 to K-252; M-1 to A-251; M-1 to I-250; M-1 to G-249; M-1 to A-248; M-1 to S-247; M-1 to Y-246; M-1 to C-245; M-1 to S-244; M-1 to N-243; M-1 to N-242; M-1 to P-241; M-1 to L-240; M-1 to T-239; M-1 to E-238; M-1 to P-237; M-1 to M-236; M-1 to N-235; M-1 to Q-234; M-1 to I-233; M-1 to C-232; M-1 to R-231; M-1 to F-230; M-1 to L-229; M-1 to T-228; M-1 to V-227; M-1 to L-226; M-1 to S-225; M-1 to L-224; M-1 to E-223; M-1 to D-222; M-1 to G-221; M-1 to F-220; M-1 to V-219; M-1 to H-218; M-1 to V-217; M-1 to K-216; M-1 to K-215; M-1 to R-214; M-1 to Q-213; M-1 to I-212; M-1 to L-211; M-1 to I-210; M-1 to G-209; M-1 to M-208; M-1 to A-207; M-1 to Y-206; M-1 to T-205; M-1 to K-204; M-1 to D-203; M-1 to T-202; M-1 to Y-201; M-1 to L-200; M-1 to V-199; M-1 to Q-198; M-1 to G-197; M-1 to Y-196; M-1 to I-195; M-1 to F-194; M-1 to F-193; M-1 to Y-192; M-1 to G-191; M-1 to T-190; M-1 to E-189; M-1 to K-188; M-1 to V-187; M-1 to L-186; M-1 to I-185; M-1 to K-184; M-1 to N-183; M-1 to E-182; M-1 to K-181; M-1 to E-180; M-1 to E-179; M-1 to L-178; M-1 to A-177; M-1 to S-176; M-1 to G-175; M-1 to R-174; M-1 to K-173; M-1 to F-172; M-1 to S-171; M-1 to L-170; M-1 to L-169; M-1 to W-168; M-1 to P-167; M-1 to V-166; M-1 to F-165; M-1 to T-164; M-1 to Y-163; M-1 to S-162; M-1 to G-161; M-1 to K-160; M-1 to Q-159; M-1 to I-158; M-1 to T-157; M-1 to P-156; M-1 to T-155; M-1 to E-154; M-1 to S-153; M-1 to D-152; M-1 to A-151; M-1 to I-150; M-1 to L-149; M-1 to Q-148; M-1 to L-147; M-1 to C-146; M-1 to D-145; M-1 to Q-144; M-1 to T-143; M-1 to V-142; M-1 to T-141; M-1 to F-140; M-1 to E-139; M-1 to P-138; M-1 to G-137; M-1 to Q-136; M-1 to V-135; M-1 to A-134; M-1 to R-133; M-1 to K-132; M-1 to N-131; M-1 to R-130; M-1 to S-129; M-1 to N-128; M-1 to Q-127; M-1 to S-126; M-1 to S-125; M-1 to N-124; M-1 to G-123; M-1 to F-122; M-1 to G-121; M-1 to P-120; M-1 to A-119; M-1 to P-118; M-1 to P-117; M-1 to E-116; M-1 to F-115; M-1 to I-114; M-1 to K-113; M-1 to L-112; M-1 to G-111; M-1 to A-110; M-1 to T-109; M-1 to V-108; M-1 to A-107; M-1 to P-106; M-1 to A-105; M-1 to E-104; M-1 to E-103; M-1 to L-102; M-1 to G-101; M-1 to A-100; M-1 to K-99; M-1 to P-98; M-1 to A-97; M-1 to G-96; M-1 to A-95; M-1 to G-94; M-1 to A-93; M-1 to P-92; M-1 to L-91; M-1 to K-90; M-1 to E-89; M-1 to A-88; M-1 to H-87; M-1 to I-86; M-1 to G-85; M-1 to Q-84; M-1 to L-83; M-1 to E-82; M-1 to A-81; M-1 to

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R-80; M-1 to L-79; M-1 to S-78; M-1 to A-77; M-1 to L-76; M-1 to D-75; M-1 to G-74; M-1 to Q-73; M-1 to L-72; M-1 to A-71; M-1 to A-70; M-1 to V-69; M-1 to Q-68; M-1 to Y-67; M-1 to F-66; M-1 to S-65; M-1 to V-64; M-1 to V-63; M-1 to T-62; M-1 to L-61; M-1 to C-60; M-1 to C-59; M-1 to S-58; M-1 to L-57; M-1 to L-56; M-1 to A-55; M-1 to L-54; M-1 to L-53; M-1 to L-52; M-1 to T-51; M-1 to A-50; M-1 to A-49; M-1 to L-48; M-1 to L-47; M-1 to K-46; M-1 to G-45; M-1 to D-44; M-1 to K-43; M-1 to S-42; M-1 to S-41; M-1 to R-40; M-1 to V-39; M-1 to S-38; M-1 to P-37; M-1 to S-36; M-1 to E-35; M-1 to K-34; M-1 to R-33; M-1 to P-32; M-1 to L-31; M-1 to I-30; M-1 to S-29; M-1 to V-28; M-1 to C-27; M-1 to E-26; M-1 to K-25; M-1 to L-24; M-1 to K-23; M-1 to M-22; M-1 to F-21; M-1 to F-20; M-1 to R-19; M-1 to K-18; M-1 to K-17; M-1 to L-16; M-1 to C-15; M-1 to S-14; M-1 to T-13; M-1 to L-12; M-1 to R-11; M-1 to S-10; M-1 to Q-9; M-1 to E-8; M-1 to R-7; and M-1 to E-6 of SEQ ID NO:2. The present application is also directed to nucleic acid molecules comprising, or alternatively, consisting of, a polynucleotide sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the polynucleotide sequence encoding the Neutrokin- α and/or Neutrokin- α SV polypeptides described above. The present invention also encompasses the above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these nucleic acids and/or polynucleotide sequences are also encompassed by the invention, as are polypeptides comprising an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the amino acid sequence described above, and polynucleotides that encode such polypeptides.

The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini of a Neutrokin- α polypeptide, which may be described generally as having residues n^3 - m^3 of SEQ ID NO:2, where n^3 and m^3 are integers as defined above.

Furthermore, since the predicted extracellular domain of the Neutrokin- α SV polypeptides of the invention may itself elicit functional activity (e.g., biological activity), deletions of N- and C-terminal amino acid residues from the predicted extracellular region of the polypeptide at positions Gln-73 to Leu-266 of SEQ ID NO:19 may retain some functional activity, such as, for example, ligand binding, to stimulation of lymphocyte (e.g., B cell) proliferation, differentiation, and/or activation, modulation of cell replication, modulation of target cell activities and/or immunogenicity. However, even if deletion of one or more amino acids from the N-terminus of the predicted extracellular domain of a Neutrokin- α SV polypeptide results in modification or loss of one or more functional activities of the polypeptide, other functional activities may still be retained. Thus, the ability of the shortened polypeptides to induce and/or bind to antibodies which recognize the complete or mature or extracellular domains of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature or extracellular domains of the polypeptides are removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence of Neutrokin- α SV shown in SEQ ID NO:19, up to the glycine residue at position number 261, and polynucleotides encoding such polypeptides. In particular, the present invention provides

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polypeptides comprising the amino acid sequence of residues n^4 -266 of SEQ ID NO:19, where n^4 is an integer in the range of the amino acid position of amino acid residues 73-261 of the amino acid sequence in SEQ ID NO:19, and 261 is the position of the first residue from the N-terminus of the predicted extracellular domain Neutrokin- α SV polypeptide (shown in SEQ ID NO:19).

More in particular, in certain embodiments, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, an amino acid sequence selected from the group consisting of residues of Q-73 to L-266; G-74 to L-266; D-75 to L-266; L-76 to L-266; A-77 to L-266; S-78 to L-266; L-79 to L-266; R-80 to L-266; A-81 to L-266; E-82 to L-266; L-83 to L-266; Q-84 to L-266; G-85 to L-266; H-86 to L-266; H-87 to L-266; A-88 to L-266; E-89 to L-266; K-90 to L-266; L-91 to L-266; P-92 to L-266; A-93 to L-266; G-94 to L-266; A-95 to L-266; G-96 to L-266; A-97 to L-266; P-98 to L-266; K-99 to L-266; A-100 to L-266; G-101 to L-266; L-102 to L-266; F-103 to L-266; F-104 to L-266; A-105 to L-266; P-106 to L-266; A-107 to L-266; V-108 to L-266; T-109 to L-266; A-110 to L-266; G-111 to L-266; L-112 to L-266; K-113 to L-266; I-114 to L-266; F-115 to L-266; E-116 to L-266; P-117 to L-266; P-118 to L-266; A-119 to L-266; P-120 to L-266; G-121 to L-266; F-122 to L-266; G-123 to L-266; N-124 to L-266; S-125 to L-266; S-126 to L-266; Q-127 to L-266; N-128 to L-266; S-129 to L-266; R-130 to L-266; N-131 to L-266; K-132 to L-266; R-133 to L-266; A-134 to L-266; V-135 to L-266; Q-136 to L-266; G-137 to L-266; P-138 to L-266; F-139 to L-266; E-140 to L-266; T-141 to L-266; G-142 to L-266; S-143 to L-266; Y-144 to L-266; T-145 to L-266; F-146 to L-266; V-147 to L-266; P-148 to L-266; W-149 to L-266; L-150 to L-266; L-151 to L-266; S-152 to L-266; F-153 to L-266; K-154 to L-266; R-155 to L-266; G-156 to L-266; S-157 to L-266; A-158 to L-266; L-159 to L-266; E-160 to L-266; E-161 to L-266; K-162 to L-266; E-163 to L-266; N-164 to L-266; K-165 to L-266; I-166 to L-266; L-167 to L-266; V-168 to L-266; K-169 to L-266; E-170 to L-266; T-171 to L-266; G-172 to L-266; Y-173 to L-266; F-174 to L-266; F-175 to L-266; I-176 to L-266; Y-177 to L-266; G-178 to L-266; Q-179 to L-266; V-180 to L-266; L-181 to L-266; Y-182 to L-266; T-183 to L-266; D-184 to L-266; K-185 to L-266; T-186 to L-266; Y-187 to L-266; A-188 to L-266; M-189 to L-266; G-190 to L-266; H-191 to L-266; L-192 to L-266; I-193 to L-266; Q-194 to L-266; R-195 to L-266; K-196 to L-266; K-197 to L-266; V-198 to L-266; I-199 to L-266; V-200 to L-266; F-201 to L-266; G-202 to L-266; D-203 to L-266; E-204 to L-266; L-205 to L-266; S-206 to L-266; L-207 to L-266; V-208 to L-266; T-209 to L-266; L-210 to L-266; F-211 to L-266; R-212 to L-266; C-213 to L-266; I-214 to L-266; Q-215 to L-266; N-216 to L-266; M-217 to L-266; P-218 to L-266; E-219 to L-266; T-220 to L-266; L-221 to L-266; P-222 to L-266; N-223 to L-266; N-224 to L-266; S-225 to L-266; C-226 to L-266; Y-227 to L-266; S-228 to L-266; A-229 to L-266; G-230 to L-266; I-231 to L-266; A-232 to L-266; K-233 to L-266; L-234 to L-266; E-235 to L-266; E-236 to L-266; G-237 to L-266; D-238 to L-266; F-239 to L-266; L-240 to L-266; Q-241 to L-266; L-242 to L-266; A-243 to L-266; I-244 to L-266; P-245 to L-266; R-246 to L-266; E-247 to L-266; N-248 to L-266; A-249 to L-266; Q-250 to L-266; I-251 to L-266; S-252 to L-266; L-253 to L-266; D-254 to L-266; G-255 to L-266; D-256 to L-266; V-257 to L-266; T-258 to L-266; F-259 to L-266; F-260 to L-266; and G-261 to L-266 of SEQ ID NO:19. The present application is also directed to nucleic acid molecules comprising, or alternatively, consisting of, a polynucleotide sequence at least 80%, 85%, 90%, 92%, 95%,

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96%, 97%, 98% or 99% identical to the polynucleotide sequence encoding the Neutrokin- α and/or Neutrokin- α SV polypeptides described above. The present invention also encompasses the above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these nucleic acids and/or polynucleotide sequences are also encompassed by the invention, as are polypeptides comprising an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the amino acid sequence described above, and polynucleotides that encode such polypeptides.

Similarly, deletions of C-terminal amino acid residues of the predicted extracellular domain of Neutrokin- α SV up to the leucine residue at position 79 of SEQ ID NO:19 may retain some functional activity, such as, for example, ligand binding, the ability to stimulate lymphocyte (e.g., B cell) proliferation, differentiation, and/or activation, modulation of cell replication, modulation of target cell activities and/or immunogenicity. Polypeptides having further C-terminal deletions including Leu-79 of SEQ ID NO:19 would not be expected to retain biological activities.

However, even if deletion of one or more amino acids from the C-terminus of a polypeptide results in modification or loss of one or more functional activities (e.g., biological activity) of the polypeptide, other functional activities may still be retained. Thus, the ability of the shortened polypeptide to induce and/or bind to antibodies which recognize the complete, mature or extracellular forms of the polypeptide generally will be retained when less than the majority of the residues of the complete, mature or extracellular forms of the polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of the predicted extracellular domain retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art.

Accordingly, the present invention further provides polypeptides having one or more residues from the carboxy terminus of the amino acid sequence of the predicted extracellular domain of Neutrokin- α SV shown in SEQ ID NO:19, up to the leucine residue at position 79 of SEQ ID NO:19, and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides having the amino acid sequence of residues 73-m⁴ of the amino acid sequence in SEQ ID NO:19, where m⁴ is any integer in the range of the amino acid position of amino acid residues 79-265 of the amino acid sequence in SEQ ID NO:19.

More in particular, in certain embodiments, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, an amino acid sequence selected from the group consisting of residues Q-73 to L-265; Q-73 to K-264; Q-73 to L-263; Q-73 to A-262; Q-73 to G-261; Q-73 to F-260; Q-73 to F-259; Q-73 to T-258; Q-73 to V-257; Q-73 to D-256; Q-73 to G-255; Q-73 to D-254; Q-73 to L-253; Q-73 to S-252; Q-73 to I-251; Q-73 to Q-250; Q-73 to A-249; Q-73 to N-248; Q-73 to E-247; Q-73 to R-246; Q-73 to P-245; Q-73 to I-244; Q-73 to A-243; Q-73 to L-242; Q-73 to Q-241; Q-73 to L-240; Q-73 to E-239; Q-73 to D-238; Q-73 to G-237; Q-73 to E-236; Q-73 to F-235; Q-73 to L-234; Q-73 to K-233; Q-73 to A-232; Q-73 to I-231; Q-73 to G-230; Q-73 to A-229; Q-73 to S-228; Q-73 to Y-227; Q-73 to C-226; Q-73 to S-225; Q-73 to N-224; Q-73 to N-223; Q-73 to P-222; Q-73 to L-221; Q-73 to T-220; Q-73 to E-219; Q-73 to P-218; Q-73 to M-217; Q-73 to N-216; Q-73 to Q-215; Q-73 to I-214; Q-73 to C-213; Q-73 to R-212; Q-73 to F-211; Q-73 to L-210; Q-73 to T-209; Q-73 to V-208; Q-73 to L-207; Q-73 to S-206; Q-73 to L-205; Q-73 to E-204; Q-73 to D-203; Q-73 to G-202; Q-73 to F-201; Q-73 to V-200; Q-73

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to H-199; Q-73 to V-198; Q-73 to K-197; Q-73 to K-196; Q-73 to R-195; Q-73 to Q-194; Q-73 to I-193; Q-73 to L-192; Q-73 to H-191; Q-73 to G-190; Q-73 to Q-7389; Q-73 to A-188; Q-73 to Y-187; Q-73 to T-186; Q-73 to K-185; Q-73 to D-184; Q-73 to T-183; Q-73 to Y-182; Q-73 to L-181; Q-73 to V-180; Q-73 to Q-179; Q-73 to G-178; Q-73 to Y-177; Q-73 to I-176; Q-73 to F-175; Q-73 to F-174; Q-73 to Y-173; Q-73 to G-172; Q-73 to T-171; Q-73 to E-170; Q-73 to K-169; Q-73 to V-168; Q-73 to L-167; Q-73 to I-166; Q-73 to K-165; Q-73 to N-164; Q-73 to E-163; Q-73 to K-162; Q-73 to E-161; Q-73 to F-160; Q-73 to L-159; Q-73 to A-158; Q-73 to S-157; Q-73 to G-156; Q-73 to R-155; Q-73 to K-154; Q-73 to F-153; Q-73 to S-152; Q-73 to I-151; Q-73 to L-150; Q-73 to W-149; Q-73 to P-148; Q-73 to V-147; Q-73 to F-146; Q-73 to T-145; Q-73 to Y-144; Q-73 to S-143; Q-73 to G-142; Q-73 to T-141; Q-73 to E-140; Q-73 to E-139; Q-73 to P-138; Q-73 to G-137; Q-73 to Q-136; Q-73 to V-135; Q-73 to A-134; Q-73 to R-133; Q-73 to K-132; Q-73 to N-131; Q-73 to R-130; Q-73 to S-129; Q-73 to N-128; Q-73 to Q-127; Q-73 to S-126; Q-73 to S-125; Q-73 to N-124; Q-73 to G-123; Q-73 to E-122; Q-73 to G-121; Q-73 to P-120; Q-73 to A-119; Q-73 to P-118; Q-73 to P-117; Q-73 to E-116; Q-73 to F-115; Q-73 to I-114; Q-73 to K-113; Q-73 to L-112; Q-73 to G-111; Q-73 to A-110; Q-73 to T-109; Q-73 to V-108; Q-73 to A-107; Q-73 to P-106; Q-73 to A-105; Q-73 to E-104; Q-73 to E-103; Q-73 to L-102; Q-73 to G-101; Q-73 to A-100; Q-73 to K-99; Q-73 to P-98; Q-73 to A-97; Q-73 to G-96; Q-73 to A-95; Q-73 to G-94; Q-73 to A-93; Q-73 to P-92; Q-73 to I-91; Q-73 to K-90; Q-73 to E-89; Q-73 to A-88; Q-73 to H-87; Q-73 to H-86; Q-73 to G-85; Q-73 to Q-84; Q-73 to L-83; Q-73 to E-82; Q-73 to A-81; Q-73 to R-80; Q-73 to L-79; and Q-73 to S-78 of SEQ ID NO:19. The present application is also directed to nucleic acid molecules comprising, or alternatively, consisting of, a polynucleotide sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the polynucleotide sequence encoding the Neutrokin- α and/or Neutrokin- α SV polypeptides described above. The present invention also encompasses the above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these nucleic acids and/or polynucleotide sequences are also encompassed by the invention, as are polypeptides comprising an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the amino acid sequence described above, and polynucleotides that encode such polypeptides.

The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini of the predicted extracellular domain of Neutrokin- α SV, which may be described generally as having residues n⁴-m⁴ of SEQ ID NO:19 where n⁴ and m⁴ are integers as defined above.

In another embodiment, a nucleotide sequence encoding a polypeptide consisting of a portion of the extracellular domain of the Neutrokin- α SV amino acid sequence encoded by the cDNA clone contained in the deposit having ATCC Accession No. 203518, where this portion excludes from 1 to about 260 amino acids from the amino terminus of the extracellular domain of the amino acid sequence encoded by cDNA clone contained in the deposit having ATCC Accession No. 203518, or from 1 to about 187 amino acids from the carboxy terminus of the extracellular domain of the amino acid sequence encoded by cDNA clone contained in the deposit having ATCC Accession No. 203518, or any combination of the above amino terminal and carboxy terminal deletions, of the entire extracellular domain of the amino acid sequence encoded by the cDNA clone contained in the deposit having ATCC Accession No. 203518.

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As mentioned above, even if deletion of one or more amino acids from the N-terminus of a polypeptide results in modification or loss of one or more functional activities (e.g., biological activity) of the polypeptide, other functional activities may still be retained. Thus, the ability of a shortened Neutrokin- α SV protein to induce and/or bind to antibodies which recognize the full-length or mature forms or the extracellular domain of the polypeptide generally will be retained when less than the majority of the residues of the full-length or mature or extracellular domain of the polypeptide are removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a Neutrokin- α SV protein with a large number of deleted N-terminal amino acid residues may retain functional (e.g., immunogenic) activities. In fact, peptides composed of as few as six Neutrokin- α SV amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the amino terminus of the predicted full-length amino acid sequence of the Neutrokin- α SV shown in SEQ ID NO:19, up to the glycine residue at position number 261 of the sequence shown SEQ ID NO:19 and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues n^5 -266 of the sequence shown in SEQ ID NO:19, where n^5 is an integer in the range of the amino acid position of amino acid residues 1 to 261 of the amino acid sequence in SEQ ID NO:19.

More in particular, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, an amino acid sequence selected from the group consisting of residues of D-2 to L-266; D-3 to L-266; S-4 to L-266; T-5 to L-266; E-6 to L-266; R-7 to L-266; E-8 to L-266; Q-9 to L-266; S-10 to L-266; R-11 to L-266; L-12 to L-266; T-13 to L-266; S-14 to L-266; C-15 to L-266; L-16 to L-266; K-17 to L-266; K-18 to L-266; R-19 to L-266; E-20 to L-266; E-21 to L-266; M-22 to L-266; K-23 to L-266; L-24 to L-266; K-25 to L-266; E-26 to L-266; C-27 to L-266; V-28 to L-266; S-29 to L-266; I-30 to L-266; L-31 to L-266; P-32 to L-266; R-33 to L-266; K-34 to L-266; E-35 to L-266; S-36 to L-266; P-37 to L-266; S-38 to L-266; V-39 to L-266; R-40 to L-266; S-41 to L-266; S-42 to L-266; K-43 to L-266; D-44 to L-266; G-45 to L-266; K-46 to L-266; L-47 to L-266; L-48 to L-266; A-49 to L-266; A-50 to L-266; T-51 to L-266; L-52 to L-266; I-53 to L-266; I-54 to L-266; A-55 to L-266; I-56 to L-266; L-57 to L-266; S-58 to L-266; C-59 to L-266; C-60 to L-266; L-61 to L-266; T-62 to L-266; V-63 to L-266; V-64 to L-266; S-65 to L-266; F-66 to L-266; Y-67 to L-266; Q-68 to L-266; V-69 to L-266; A-70 to L-266; A-71 to L-266; L-72 to L-266; Q-73 to L-266; G-74 to L-266; D-75 to L-266; L-76 to L-266; A-77 to L-266; S-78 to L-266; L-79 to L-266; R-80 to L-266; A-81 to L-266; E-82 to L-266; L-83 to L-266; Q-84 to L-266; G-85 to L-266; H-86 to L-266; H-87 to L-266; A-88 to L-266; E-89 to L-266; K-90 to L-266; I-91 to L-266; P-92 to L-266; A-93 to L-266; G-94 to L-266; A-95 to L-266; G-96 to L-266; A-97 to L-266; P-98 to L-266; K-99 to L-266; A-100 to L-266; G-101 to L-266; L-102 to L-266; E-103 to L-266; E-104 to L-266; A-105 to L-266; P-106 to L-266; A-107 to L-266; V-108 to L-266; T-109 to L-266; A-110 to L-266; G-111 to L-266; L-112 to L-266; K-113 to L-266; I-114 to L-266; F-115 to L-266; E-116 to L-266; P-117 to L-266; P-118 to L-266; A-119 to L-266; P-120 to L-266; G-121 to L-266; E-122 to L-266; G-123 to L-266; N-124 to L-266;

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S-125 to L-266; S-126 to L-266; Q-127 to L-266; N-128 to L-266; S-129 to L-266; R-130 to L-266; N-131 to L-266; K-132 to L-266; R-133 to L-266; A-134 to L-266; V-135 to L-266; Q-136 to L-266; G-137 to L-266; P-138 to L-266; E-139 to L-266; E-140 to L-266; T-141 to L-266; G-142 to L-266; S-143 to L-266; Y-144 to L-266; T-145 to L-266; F-146 to L-266; V-147 to L-266; P-148 to L-266; W-149 to L-266; I-150 to L-266; I-151 to L-266; S-152 to L-266; F-153 to L-266; K-154 to L-266; R-155 to L-266; G-156 to L-266; S-157 to L-266; A-158 to L-266; L-159 to L-266; E-160 to L-266; E-161 to L-266; K-162 to L-266; E-163 to L-266; N-164 to L-266; K-165 to L-266; I-166 to L-266; L-167 to L-266; V-168 to L-266; K-169 to L-266; E-170 to L-266; T-171 to L-266; G-172 to L-266; Y-173 to L-266; F-174 to L-266; F-175 to L-266; I-176 to L-266; Y-177 to L-266; G-178 to L-266; Q-179 to L-266; V-180 to L-266; L-181 to L-266; Y-182 to L-266; T-183 to L-266; D-184 to L-266; K-185 to L-266; T-186 to L-266; Y-187 to L-266; A-188 to L-266; M-189 to L-266; G-190 to L-266; H-191 to L-266; L-192 to L-266; I-193 to L-266; Q-194 to L-266; R-195 to L-266; K-196 to L-266; K-197 to L-266; V-198 to L-266; H-199 to L-266; V-200 to L-266; F-201 to L-266; G-202 to L-266; D-203 to L-266; E-204 to L-266; L-205 to L-266; S-206 to L-266; I-207 to L-266; V-208 to L-266; T-209 to L-266; L-210 to L-266; F-211 to L-266; R-212 to L-266; C-213 to L-266; I-214 to L-266; Q-215 to L-266; N-216 to L-266; M-217 to L-266; P-218 to L-266; E-219 to L-266; T-220 to L-266; L-221 to L-266; P-222 to L-266; N-223 to L-266; N-224 to L-266; S-225 to L-266; C-226 to L-266; Y-227 to L-266; S-228 to L-266; A-229 to L-266; G-230 to L-266; I-231 to L-266; A-232 to L-266; K-233 to L-266; L-234 to L-266; E-235 to L-266; E-236 to L-266; G-237 to L-266; D-238 to L-266; E-239 to L-266; L-240 to L-266; Q-241 to L-266; I-242 to L-266; A-243 to L-266; I-244 to L-266; P-245 to L-266; R-246 to L-266; E-247 to L-266; N-248 to L-266; A-249 to L-266; Q-250 to L-266; I-251 to L-266; S-252 to L-266; L-253 to L-266; D-254 to L-266; G-255 to L-266; D-256 to L-266; V-257 to L-266; T-258 to L-266; F-259 to L-266; F-260 to L-266; and G-261 to L-266 of SEQ ID NO:19. The present application is also directed to nucleic acid molecules comprising, or alternatively, consisting of, a polynucleotide sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the polynucleotide sequence encoding the Neutrokin- α SV and/or Neutrokin- α SV polypeptides described above. The present invention also encompasses the above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these nucleic acids and/or polynucleotide sequences are also encompassed by the invention, as are polypeptides comprising an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the amino acid sequence described above, and polynucleotides that encode such polypeptides.

Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification or loss of one or more functional activities (e.g., biological activities) of the protein, other functional activities may still be retained. Thus, the ability of a shortened Neutrokin- α SV protein to induce and/or bind to antibodies which recognize the complete or mature form or the extracellular domain of the polypeptide generally will be retained when less than the majority of the residues of the complete or mature form or the extracellular domain of the polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and oth-

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erwise known in the art. It is not unlikely that a Neurokinine-alphaSV mucin with a large number of deleted C-terminal amino acid residues may retain some functional (e.g., immunogenic) activities. In fact, peptides composed of as few as six Neurokinine-alphaSV amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides in another embodiment, polypeptides having one or more residues deleted from the carboxy terminus of the amino acid sequence of the Neurokinine-alphaSV shown in SEQ ID NO: 19, up to the glutamic acid residue at position number 6, and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues 1-m⁵ of SEQ ID NO: 19, where m⁵ is an integer in the range of the amino acid position of amino acid residues 6 to 265 in the amino acid sequence of SEQ ID NO: 19.

More in particular, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, an amino acid sequence selected from the group consisting of residues M-1 to L-265; M-1 to K-264; M-1 to L-263; M-1 to A-262; M-1 to G-261; M-1 to F-260; M-1 to F-259; M-1 to T-258; M-1 to V-257; M-1 to D-256; M-1 to G-255; M-1 to D-254; M-1 to L-253; M-1 to S-252; M-1 to I-251; M-1 to Q-250; M-1 to A-249; M-1 to N-248; M-1 to E-247; M-1 to R-246; M-1 to P-245; M-1 to I-244; M-1 to A-243; M-1 to L-242; M-1 to Q-241; M-1 to L-240; M-1 to E-239; M-1 to D-238; M-1 to G-237; M-1 to E-236; M-1 to F-235; M-1 to L-234; M-1 to K-233; M-1 to A-232; M-1 to I-231; M-1 to G-230; M-1 to A-229; M-1 to S-228; M-1 to Y-227; M-1 to C-226; M-1 to S-225; M-1 to N-224; M-1 to N-223; M-1 to P-222; M-1 to L-221; M-1 to T-220; M-1 to E-219; M-1 to P-218; M-1 to M-217; M-1 to N-216; M-1 to Q-215; M-1 to I-214; M-1 to C-213; M-1 to R-212; M-1 to F-211; M-1 to L-210; M-1 to T-209; M-1 to V-208; M-1 to L-207; M-1 to S-206; M-1 to L-205; M-1 to E-204; M-1 to D-203; M-1 to G-202; M-1 to F-201; M-1 to V-200; M-1 to H-199; M-1 to V-198; M-1 to K-197; M-1 to K-196; M-1 to R-195; M-1 to Q-194; M-1 to I-193; M-1 to L-192; M-1 to H-191; M-1 to G-190; M-1 to M-189; M-1 to A-188; M-1 to Y-187; M-1 to T-186; M-1 to K-185; M-1 to D-184; M-1 to T-183; M-1 to Y-182; M-1 to L-181; M-1 to V-180; M-1 to Q-179; M-1 to G-178; M-1 to Y-177; M-1 to I-176; M-1 to F-175; M-1 to I-174; M-1 to Y-173; M-1 to G-172; M-1 to T-171; M-1 to E-170; M-1 to K-169; M-1 to V-168; M-1 to L-167; M-1 to I-166; M-1 to K-165; M-1 to N-164; M-1 to E-163; M-1 to K-162; M-1 to E-161; M-1 to E-160; M-1 to L-159; M-1 to A-158; M-1 to S-157; M-1 to G-156; M-1 to R-155; M-1 to K-154; M-1 to F-153; M-1 to S-152; M-1 to L-151; M-1 to L-150; M-1 to W-149; M-1 to P-148; M-1 to V-147; M-1 to F-146; M-1 to T-145; M-1 to Y-144; M-1 to S-143; M-1 to G-142; M-1 to T-141; M-1 to E-140; M-1 to F-139; M-1 to P-138; M-1 to G-137; M-1 to Q-136; M-1 to V-135; M-1 to A-134; M-1 to R-133; M-1 to K-132; M-1 to N-131; M-1 to R-130; M-1 to S-129; M-1 to N-128; M-1 to Q-127; M-1 to S-126; M-1 to S-125; M-1 to N-124; M-1 to G-123; M-1 to E-122; M-1 to G-121; M-1 to P-120; M-1 to A-119; M-1 to P-118; M-1 to P-117; M-1 to E-116; M-1 to F-115; M-1 to I-114; M-1 to K-113; M-1 to L-112; M-1 to G-111; M-1 to A-110; M-1 to T-109; M-1 to V-108; M-1 to A-107; M-1 to P-106; M-1 to A-105; M-1 to E-104; M-1 to E-103; M-1 to L-102; M-1 to G-101; M-1 to A-100; M-1 to K-99; M-1 to P-98; M-1 to A-97; M-1 to G-96; M-1 to A-95; M-1 to G-94; M-1 to A-93; M-1 to P-92; M-1 to L-91; M-1 to K-90; M-1 to E-89; M-1 to A-88; M-1 to H-87; M-1 to H-86; M-1 to G-85; M-1 to Q-84; M-1 to L-83; M-1 to E-82; M-1 to A-81; M-1 to R-80; M-1 to L-79; M-1 to S-78; M-1 to A-77;

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M-1 to L-76; M-1 to D-75; M-1 to G-74; M-1 to Q-73; M-1 to L-72; M-1 to A-71; M-1 to A-70; M-1 to V-69; M-1 to Q-68; M-1 to Y-67; M-1 to F-66; M-1 to S-65; M-1 to V-64; M-1 to V-63; M-1 to F-62; M-1 to L-61; M-1 to C-60; M-1 to C-59; M-1 to S-58; M-1 to L-57; M-1 to L-56; M-1 to A-55; M-1 to L-54; M-1 to L-53; M-1 to L-52; M-1 to T-51; M-1 to A-50; M-1 to A-49; M-1 to L-48; M-1 to L-47; M-1 to K-46; M-1 to G-45; M-1 to D-44; M-1 to K-43; M-1 to S-42; M-1 to S-41; M-1 to R-40; M-1 to V-39; M-1 to S-38; M-1 to P-37; M-1 to S-36; M-1 to E-35; M-1 to K-34; M-1 to R-33; M-1 to P-32; M-1 to L-31; M-1 to I-30; M-1 to S-29; M-1 to V-28; M-1 to C-27; M-1 to F-26; M-1 to K-25; M-1 to L-24; M-1 to K-23; M-1 to M-22; M-1 to E-21; M-1 to E-20; M-1 to R-19; M-1 to K-18; M-1 to K-17; M-1 to L-16; M-1 to C-15; M-1 to S-14; M-1 to T-13; M-1 to L-12; M-1 to R-11; M-1 to S-10; M-1 to Q-9; M-1 to E-8; M-1 to R-7; and M-1 to E-6 of SEQ ID NO: 19. The present application is also directed to nucleic acid molecules comprising, or alternatively, consisting of, a polynucleotide sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the polynucleotide sequence encoding the Neurokinine-alpha and/or Neurokinine-alphaSV polypeptides described above. The present invention also encompasses the above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these nucleic acids and/or polynucleotide sequences are also encompassed by the invention, as are polypeptides comprising an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the amino acid sequence described above, and polynucleotides that encode such polypeptides.

The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini of a Neurokinine-alphaSV polypeptide, which may be described generally as having residues n⁵-m⁵ of SEQ ID NO: 19, where n⁵ and m⁵ are integers as defined above.

In additional embodiments, the present invention provides polypeptides comprising the amino acid sequence of residues 134-m⁶ of SEQ ID NO: 2, where m⁶ is an integer from 140 to 285, corresponding to the position of the amino acid residue in SEQ ID NO: 2. For example, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, an amino acid sequence selected from the group consisting of residues A-134 to Leu-285; A-134 to L-284; A-134 to K-283; A-134 to L-282; A-134 to A-281; A-134 to G-280; A-134 to F-279; A-134 to F-278; A-134 to T-277; A-134 to V-276; A-134 to D-275; A-134 to G-274; A-134 to D-273; A-134 to L-272; A-134 to S-271; A-134 to I-270; A-134 to Q-269; A-134 to A-268; A-134 to N-267; A-134 to F-266; A-134 to R-265; A-134 to P-264; A-134 to I-263; A-134 to A-262; A-134 to L-261; A-134 to Q-260; A-134 to L-259; A-134 to E-258; A-134 to D-257; A-134 to G-256; A-134 to E-255; A-134 to E-254; A-134 to L-253; A-134 to K-252; A-134 to A-251; A-134 to I-250; A-134 to G-249; A-134 to A-248; A-134 to S-247; A-134 to Y-246; A-134 to C-245; A-134 to S-244; A-134 to N-243; A-134 to N-242; A-134 to P-241; A-134 to L-240; A-134 to T-239; A-134 to E-238; A-134 to P-237; A-134 to M-236; A-134 to N-235; A-134 to Q-234; A-134 to I-233; A-134 to C-232; A-134 to R-231; A-134 to F-230; A-134 to L-229; A-134 to T-228; A-134 to V-227; A-134 to L-226; A-134 to S-225; A-134 to L-224; A-134 to E-223; A-134 to D-222; A-134 to G-221; A-134 to F-220; A-134 to V-219; A-134 to H-218; A-134 to V-217; A-134 to K-216; A-134 to K-215; A-134 to R-214; A-134 to Q-213; A-134 to I-212; A-134 to L-211; A-134 to H-210; A-134 to G-209; A-134 to M-208; A-134 to A-207; A-134 to Y-206; A-134 to T-205; A-134 to K-204; A-134 to D-203; A-134 to T-202; A-134 to Y-201; A-134 to

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L-200; A-134 to V-199; A-134 to Q-198; A-134 to G-197; A-134 to Y-196; A-134 to I-195; A-134 to F-194; A-134 to F-193; A-134 to Y-192; A-134 to G-191; A-134 to T-190; A-134 to E-189; A-134 to K-188; A-134 to V-187; A-134 to L-186; A-134 to I-185; A-134 to K-184; A-134 to N-183; A-134 to E-182; A-134 to K-181; A-134 to E-180; A-134 to E-179; A-134 to L-178; A-134 to A-177; A-134 to S-176; A-134 to G-175; A-134 to R-174; A-134 to K-173; A-134 to F-172; A-134 to S-171; A-134 to L-170; A-134 to L-169; A-134 to W-168; A-134 to P-167; A-134 to V-166; A-134 to F-165; A-134 to T-164; A-134 to Y-163; A-134 to S-162; A-134 to G-161; A-134 to K-160; A-134 to Q-159; A-134 to I-158; A-134 to T-157; A-134 to P-156; A-134 to T-155; A-134 to E-154; A-134 to S-153; A-134 to D-152; A-134 to A-151; A-134 to I-150; A-134 to L-149; A-134 to Q-148; A-134 to L-147; A-134 to C-146; A-134 to D-145; A-134 to Q-144; A-134 to T-143; A-134 to V-142; A-134 to T-141; and A-134 to E-140 of SEQ ID NO:2. The present application is also directed to nucleic acid molecules comprising, or alternatively, consisting of, a polynucleotide sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the polynucleotide sequence encoding the Neutrokine-alpha and/or Neutrokine-alphaSV polypeptides described above. The present invention also encompasses the above polynucleotide sequences fused to a heterologous polynucleotide sequence. Polypeptides encoded by these nucleic acids and/or polynucleotide sequences are also encompassed by the invention, as are polypeptides comprising an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to the amino acid sequence described above, and polynucleotides that encode such polypeptides.

Additional preferred polypeptide fragments of the invention comprise, or alternatively consist of, an amino acid sequence selected from the group consisting of residues: M-1 to C-15; D-2 to L-16; D-3 to K-17; S-4 to K-18; T-5 to R-19; E-6 to E-20; R-7 to E-21; E-8 to M-22; Q-9 to K-23; S-10 to L-24; R-11 to K-25; L-12 to E-26; T-13 to C-27; S-14 to V-28; C-15 to S-29; L-16 to I-30; K-17 to L-31; K-18 to P-32; R-19 to R-33; E-20 to K-34; E-21 to E-35; M-22 to S-36; K-23 to P-37; L-24 to S-38; K-25 to V-39; E-26 to R-40; C-27 to S-41; V-28 to S-42; S-29 to K-43; I-30 to D-44; L-31 to G-45; P-32 to K-46; R-33 to L-47; K-34 to L-48; E-35 to A-49; S-36 to A-50; P-37 to T-51; S-38 to L-52; V-39 to L-53; R-40 to L-54; S-41 to A-55; S-42 to L-56; K-43 to L-57; D-44 to S-58; G-45 to C-59; K-46 to C-60; L-47 to L-61; L-48 to T-62; A-49 to V-63; A-50 to V-64; T-51 to S-65; L-52 to F-66; L-53 to Y-67; L-54 to Q-68; A-55 to V-69; L-56 to A-70; L-57 to A-71; S-58 to L-72; C-59 to Q-73; C-60 to G-74; L-61 to D-75; T-62 to L-76; V-63 to A-77; V-64 to S-78; S-65 to L-79; F-66 to R-80; Y-67 to A-81; Q-68 to E-82; V-69 to L-83; A-70 to Q-84; A-71 to G-85; L-72 to I-86; Q-73 to I-87; G-74 to A-88; D-75 to E-89; L-76 to K-90; A-77 to L-91; S-78 to P-92; L-79 to A-93; R-80 to G-94; A-81 to A-95; E-82 to G-96; L-83 to A-97; Q-84 to P-98; G-85 to K-99; H-86 to A-100; H-87 to G-101; A-88 to L-102; E-89 to E-103; K-90 to E-104; L-91 to A-105; P-92 to P-106; A-93 to A-107; G-94 to V-108; A-95 to T-109; G-96 to A-110; A-97 to G-111; P-98 to L-112; K-99 to K-113; A-100 to I-114; G-101 to F-115; L-102 to E-116; E-103 to P-117; E-104 to P-118; A-105 to A-119; P-106 to P-120; A-107 to G-121; V-108 to E-122; T-109 to G-123; A-110 to N-124; G-111 to S-125; L-112 to S-126; K-113 to Q-127; I-114 to N-128; F-115 to S-129; E-116 to R-130; P-117 to N-131; P-118 to K-132; A-119 to R-133; P-120 to A-134; G-121 to V-135; E-122 to Q-136; G-123 to G-137; N-124 to P-138; S-125 to E-139; S-126 to E-140; Q-127 to T-141; N-128 to V-142; S-129 to T-143; R-130 to Q-144; N-131 to D-145; K-132 to C-146; R-133 to L-147; A-134 to Q-148;

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V-135 to L-149; Q-136 to I-150; G-137 to A-151; P-138 to D-152; E-139 to S-153; E-140 to F-154; T-141 to T-155; V-142 to P-156; T-143 to T-157; Q-144 to I-158; D-145 to Q-159; C-146 to K-160; L-147 to G-161; Q-148 to S-162; L-149 to Y-163; I-150 to T-164; A-151 to F-165; D-152 to V-166; S-153 to P-167; E-154 to W-168; T-155 to L-169; P-156 to L-170; T-157 to S-171; I-158 to F-172; Q-159 to K-173; K-160 to R-174; G-161 to G-175; S-162 to S-176; Y-163 to A-177; T-164 to L-178; F-165 to E-179; V-166 to E-180; P-167 to K-181; W-168 to E-182; L-169 to N-183; L-170 to K-184; S-171 to I-185; F-172 to L-186; K-173 to V-187; R-174 to K-188; G-175 to E-189; S-176 to T-190; A-177 to G-191; L-178 to Y-192; E-179 to F-193; E-180 to F-194; K-181 to I-195; E-182 to Y-196; N-183 to G-197; K-184 to Q-198; I-185 to V-199; L-186 to L-200; V-187 to Y-201; K-188 to T-202; E-189 to D-203; T-190 to K-204; G-191 to T-205; Y-192 to Y-206; F-193 to G-221; M-208 to M-208; I-195 to G-209; Y-196 to I-210; G-197 to L-211; Q-198 to I-212; V-199 to Q-213; L-200 to R-214; Y-201 to K-215; T-202 to K-216; D-203 to V-217; K-204 to H-218; T-205 to V-219; Y-206 to F-220; A-207 to G-221; M-208 to D-222; G-209 to E-223; H-210 to L-224; L-211 to S-225; I-212 to L-226; Q-213 to V-227; R-214 to T-228; K-215 to L-229; K-216 to F-230; V-217 to R-231; H-218 to C-232; V-219 to I-233; F-220 to Q-234; G-221 to N-235; D-222 to M-236; E-223 to P-237; L-224 to E-238; S-225 to T-239; L-226 to L-240; V-227 to P-241; T-228 to N-242; L-229 to N-243; F-230 to S-244; R-231 to C-245; C-232 to Y-246; I-233 to S-247; Q-234 to A-248; N-235 to G-249; M-236 to I-250; P-237 to A-251; E-238 to K-252; T-239 to L-253; L-240 to E-254; P-241 to E-255; N-242 to G-256; N-243 to D-257; S-244 to E-258; C-245 to L-259; Y-246 to Q-260; S-247 to L-261; A-248 to A-262; G-249 to I-263; I-250 to P-264; A-251 to R-265; K-252 to E-266; L-253 to N-267; E-254 to A-268; E-255 to Q-269; G-256 to I-270; D-257 to S-271; E-258 to L-272; L-259 to D-273; Q-260 to Y-274; L-261 to D-275; A-262 to V-276; I-263 to T-277; P-264 to F-278; R-265 to F-279; E-266 to G-280; N-267 to A-281; A-268 to L-282; Q-269 to K-283; I-270 to L-284; and S-271 to L-285 of SEQ ID NO:2. Preferably, these polypeptide fragments have one or more functional activities (e.g., biological activity, antigenicity, and immunogenicity) of Neutrokine-alpha and/or Neutrokine-alpha SV polypeptides of the invention and may be used, for example, to generate or screen for antibodies, as described further below. The present invention is also directed to polypeptides comprising, or alternatively, consisting of, an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to an amino acid sequence described above. The present invention also encompasses the above amino acid sequences fused to a heterologous amino acid sequence as described herein. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Additional preferred polypeptide fragments of the invention comprise, or alternatively consist of, an amino acid sequence selected from the group consisting of residues: M-1 to C-15; D-2 to L-16; D-3 to K-17; S-4 to K-18; T-5 to R-19; E-6 to E-20; R-7 to E-21; E-8 to M-22; Q-9 to K-23; S-10 to L-24; R-11 to K-25; L-12 to E-26; T-13 to C-27; S-14 to V-28; C-15 to S-29; L-16 to I-30; K-17 to L-31; K-18 to P-32; R-19 to R-33; E-20 to K-34; E-21 to E-35; M-22 to S-36; K-23 to P-37; L-24 to S-38; K-25 to V-39; E-26 to R-40; C-27 to S-41; V-28 to S-42; S-29 to K-43; I-30 to D-44; L-31 to G-45; P-32 to K-46; R-33 to L-47; K-34 to L-48; E-35 to A-49; S-36 to A-50; P-37 to T-51; S-38 to L-52; V-39 to L-53; R-40 to L-54; S-41 to A-55; S-42 to L-56; K-43 to L-57; D-44 to S-58; G-45 to C-59; K-46 to C-60; L-47 to L-61; L-48 to T-62; A-49 to

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V-63; A-50 to V-64; T-51 to S-65; L-52 to F-66; L-53 to Y-67; L-54 to Q-68; A-55 to V-69; L-56 to A-70; L-57 to A-71; S-58 to L-72; C-59 to Q-73; C-60 to G-74; L-61 to D-75; T-62 to L-76; V-63 to A-77; V-64 to S-78; S-65 to L-79; F-66 to R-80; Y-67 to A-81; Q-68 to E-82; V-69 to L-83; A-70 to Q-84; A-71 to G-85; L-72 to H-86; Q-73 to H-87; G-74 to A-88; D-75 to E-89; L-76 to K-90; A-77 to L-91; S-78 to P-92; L-79 to A-93; R-80 to G-94; A-81 to A-95; E-82 to G-96; L-83 to A-97; Q-84 to P-98; G-85 to K-99; H-86 to A-100; H-87 to G-101; A-88 to L-102; E-89 to E-103; K-90 to E-104; L-91 to A-105; P-92 to P-106; A-93 to A-107; G-94 to V-108; A-95 to T-109; G-96 to A-110; A-97 to G-111; P-98 to L-112; K-99 to K-113; A-100 to L-114; G-101 to F-115; L-102 to E-116; E-103 to P-117; F-104 to P-118; A-105 to A-119; P-106 to P-120; A-107 to G-121; V-108 to E-122; T-109 to G-123; A-110 to N-124; G-111 to S-125; L-112 to S-126; K-113 to Q-127; L-114 to N-128; S-115 to S-129; E-116 to R-130; P-117 to N-131; P-118 to K-132; A-119 to R-133; P-120 to A-134; G-121 to V-135; F-122 to Q-136; G-123 to G-137; N-124 to P-138; S-125 to E-139; S-126 to E-140; Q-127 to T-141; G-156 to G-142; S-129 to S-143; R-130 to Y-144; N-131 to T-145; K-132 to F-146; R-133 to V-147; A-134 to P-148; V-135 to W-149; Q-136 to L-150; G-137 to L-151; P-138 to S-152; F-139 to F-153; F-140 to K-154; T-141 to R-155; G-142 to G-156; S-143 to S-157; Y-144 to A-158; T-145 to L-159; F-146 to E-160; V-147 to E-161; P-148 to K-162; W-149 to E-163; L-150 to N-164; L-151 to K-165; S-152 to L-166; F-153 to L-167; K-154 to V-168; R-155 to K-169; G-156 to E-170; S-157 to T-171; A-158 to G-172; L-159 to Y-173; E-160 to F-174; E-161 to F-175; K-162 to L-176; E-163 to Y-177; N-164 to G-178; K-165 to Q-179; L-166 to V-180; L-167 to L-181; V-168 to Y-182; K-169 to T-183; E-170 to D-184; T-171 to K-185; G-172 to T-186; Y-173 to Y-187; F-174 to A-188; F-175 to M-189; L-176 to G-190; Y-177 to H-191; G-178 to L-192; Q-179 to L-193; V-180 to Q-194; L-181 to R-195; Y-182 to K-196; T-183 to K-197; D-184 to V-198; K-185 to H-199; T-186 to V-200; Y-187 to F-201; A-188 to G-202; M-189 to D-203; G-190 to E-204; H-191 to L-205; L-192 to S-206; L-193 to L-207; Q-194 to V-208; R-195 to T-209; K-196 to L-210; K-197 to F-211; V-198 to R-212; H-199 to C-213; V-200 to L-214; F-201 to Q-215; G-202 to N-216; D-203 to M-217; E-204 to P-218; L-205 to E-219; S-206 to T-220; L-207 to L-221; V-208 to P-222; T-209 to N-223; L-210 to N-224; F-211 to S-225; R-212 to C-226; C-213 to Y-227; L-214 to S-228; Q-215 to A-229; N-216 to G-230; M-217 to L-231; P-218 to A-232; E-219 to K-233; T-220 to L-234; L-221 to E-235; P-222 to E-236; N-223 to G-237; N-224 to D-238; S-225 to E-239; C-226 to L-240; Y-227 to Q-241; S-228 to L-242; A-229 to A-243; G-230 to L-244; L-231 to P-245; A-232 to R-246; K-233 to E-247; L-234 to N-248; E-235 to A-249; E-236 to Q-250; G-237 to L-251; D-238 to S-252; E-239 to L-253; L-240 to D-254; Q-241 to G-255; L-242 to D-256; A-243 to V-257; L-244 to T-258; P-245 to F-259; R-246 to F-260; E-247 to G-261; N-248 to A-262; A-249 to L-263; Q-250 to K-264; L-251 to L-265; and S-252 to L-266 of SEQ ID NO: 19. Preferably, these polypeptide fragments have one or more functional activities (e.g., biological activity, antigenicity, and immunogenicity) of Neurotrophin- α and/or Neurotrophin- α SV polypeptides of the invention and may be used, for example, to generate or screen for antibodies, as described further below. The present invention is also directed to polypeptides comprising, or alternatively, consisting of, an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to an amino acid sequence described above. The present invention also encompasses the above amino acid sequences fused to a heterologous amino

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acid sequence as described herein. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Additional preferred polypeptide fragments of the invention comprise, or alternatively consist of, an amino acid sequence selected from the group consisting of residues: M-1 to F-15; D-2 to C-16; E-3 to S-17; S-4 to E-18; A-5 to K-19; K-6 to G-20; T-7 to E-21; L-8 to D-22; P-9 to M-23; P-10 to K-24; P-11 to V-25; C-12 to G-26; L-13 to Y-27; C-14 to D-28; F-15 to P-29; C-16 to L-30; S-17 to T-31; E-18 to P-32; K-19 to Q-33; G-20 to K-34; E-21 to E-35; D-22 to E-36; M-23 to G-37; K-24 to A-38; V-25 to W-39; G-26 to F-40; Y-27 to G-41; D-28 to L-42; P-29 to C-43; L-30 to R-44; T-31 to D-45; P-32 to G-46; Q-33 to R-47; K-34 to L-48; E-35 to L-49; F-36 to A-50; G-37 to A-51; A-38 to F-52; W-39 to L-53; F-40 to L-54; G-41 to L-55; L-42 to A-56; C-43 to L-57; R-44 to L-58; D-45 to S-59; G-46 to S-60; R-47 to S-61; L-48 to F-62; L-49 to T-63; A-50 to A-64; A-51 to M-65; T-52 to S-66; L-53 to L-67; L-54 to Y-68; L-55 to Q-69; A-56 to L-70; L-57 to A-71; L-58 to A-72; S-59 to L-73; S-60 to Q-74; S-61 to A-75; F-62 to D-76; T-63 to L-77; A-64 to M-78; M-65 to N-79; S-66 to L-80; L-67 to R-81; Y-68 to A-98; Q-69 to E-83; L-70 to L-84; A-71 to Q-85; A-72 to S-86; L-73 to Y-87; Q-74 to R-88; A-75 to G-89; D-76 to S-90; L-77 to A-91; M-78 to T-92; N-79 to P-93; L-80 to A-94; R-81 to A-95; M-82 to A-96; E-83 to G-97; L-84 to A-98; Q-85 to P-99; S-86 to E-100; Y-87 to L-101; R-88 to T-102; G-89 to A-103; S-90 to G-104; A-91 to V-105; T-92 to K-106; P-93 to L-107; A-94 to L-108; A-95 to T-109; A-96 to P-110; G-97 to A-111; A-98 to A-112; P-99 to P-113; F-100 to R-114; L-101 to P-115; T-102 to H-116; A-103 to N-117; G-104 to S-118; V-105 to S-119; K-106 to R-120; L-107 to G-121; L-108 to H-122; T-109 to R-123; P-110 to N-124; A-111 to R-125; A-112 to R-126; P-113 to A-127; R-114 to A-142; P-115 to Q-129; H-116 to G-130; N-117 to P-131; S-118 to E-132; S-119 to E-133; R-120 to T-134; G-121 to E-135; H-122 to Q-136; R-123 to D-137; N-124 to V-138; R-125 to D-139; R-126 to L-140; A-127 to S-141; F-128 to A-142; Q-129 to P-143; G-130 to P-144; P-131 to A-145; E-132 to P-146; E-133 to C-147; T-134 to L-148; E-135 to P-149; Q-136 to G-150; D-137 to C-151; V-138 to R-152; D-139 to H-153; L-140 to S-154; S-141 to Q-155; A-142 to L-156; P-143 to D-157; P-144 to D-158; A-145 to N-159; P-146 to G-160; C-147 to M-161; L-148 to N-162; P-149 to L-163; G-150 to R-164; C-151 to N-165; R-152 to L-166; H-153 to L-167; S-154 to Q-168; Q-155 to D-169; H-156 to C-170; D-157 to L-171; D-158 to Q-172; N-159 to L-173; G-160 to L-174; M-161 to A-175; N-162 to D-176; L-163 to S-177; R-164 to D-178; N-165 to T-179; L-166 to P-180; L-167 to A-181; Q-168 to L-182; D-169 to E-183; C-170 to E-184; L-171 to K-185; Q-172 to E-186; L-173 to N-187; L-174 to K-188; A-175 to L-189; D-176 to V-190; S-177 to V-191; D-178 to R-192; T-179 to Q-193; P-180 to T-194; A-181 to G-195; L-182 to Y-196; E-183 to F-197; E-184 to F-198; K-185 to L-199; E-186 to Y-200; N-187 to S-201; K-188 to Q-202; L-189 to V-203; V-190 to L-204; V-191 to Y-205; R-192 to T-206; Q-193 to D-207; T-194 to P-208; G-195 to L-209; Y-196 to F-210; F-197 to A-211; F-198 to M-212; L-199 to G-213; Y-200 to H-214; S-201 to V-215; Q-202 to L-216; V-203 to Q-217; L-204 to R-218; Y-205 to K-219; T-206 to K-220; D-207 to V-221; P-208 to H-222; L-209 to V-223; F-210 to F-224; A-211 to G-225; M-212 to D-226; G-213 to E-227; H-214 to L-228; V-215 to S-229; L-216 to L-230; Q-217 to V-231; R-218 to T-232; K-219 to L-233; K-220 to F-234; V-221 to R-235; H-222 to C-236; V-223 to L-237; F-224 to Q-238; G-225 to N-239; D-226 to M-240; E-227 to P-241; L-228 to K-242; S-229 to T-243; L-230 to L-244; V-231 to P-245; T-232 to N-246; L-233 to N-247; F-234 to

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S-248; R-235 to C-249; C-236 to Y-250; I-237 to S-251; Q-238 to A-252; N-239 to G-253; M-240 to I-254; P-241 to A-255; K-242 to R-256; T-243 to L-257; L-244 to E-258; P-245 to F-259; N-246 to G-260; N-247 to D-261; S-248 to E-262; C-249 to I-263; Y-250 to Q-264; S-251 to L-265; A-252 to A-266; G-253 to I-267; I-254 to P-268; A-255 to R-269; R-256 to E-270; L-257 to N-271; E-258 to A-272; E-259 to Q-273; G-260 to I-274; D-261 to S-275; E-262 to R-276; I-263 to N-277; Q-264 to G-278; L-265 to D-279; A-266 to D-280; I-267 to T-281; P-268 to F-282; R-269 to F-283; E-270 to G-284; N-271 to A-285; A-272 to L-286; Q-273 to K-287; I-274 to L-288; and S-275 to L-289 of SEQ ID NO:38. Preferably, these polypeptide fragments have one or more functional activities (e.g., biological activity, antigenicity, and immunogenicity) of Neutrokin- α and/or Neutrokin- α SV polypeptides of the invention and may be used, for example, to generate or screen for antibodies, as described further below. The present invention is also directed to polypeptides comprising, or alternatively, consisting of, an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to an amino acid sequence described above. The present invention also encompasses the above amino acid sequences fused to a heterologous amino acid sequence as described herein. Polynucleotides encoding these polypeptides are also encompassed by the invention.

It will be recognized by one of ordinary skill in the art that some amino acid sequences of the Neutrokin- α and Neutrokin- α SV polypeptides can be varied without significant effect of the structure or function of the polypeptide. If such differences in sequence are contemplated, it should be remembered that there will be critical areas on the polypeptide which determine activity.

Thus, the invention further includes variations of the Neutrokin- α polypeptide which show Neutrokin- α polypeptide functional activity (e.g., biological activity) or which include regions of Neutrokin- α polypeptide such as the polypeptide fragments described herein. The invention also includes variations of the Neutrokin- α SV polypeptide which show Neutrokin- α SV polypeptide functional activity (e.g., biological activity) or which include regions of Neutrokin- α SV polypeptide such as the polypeptide fragments described herein. Such mutants include deletions, insertions, inversions, repeats, and type substitutions selected according to general rules known in the art so as to have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," *Science* 247:1306-1310 (1990), wherein the authors indicate that there are two main approaches for studying the tolerance of an amino acid sequence to change. The first method relies on the process of evolution, in which mutations are either accepted or rejected by natural selection. The second approach uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene and selections or screens to identify sequences that maintain functionality.

As the authors state, these studies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at a certain position of the protein. For example, most buried amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Other such phenotypically silent substitutions are described in Bowie, J. U. et al., *supra*, and the references cited therein. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the

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hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe, Tyr.

Thus, the fragment, derivative or analog of the polypeptide of FIGS. 1A and 1B (SEQ ID NO:2), or that encoded by the deposited cDNA plasmid, may be (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the extracellular domain of the polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the extracellular domain of the polypeptide, such as an IgG Fc fusion region peptide or leader or secretory sequence or a sequence which is employed for purification of the extracellular domain of the polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

Furthermore, the fragment, derivative or analog of the polypeptide of FIGS. 5A and 5B (SEQ ID NO:19), or that encoded by the deposited cDNA plasmid, may be (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the extracellular domain of the polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the extracellular domain of the polypeptide, such as, a soluble biologically active fragment of another TNF ligand family member (e.g., CD40 Ligand), an IgG Fc fusion region peptide or leader or secretory sequence or a sequence which is employed for purification of the extracellular domain of the polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

Thus, the Neutrokin- α and/or Neutrokin- α SV polypeptides of the present invention may include one or more amino acid substitutions, deletions or additions, either from natural mutations or human manipulation. As indicated, changes are preferably of a minor nature, such as conservative amino acid substitutions that do not significantly affect the folding or activity of the protein (see Table II).

TABLE II

Conservative Amino Acid Substitutions.	
Aromatic	Phenylalanine Tryptophan Tyrosine
Hydrophobic	Isoleucine Leucine Valine
Polar	Glutamine Asparagine
Basic	Arginine Lysine Histidine
Acidic	Aspartic Acid Glutamic Acid

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TABLE II-continued

Conservative Amino Acid Substitutions	
Small	Alanine Serine Threonine Methionine Glycine

In one embodiment of the invention, polypeptide comprises, or alternatively consists of, the amino acid sequence of a Neurokinine-alpha or Neurokinine-alphaSV polypeptide having an amino acid sequence which contains at least one conservative amino acid substitution, but not more than 50 conservative amino acid substitutions, even more preferably, not more than 40 conservative amino acid substitutions, still more preferably, not more than 30 conservative amino acid substitutions, and still even more preferably, not more than 20 conservative amino acid substitutions. Of course, in order of ever-increasing preference, it is highly preferable for a peptide or polypeptide to have an amino acid sequence which comprises the amino acid sequence of a Neurokinine-alpha polypeptide, which contains at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 conservative amino acid substitutions.

For example, site directed changes at the amino acid level of Neurokinine-alpha can be made by replacing a particular amino acid with a conservative substitution. Preferred conservative substitution mutations of the Neurokinine-alpha amino acid sequence provided in SEQ ID NO:2 include: M1 replaced with A, G, I, L, S, T, or V; D2 replaced with E; D3 replaced with E; S4 replaced with A, G, I, L, T, M, or V; T5 replaced with A, G, I, L, S, M, or V; E6 replaced with D; R7 replaced with H, or K; E8 replaced with D; Q9 replaced with N; S10 replaced with A, G, I, L, T, M, or V; R11 replaced with H, or K; L12 replaced with A, G, I, S, T, M, or V; T13 replaced with A, G, I, L, S, M, or V; S14 replaced with A, G, I, L, T, M, or V; L16 replaced with A, G, I, S, T, M, or V; K17 replaced with H, or R; K18 replaced with H, or R; R19 replaced with H, or K; E20 replaced with D; E21 replaced with D; M22 replaced with A, G, I, L, S, T, or V; K23 replaced with H, or R; L24 replaced with A, G, I, S, T, M, or V; K25 replaced with H, or R; E26 replaced with D; V28 replaced with A, G, I, L, S, T, or M; S29 replaced with A, G, I, L, T, M, or V; I30 replaced with A, G, L, S, T, M, or V; L31 replaced with A, G, I, S, T, M, or V; R33 replaced with H, or K; K34 replaced with H, or R; E35 replaced with D; S36 replaced with A, G, I, L, T, M, or V; S38 replaced with A, G, I, L, T, M, or V; V39 replaced with A, G, I, L, S, T, or M; R40 replaced with H, or K; S41 replaced with A, G, I, L, T, M, or V; S42 replaced with A, G, I, L, T, M, or V; K43 replaced with H, or R; D44 replaced with E; G45 replaced with A, I, L, S, T, M, or V; K46 replaced with H, or R; I47 replaced with A, G, I, S, T, M, or V; I48 replaced with A, G, I, S, T, M, or V; A49 replaced with G, I, L, S, T, M, or V; A50 replaced with G, I, L, S, T, M, or V; T51 replaced with A, G, I, L, S, M, or V; L52 replaced with A, G, I, S, T, M, or V; L53 replaced with A, G, I, S, T, M, or V; L54 replaced with A, G, I, S, T, M, or V; A55 replaced with G, I, L, S, T, M, or V; L56 replaced with A, G, I, S, T, M, or V; L57 replaced with A, G, I, S, T, M, or V; S58 replaced with A, G, I, L, T, M, or V; L61 replaced with A, G, I, S, T, M, or V; T62 replaced with A, G, I, L, S, M, or V; V63 replaced with A, G, I, L, S, T, or M; V64 replaced with A, G, I, L, S, T, or M; S65 replaced with A, G, I, L, T, M, or V; F66 replaced with W, or Y; Y67 replaced with F, or W; Q68 replaced with N; V69 replaced with A, G, I, L, S, T, or M; A70 replaced with G, I, L, S, T, M, or V; A71 replaced with G, I, L, S, T, M, or V; L72 replaced with A, G, I,

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I, L, S, T, M, or V; Q73 replaced with N; G74 replaced with A, I, L, S, T, M, or V; D75 replaced with E; L76 replaced with A, G, I, L, S, T, M, or V; A77 replaced with G, I, L, S, T, M, or V; S78 replaced with A, G, I, L, T, M, or V; I79 replaced with A, G, I, L, S, T, M, or V; R80 replaced with H, or K; A81 replaced with G, I, L, S, T, M, or V; E82 replaced with D; L83 replaced with A, G, I, L, S, T, M, or V; Q84 replaced with N; G85 replaced with A, I, L, S, T, M, or V; H86 replaced with K, or R; H87 replaced with K, or R; A88 replaced with G, I, L, S, T, M, or V; E89 replaced with D; K90 replaced with H, or R; L91 replaced with A, G, I, L, S, T, M, or V; A93 replaced with G, I, L, S, T, M, or V; G94 replaced with A, I, L, S, T, M, or V; A95 replaced with G, I, L, S, T, M, or V; G96 replaced with A, I, L, S, T, M, or V; A97 replaced with G, I, L, S, T, M, or V; K99 replaced with H, or R; A100 replaced with G, I, L, S, T, M, or V; G101 replaced with A, I, L, S, T, M, or V; L102 replaced with A, G, I, L, S, T, M, or V; E103 replaced with D; E104 replaced with D; A105 replaced with G, I, L, S, T, M, or V; A107 replaced with G, I, L, S, T, M, or V; V108 replaced with A, G, I, L, S, T, or M; T109 replaced with A, G, I, L, S, M, or V; A110 replaced with G, I, L, S, T, M, or V; G111 replaced with A, I, L, S, T, M, or V; L112 replaced with A, G, I, L, S, T, M, or V; K113 replaced with H, or R; I114 replaced with A, G, L, S, T, M, or V; F115 replaced with W, or Y; F116 replaced with D; A119 replaced with G, I, L, S, T, M, or V; G121 replaced with A, I, L, S, T, M, or V; E122 replaced with D; G123 replaced with A, I, L, S, T, M, or V; N124 replaced with Q; S125 replaced with A, G, I, L, T, M, or V; S126 replaced with A, G, I, L, T, M, or V; Q127 replaced with N; N128 replaced with Q; S129 replaced with A, G, I, L, T, M, or V; R130 replaced with H, or K; N131 replaced with Q; K132 replaced with H, or R; R133 replaced with H, or K; A134 replaced with G, I, L, S, T, M, or V; V135 replaced with A, G, I, L, S, T, or M; Q136 replaced with N; G137 replaced with A, I, L, S, T, M, or V; E139 replaced with D; E140 replaced with D; T141 replaced with A, G, I, L, S, M, or V; V142 replaced with A, G, I, L, S, T, or M; T143 replaced with A, G, I, L, S, M, or V; Q144 replaced with N; D145 replaced with E; L147 replaced with A, G, I, S, T, M, or V; Q148 replaced with N; L149 replaced with A, G, I, S, T, M, or V; I150 replaced with A, G, L, S, T, M, or V; A151 replaced with G, I, L, S, T, M, or V; D152 replaced with E; S153 replaced with A, G, I, L, T, M, or V; E154 replaced with D; T155 replaced with A, G, I, L, S, M, or V; T157 replaced with A, G, I, L, S, M, or V; I158 replaced with A, G, L, S, T, M, or V; Q159 replaced with N; K160 replaced with H, or R; G161 replaced with A, I, L, S, T, M, or V; S162 replaced with A, G, I, L, T, M, or V; Y163 replaced with F, or W; T164 replaced with A, G, I, L, S, M, or V; F165 replaced with W, or Y; V166 replaced with A, G, I, L, S, T, or M; W168 replaced with F, or Y; L169 replaced with A, G, I, S, T, M, or V; L170 replaced with A, G, I, S, T, M, or V; S171 replaced with A, G, I, L, T, M, or V; F172 replaced with W, or Y; K173 replaced with H, or R; R174 replaced with H, or K; G175 replaced with A, I, L, S, T, M, or V; S176 replaced with A, G, I, L, T, M, or V; A177 replaced with G, I, L, S, T, M, or V; L178 replaced with A, G, I, S, T, M, or V; E179 replaced with D; E180 replaced with D; K181 replaced with H, or R; E182 replaced with D; N183 replaced with Q; K184 replaced with H, or R; I185 replaced with A, G, L, S, T, M, or V; L186 replaced with A, G, I, S, T, M, or V; V187 replaced with A, G, I, L, S, T, or M; K188 replaced with H, or R; E189 replaced with D; T190 replaced with A, G, I, L, S, M, or V; G191 replaced with A, I, L, S, T, M, or V; Y192 replaced with F, or W; F193 replaced with W, or Y; F194 replaced with W, or Y; I195 replaced with A, G, L, S, T, M, or V; Y196 replaced with F, or W; G197 replaced with A, I, L, S, T, M, or V; Q198 replaced with N; V199 replaced with A, G, I, L, S, T, or M; L200 replaced with A, G, I, S, T,

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M, or V: Y201 replaced with F, or W: T202 replaced with A, G, I, L, S, M, or V: D203 replaced with E: K204 replaced with H, or R: T205 replaced with A, G, I, L, S, M, or V: Y206 replaced with F, or W: A207 replaced with G, I, L, S, T, M, or V: M208 replaced with A, G, I, L, S, T, or V: G209 replaced with A, I, L, S, T, M, or V: H210 replaced with K, or R: L211 replaced with A, G, I, S, T, M, or V: I212 replaced with A, G, I, S, T, M, or V: Q213 replaced with N: R214 replaced with H, or K: K215 replaced with H, or R: K216 replaced with H, or R: V217 replaced with A, G, I, L, S, T, or M: H218 replaced with K, or R: V219 replaced with A, G, I, L, S, T, or M: F220 replaced with W, or Y: G221 replaced with A, I, L, S, T, M, or V: D222 replaced with E: F223 replaced with D: L224 replaced with A, G, I, S, T, M, or V: S225 replaced with A, G, I, L, T, M, or V: L226 replaced with A, G, I, S, T, M, or V: V227 replaced with A, G, I, L, S, T, or M: T228 replaced with A, G, I, L, S, M, or V: L229 replaced with A, G, I, S, T, M, or V: F230 replaced with W, or Y: R231 replaced with H, or K: I233 replaced with A, G, I, S, T, M, or V: Q234 replaced with N: N235 replaced with Q: M236 replaced with A, G, I, L, S, T, or V: E238 replaced with D: T239 replaced with A, G, I, L, S, M, or V: I240 replaced with A, G, I, S, T, M, or V: N242 replaced with Q: N243 replaced with Q: S244 replaced with A, G, I, L, T, M, or V: Y246 replaced with F, or W: S247 replaced with A, G, I, L, T, M, or V: A248 replaced with G, I, L, S, T, M, or V: K252 replaced with H, or R: I253 replaced with A, G, I, S, T, M, or V: F254 replaced with D: F255 replaced with D: G256 replaced with A, I, L, S, T, M, or V: D257 replaced with E: E258 replaced with D: L259 replaced with A, G, I, S, T, M, or V: Q260 replaced with N: L261 replaced with A, G, I, S, T, M, or V: A262 replaced with G, I, L, S, T, M, or V: I263 replaced with A, G, I, S, T, M, or V: R265 replaced with H, or K: E266 replaced with D: N267 replaced with Q: A268 replaced with G, I, L, S, T, M, or V: Q269 replaced with N: I270 replaced with A, G, I, L, S, T, M, or V: S271 replaced with A, G, I, L, T, M, or V: L272 replaced with A, G, I, S, T, M, or V: D273 replaced with E: G274 replaced with A, I, L, S, T, M, or V: D275 replaced with E: V276 replaced with A, G, I, L, S, T, or M: T277 replaced with A, G, I, L, S, M, or V: F278 replaced with W, or Y: F279 replaced with W, or Y: G280 replaced with A, I, L, S, T, M, or V: A281 replaced with G, I, L, S, T, M, or V: I282 replaced with A, G, I, S, T, M, or V: K283 replaced with H, or R: I284 replaced with A, G, I, L, S, T, M, or V: and/or I285 replaced with A, G, I, S, T, M, or V. Polynucleotides encoding these polypeptides are also encompassed by the invention. The resulting Neutrokin- α proteins of the invention may be routinely screened for Neutrokin- α and/or Neutrokin- α SV functional activity and/or physical properties (such as, for example, enhanced or reduced stability and/or solubility). Preferably, the resulting proteins of the invention have an increased and/or a decreased Neutrokin- α and/or Neutrokin- α SV functional activity. More preferably, the resulting Neutrokin- α and/or Neutrokin- α SV proteins of the invention have more than one increased and/or decreased Neutrokin- α and/or Neutrokin- α SV functional activity and/or physical property.

In another embodiment, site directed changes at the amino acid level of Neutrokin- α SV can be made by replacing a particular amino acid with a conservative substitution. Preferred conservative substitution mutations of the Neutrokin- α SV amino acid sequence provided in SEQ ID NO:19 include: M1 replaced with A, G, I, L, S, T, or V: D2 replaced with E: D3 replaced with E: S4 replaced with A, G, I, L, T, M, or V: T5 replaced with A, G, I, L, S, M, or V: I36 replaced with

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D: R7 replaced with H, or K: E8 replaced with D: Q9 replaced with N: S10 replaced with A, G, I, L, T, M, or V: R11 replaced with H, or K: I12 replaced with A, G, I, S, T, M, or V: T13 replaced with A, G, I, L, S, M, or V: S14 replaced with A, G, I, L, T, M, or V: I16 replaced with A, G, I, S, T, M, or V: K17 replaced with H, or R: K18 replaced with H, or R: R19 replaced with H, or K: I20 replaced with D: E21 replaced with D: M22 replaced with A, G, I, L, S, T, or V: K23 replaced with H, or R: L24 replaced with A, G, I, S, T, M, or V: K25 replaced with H, or R: E26 replaced with D: S36 replaced with A, G, I, L, S, T, or M: S29 replaced with A, G, I, L, T, M, or V: I30 replaced with A, G, L, S, T, M, or V: L31 replaced with A, G, I, S, T, M, or V: R33 replaced with H, or K: K34 replaced with H, or R: I35 replaced with D: V38 replaced with A, G, I, L, T, M, or V: S38 replaced with A, G, I, L, T, M, or V: V39 replaced with A, G, I, L, S, T, or M: R40 replaced with H, or K: S41 replaced with A, G, I, L, T, M, or V: S42 replaced with A, G, I, L, T, M, or V: K43 replaced with H, or R: D44 replaced with E: G45 replaced with A, I, L, S, T, M, or V: K46 replaced with H, or R: L47 replaced with A, G, I, S, T, M, or V: I48 replaced with A, G, I, S, T, M, or V: A49 replaced with G, I, L, S, T, M, or V: A50 replaced with G, I, L, S, T, M, or V: T51 replaced with A, G, I, L, S, M, or V: I52 replaced with A, G, I, S, T, M, or V: I53 replaced with A, G, I, S, T, M, or V: I54 replaced with A, G, I, S, T, M, or V: A55 replaced with G, I, L, S, T, M, or V: I56 replaced with A, G, I, S, T, M, or V: I57 replaced with A, G, I, S, T, M, or V: S58 replaced with A, G, I, L, T, M, or V: I61 replaced with A, G, I, S, T, M, or V: T62 replaced with A, G, I, L, S, M, or V: V63 replaced with A, G, I, L, S, T, or M: V64 replaced with A, G, I, L, S, T, or M: S65 replaced with A, G, I, L, T, M, or V: F66 replaced with W, or Y: Y67 replaced with F, or W: Q68 replaced with N: V69 replaced with A, G, I, L, S, T, or M: A70 replaced with G, I, L, S, T, M, or V: A71 replaced with G, I, L, S, T, M, or V: L72 replaced with A, G, I, S, T, M, or V: Q73 replaced with N: G74 replaced with A, I, L, S, T, M, or V: D75 replaced with E: I76 replaced with A, G, I, S, T, M, or V: A77 replaced with G, I, L, S, T, M, or V: S78 replaced with A, G, I, L, T, M, or V: I79 replaced with A, G, I, S, T, M, or V: R80 replaced with H, or K: A81 replaced with G, I, L, S, T, M, or V: E82 replaced with D: I83 replaced with A, G, I, S, T, M, or V: Q84 replaced with N: G85 replaced with A, I, L, S, T, M, or V: H86 replaced with K, or R: H87 replaced with K, or R: A88 replaced with G, I, L, S, T, M, or V: E89 replaced with D: K90 replaced with H, or R: I91 replaced with A, G, I, S, T, M, or V: A93 replaced with G, I, L, S, T, M, or V: G94 replaced with A, I, L, S, T, M, or V: A95 replaced with G, I, L, S, T, M, or V: G96 replaced with A, I, L, S, T, M, or V: A97 replaced with G, I, L, S, T, M, or V: K99 replaced with H, or R: A100 replaced with G, I, L, S, T, M, or V: G101 replaced with A, I, L, S, T, M, or V: I102 replaced with A, G, I, S, T, M, or V: E103 replaced with D: F104 replaced with D: A105 replaced with G, I, L, S, T, M, or V: A107 replaced with G, I, L, S, T, M, or V: V108 replaced with A, G, I, L, S, T, or M: T109 replaced with A, G, I, L, S, M, or V: A110 replaced with G, I, L, S, T, M, or V: G111 replaced with A, I, L, S, T, M, or V: L112 replaced with A, G, I, S, T, M, or V: K113 replaced with H, or R: H114 replaced with A, G, I, S, T, M, or V: F115 replaced with W, or Y: E116 replaced with D: A119 replaced with G, I, L, S, T, M, or V: G121 replaced with A, I, L, S, T, M, or V: E122 replaced with D: G123 replaced with A, I, L, S, T, M, or V: N124 replaced with Q: S125 replaced with A, G, I, L, T, M, or V: S126 replaced with A, G, I, L, T, M, or V: Q127 replaced with N: N128 replaced with Q: S129 replaced with A, G, I, L, T, M, or V: R130 replaced with H, or K: N131 replaced with Q: K132 replaced with H, or R: R133 replaced with H, or K: A134 replaced with G, I, L, S, T, M, or V: V135 replaced with A, G,

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I, L, S, T, or M; Q136 replaced with N; G137 replaced with A, I, L, S, T, M, or V; F139 replaced with D; F140 replaced with D; T141 replaced with A, G, I, L, S, M, or V; G142 replaced with A, I, L, S, T, M, or V; S143 replaced with A, G, I, L, T, M, or V; Y144 replaced with F, or W; T145 replaced with A, G, I, L, S, M, or V; F146 replaced with W, or Y; V147 replaced with A, G, I, L, S, T, or M; W149 replaced with F, or Y; I150 replaced with A, G, I, S, T, M, or V; I151 replaced with A, G, I, S, T, M, or V; S152 replaced with A, G, I, L, T, M, or V; F153 replaced with W, or Y; K154 replaced with H, or R; R155 replaced with H, or K; G156 replaced with A, I, L, S, T, M, or V; S157 replaced with A, G, I, L, T, M, or V; A158 replaced with G, I, L, S, T, M, or V; I159 replaced with A, G, I, S, T, M, or V; E160 replaced with D; E161 replaced with D; K162 replaced with H, or R; E163 replaced with D; N164 replaced with Q; K165 replaced with H, or R; I166 replaced with A, G, I, L, S, T, M, or V; I167 replaced with A, G, I, S, T, M, or V; V168 replaced with A, G, I, L, S, T, or M; K169 replaced with H, or R; F170 replaced with D; T171 replaced with A, G, I, L, S, M, or V; G172 replaced with A, I, L, S, T, M, or V; Y173 replaced with F, or W; F174 replaced with W, or Y; F175 replaced with F, or Y; I176 replaced with A, G, I, L, S, T, M, or V; Y177 replaced with F, or W; G178 replaced with A, I, L, S, T, M, or V; Q179 replaced with N; V180 replaced with A, G, I, L, S, T, or M; L181 replaced with A, G, I, S, T, M, or V; Y182 replaced with F, or W; T183 replaced with A, G, I, L, S, M, or V; D184 replaced with E; K185 replaced with H, or R; T186 replaced with A, G, I, L, S, M, or V; Y187 replaced with F, or W; A188 replaced with A, G, I, L, S, T, M, or V; M189 replaced with A, G, I, L, S, T, or V; G190 replaced with A, I, L, S, T, M, or V; H191 replaced with K, or R; I192 replaced with A, G, I, S, T, M, or V; H193 replaced with A, G, I, L, S, T, M, or V; Q194 replaced with N; R195 replaced with H, or K; K196 replaced with H, or R; K197 replaced with H, or R; V198 replaced with A, G, I, L, S, T, or M; H199 replaced with K, or R; V200 replaced with A, G, I, L, S, T, or M; F201 replaced with W, or Y; G202 replaced with A, I, L, S, T, M, or V; D203 replaced with E; F204 replaced with D; L205 replaced with A, G, I, S, T, M, or V; S206 replaced with A, G, I, L, T, M, or V; I207 replaced with A, G, I, S, T, M, or V; V208 replaced with A, G, I, L, S, T, or M; T209 replaced with A, G, I, L, S, M, or V; I210 replaced with A, G, I, S, T, M, or V; F211 replaced with W, or Y; R212 replaced with H, or K; I214 replaced with A, G, I, S, T, M, or V; Q215 replaced with N; N216 replaced with Q; M217 replaced with A, G, I, L, S, T, or V; E219 replaced with D; T220 replaced with A, G, I, L, S, M, or V; I221 replaced with A, G, I, S, T, M, or V; N223 replaced with Q; N224 replaced with Q; S225 replaced with A, G, I, L, T, M, or V; Y227 replaced with F, or W; S228 replaced with A, G, I, L, T, M, or V; A229 replaced with G, I, L, S, T, M, or V; G230 replaced with A, I, L, S, T, M, or V; I231 replaced with A, G, I, L, S, T, M, or V; A232 replaced with G, I, L, S, T, M, or V; K233 replaced with H, or R; I234 replaced with A, G, I, S, T, M, or V; E235 replaced with D; E236 replaced with D; G237 replaced with A, I, L, S, T, M, or V; D238 replaced with E; E239 replaced with D; I240 replaced with A, G, I, S, T, M, or V; Q241 replaced with N; I242 replaced with A, G, I, S, T, M, or V; A243 replaced with G, I, L, S, T, M, or V; I244 replaced with A, G, I, L, S, T, M, or V; R246 replaced with H, or K; F247 replaced with D; N248 replaced with Q; A249 replaced with G, I, L, S, T, M, or V; Q250 replaced with N; I251 replaced with A, G, I, L, S, T, M, or V; S252 replaced with A, G, I, L, T, M, or V; I253 replaced with A, G, I, S, T, M, or V; D254 replaced with E; G255 replaced with A, I, L, S, T, M, or V; D256 replaced with E; V257 replaced with A, G, I, L, S, T, or M; T258 replaced with A, G, I, L, S, M, or V; F259 replaced with W, or Y; F260 replaced with W, or Y; G261 replaced with

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A, I, L, S, T, M, or V; A262 replaced with G, I, L, S, T, M, or V; I263 replaced with A, G, I, S, T, M, or V; K264 replaced with H, or R; I265 replaced with A, G, I, S, T, M, or V; and/or I266 replaced with A, G, I, S, T, M, or V. Polynucleotides encoding these polypeptides are also encompassed by the invention. The resulting Neutrokin- α proteins of the invention may be routinely screened for Neutrokin- α and/or Neutrokin- α SV functional activity and/or physical properties (such as, for example, enhanced or reduced stability and/or solubility). Preferably, the resulting proteins of the invention have an increased and/or a decreased Neutrokin- α and/or Neutrokin- α SV functional activity. More preferably, the resulting Neutrokin- α and/or Neutrokin- α SV proteins of the invention have more than one increased and/or decreased Neutrokin- α and/or Neutrokin- α SV functional activity and/or physical property.

In another embodiment, site directed changes at the amino acid level of Neutrokin- α can be made by replacing a particular amino acid with a conservative substitution. Preferred conservative substitution mutations of the Neutrokin- α amino acid sequence provided in SEQ ID NO:23 include: R1 replaced with H, or K; V2 replaced with A, G, I, L, S, T, or M; V3 replaced with A, G, I, L, S, T, or M; D4 replaced with E; I5 replaced with A, G, I, S, T, M, or V; S6 replaced with A, G, I, L, T, M, or V; A7 replaced with G, I, L, S, T, M, or V; A10 replaced with G, I, L, S, T, M, or V; L13 replaced with A, G, I, S, T, M, or V; G15 replaced with A, I, L, S, T, M, or V; R17 replaced with H, or K; H18 replaced with K, or R; S19 replaced with A, G, I, L, T, M, or V; Q20 replaced with N; I21 replaced with K, or R; D22 replaced with E; D23 replaced with E; N24 replaced with Q; G25 replaced with A, I, L, S, T, M, or V; M26 replaced with A, G, I, L, S, T, or V; N27 replaced with Q; I28 replaced with A, G, I, S, T, M, or V; R29 replaced with H, or K; N30 replaced with Q; R31 replaced with H, or K; T32 replaced with A, G, I, L, S, M, or V; Y33 replaced with F, or W; T34 replaced with A, G, I, L, S, M, or V; F35 replaced with W, or Y; V36 replaced with A, G, I, L, S, T, or M; W38 replaced with F, or Y; I39 replaced with A, G, I, S, T, M, or V; I40 replaced with A, G, I, S, T, M, or V; S41 replaced with A, G, I, L, T, M, or V; F42 replaced with W, or Y; K43 replaced with H, or R; R44 replaced with H, or K; G45 replaced with A, I, L, S, T, M, or V; N46 replaced with Q; A47 replaced with G, I, L, S, T, M, or V; I48 replaced with A, G, I, S, T, M, or V; E49 replaced with D; E50 replaced with D; K51 replaced with H, or R; E52 replaced with D; N53 replaced with Q; K54 replaced with H, or R; I55 replaced with A, G, I, S, T, M, or V; V56 replaced with A, G, I, L, S, T, or M; V57 replaced with A, G, I, L, S, T, or M; R58 replaced with H, or K; Q59 replaced with N; T60 replaced with A, G, I, L, S, M, or V; G61 replaced with A, I, L, S, T, M, or V; Y62 replaced with F, or W; F63 replaced with W, or Y; F64 replaced with W, or Y; I65 replaced with A, G, I, S, T, M, or V; Y66 replaced with F, or W; S67 replaced with A, G, I, L, T, M, or V; Q68 replaced with N; V69 replaced with A, G, I, L, S, T, or M; I70 replaced with A, G, I, S, T, M, or V; Y71 replaced with F, or W; T72 replaced with A, G, I, L, S, M, or V; D73 replaced with E; I75 replaced with A, G, I, S, T, M, or V; F76 replaced with W, or Y; A77 replaced with G, I, L, S, T, M, or V; M78 replaced with A, G, I, L, S, T, or V; G79 replaced with A, I, L, S, T, M, or V; I180 replaced with K, or R; V81 replaced with A, G, I, L, S, T, or M; I82 replaced with A, G, I, S, T, M, or V; Q83 replaced with N; R84 replaced with H, or K; K85 replaced with H, or R; K86 replaced with H, or R; V87 replaced with A, G, I, L, S, T, or M; H88 replaced with K, or R; V89 replaced with A, G, I, L, S, T, or M; F90 replaced with W, or Y; G91 replaced with A, I, L, S, T, M, or V; D92 replaced with E; E93 replaced with D; L94 replaced with A, G, I, S, T,

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M. or V: S95 replaced with A. G. I. L. S. T. M. or V: I.96 replaced with A. G. I. L. S. T. M. or V: V97 replaced with A. G. I. L. S. T. M. or V: T98 replaced with A. G. I. L. S. T. M. or V: I.99 replaced with A. G. I. L. S. T. M. or V: F100 replaced with W. or Y: R10 replaced with H. or K: I103 replaced with A. G. I. L. S. T. M. or V: Q104 replaced with N: N105 replaced with Q: M106 replaced with A. G. I. L. S. T. M. or V: K108 replaced with H. or R: T109 replaced with A. G. I. L. S. T. M. or V: I.110 replaced with A. G. I. L. S. T. M. or V: N112 replaced with Q: N113 replaced with Q: S114 replaced with A. G. I. L. S. T. M. or V: Y116 replaced with F. or W: S117 replaced with A. G. I. L. S. T. M. or V: A118 replaced with G. I. L. S. T. M. or V: G119 replaced with A. G. I. L. S. T. M. or V: I120 replaced with A. G. I. L. S. T. M. or V: A121 replaced with G. I. L. S. T. M. or V: R122 replaced with H. or K: I.123 replaced with A. G. I. L. S. T. M. or V: E124 replaced with D: E125 replaced with D: G126 replaced with A. G. I. L. S. T. M. or V: D127 replaced with E: E128 replaced with D: I129 replaced with A. G. I. L. S. T. M. or V: Q130 replaced with N: I131 replaced with A. G. I. L. S. T. M. or V: A132 replaced with G. I. L. S. T. M. or V: I133 replaced with A. G. I. L. S. T. M. or V: R135 replaced with H. or K: E136 replaced with D: N137 replaced with Q: A138 replaced with G. I. L. S. T. M. or V: Q139 replaced with N: I140 replaced with A. G. I. L. S. T. M. or V: S141 replaced with A. G. I. L. S. T. M. or V: R142 replaced with H. or K: N143 replaced with Q: G144 replaced with A. G. I. L. S. T. M. or V: D145 replaced with E: D146 replaced with E: T147 replaced with A. G. I. L. S. T. M. or V: F148 replaced with W. or Y: F149 replaced with W. or Y: G150 replaced with A. G. I. L. S. T. M. or V: A151 replaced with G. I. L. S. T. M. or V: I152 replaced with A. G. I. L. S. T. M. or V: K153 replaced with H. or R: I.154 replaced with A. G. I. L. S. T. M. or V: and/or I.155 replaced with A. G. I. L. S. T. M. or V. Polynucleotides encoding these polypeptides are also encompassed by the invention. The resulting Neutrokin- α proteins of the invention may be routinely screened for Neutrokin- α and/or Neutrokin- α SV functional activity and/or physical properties (such as, for example, enhanced or reduced stability and/or solubility). Preferably, the resulting proteins of the invention have an increased and/or a decreased Neutrokin- α and/or Neutrokin- α SV functional activity. More preferably, the resulting Neutrokin- α and/or Neutrokin- α SV proteins of the invention have more than one increased and/or decreased Neutrokin- α and/or Neutrokin- α SV functional activity and/or physical property.

In another embodiment, site directed changes at the amino acid level of Neutrokin- α can be made by replacing a particular amino acid with a conservative substitution. Preferred conservative substitution mutations of the Neutrokin- α amino acid sequence provided in SEQ ID NO:38 include: M1 replaced with A. G. I. L. S. T. M. or V: D2 replaced with E: E3 replaced with D: S4 replaced with A. G. I. L. S. T. M. or V: A5 replaced with G. I. L. S. T. M. or V: K6 replaced with H. or R: T7 replaced with A. G. I. L. S. T. M. or V: I.8 replaced with A. G. I. L. S. T. M. or V: I.13 replaced with A. G. I. L. S. T. M. or V: F15 replaced with W. or Y: S17 replaced with A. G. I. L. S. T. M. or V: E18 replaced with D: K19 replaced with H. or R: G20 replaced with A. G. I. L. S. T. M. or V: E21 replaced with D: D22 replaced with E: M23 replaced with A. G. I. L. S. T. M. or V: K24 replaced with H. or R: V25 replaced with A. G. I. L. S. T. M. or V: G26 replaced with A. G. I. L. S. T. M. or V: Y27 replaced with F. or W: D28 replaced with E: I30 replaced with A. G. I. L. S. T. M. or V: T31 replaced with A. G. I. L. S. T. M. or V: Q33 replaced with N: K34 replaced with H. or R: F35 replaced with D: E36 replaced with D: G37 replaced with A. G. I. L. S. T. M. or V: A38 replaced with G. I. L. S. T. M. or V: W39 replaced with F. or Y: F40 replaced with W. or Y: G41 replaced

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with A. G. I. L. S. T. M. or V: I42 replaced with A. G. I. L. S. T. M. or V: R44 replaced with H. or K: D45 replaced with E: G46 replaced with A. G. I. L. S. T. M. or V: R47 replaced with H. or K: I.48 replaced with A. G. I. L. S. T. M. or V: I.49 replaced with A. G. I. L. S. T. M. or V: A50 replaced with G. I. L. S. T. M. or V: A51 replaced with G. I. L. S. T. M. or V: T52 replaced with A. G. I. L. S. T. M. or V: I.53 replaced with A. G. I. L. S. T. M. or V: I.54 replaced with A. G. I. L. S. T. M. or V: I.55 replaced with A. G. I. L. S. T. M. or V: A56 replaced with G. I. L. S. T. M. or V: I.57 replaced with A. G. I. L. S. T. M. or V: I.58 replaced with A. G. I. L. S. T. M. or V: S59 replaced with A. G. I. L. S. T. M. or V: S60 replaced with A. G. I. L. S. T. M. or V: S61 replaced with A. G. I. L. S. T. M. or V: F62 replaced with W. or Y: T63 replaced with A. G. I. L. S. T. M. or V: A64 replaced with G. I. L. S. T. M. or V: M65 replaced with A. G. I. L. S. T. M. or V: S66 replaced with A. G. I. L. S. T. M. or V: I.67 replaced with A. G. I. L. S. T. M. or V: Y68 replaced with F. or W: Q69 replaced with N: I.70 replaced with A. G. I. L. S. T. M. or V: A71 replaced with G. I. L. S. T. M. or V: A72 replaced with G. I. L. S. T. M. or V: I.73 replaced with A. G. I. L. S. T. M. or V: Q74 replaced with N: A75 replaced with G. I. L. S. T. M. or V: D76 replaced with E: I.77 replaced with A. G. I. L. S. T. M. or V: M78 replaced with A. G. I. L. S. T. M. or V: N79 replaced with Q: I.80 replaced with A. G. I. L. S. T. M. or V: R81 replaced with H. or K: M82 replaced with A. G. I. L. S. T. M. or V: E83 replaced with D: I.84 replaced with A. G. I. L. S. T. M. or V: Q85 replaced with N: S86 replaced with A. G. I. L. S. T. M. or V: Y87 replaced with F. or W: R88 replaced with H. or K: G89 replaced with A. G. I. L. S. T. M. or V: S90 replaced with A. G. I. L. S. T. M. or V: A91 replaced with G. I. L. S. T. M. or V: T92 replaced with A. G. I. L. S. T. M. or V: A94 replaced with G. I. L. S. T. M. or V: A95 replaced with G. I. L. S. T. M. or V: A96 replaced with G. I. L. S. T. M. or V: G97 replaced with A. G. I. L. S. T. M. or V: A98 replaced with G. I. L. S. T. M. or V: E100 replaced with D: I.101 replaced with A. G. I. L. S. T. M. or V: T102 replaced with A. G. I. L. S. T. M. or V: A103 replaced with G. I. L. S. T. M. or V: G104 replaced with A. G. I. L. S. T. M. or V: V105 replaced with A. G. I. L. S. T. M. or V: K106 replaced with H. or R: I.107 replaced with A. G. I. L. S. T. M. or V: I.108 replaced with A. G. I. L. S. T. M. or V: T109 replaced with A. G. I. L. S. T. M. or V: A111 replaced with G. I. L. S. T. M. or V: A112 replaced with G. I. L. S. T. M. or V: R114 replaced with H. or K: I116 replaced with K. or R: N117 replaced with Q: S118 replaced with A. G. I. L. S. T. M. or V: S119 replaced with A. G. I. L. S. T. M. or V: R120 replaced with H. or K: G121 replaced with A. G. I. L. S. T. M. or V: I122 replaced with K. or R: R123 replaced with H. or K: N124 replaced with Q: R125 replaced with H. or K: R126 replaced with H. or K: A127 replaced with G. I. L. S. T. M. or V: F128 replaced with W. or Y: Q129 replaced with N: G130 replaced with A. G. I. L. S. T. M. or V: E132 replaced with D: E133 replaced with D: T134 replaced with A. G. I. L. S. T. M. or V: E135 replaced with D: Q136 replaced with N: D137 replaced with E: V138 replaced with A. G. I. L. S. T. M. or V: D139 replaced with E: L140 replaced with A. G. I. L. S. T. M. or V: S141 replaced with A. G. I. L. S. T. M. or V: A142 replaced with G. I. L. S. T. M. or V: A145 replaced with G. I. L. S. T. M. or V: I.148 replaced with A. G. I. L. S. T. M. or V: G150 replaced with A. G. I. L. S. T. M. or V: R152 replaced with H. or K: H153 replaced with K. or R: S154 replaced with A. G. I. L. S. T. M. or V: Q155 replaced with N: H156 replaced with K. or R: D157 replaced with E: D158 replaced with E: N159 replaced with Q: G160 replaced with A. G. I. L. S. T. M. or V: M161 replaced with A. G. I. L. S. T. M. or V: N162 replaced with Q: L163 replaced with A. G. I. L. S. T. M. or V: R164 replaced with H. or K: N165 replaced with Q: I166 replaced with A. G. I. L. S. T. M. or V: I167 replaced with A. G. I. L. S. T. M. or V: Q168 replaced with N: D169 replaced with E: I.171 replaced with A. G. I. L. S.

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T, M, or V: Q172 replaced with N; I:173 replaced with A, G, I, S, T, M, or V: I:174 replaced with A, G, I, S, T, M, or V: A175 replaced with G, I, L, S, T, M, or V: D176 replaced with E; S177 replaced with A, G, I, L, T, M, or V: D178 replaced with E; T179 replaced with A, G, I, L, S, M, or V: A181 replaced with G, I, L, S, T, M, or V: I:182 replaced with A, G, I, S, T, M, or V: F183 replaced with D; F184 replaced with D; K185 replaced with H, or R; F186 replaced with D; N187 replaced with Q; K188 replaced with H, or R; I189 replaced with A, G, I, S, T, M, or V: V190 replaced with A, G, I, L, S, T, or M; V191 replaced with A, G, I, L, S, T, or M; R192 replaced with H, or K; Q193 replaced with N; T194 replaced with A, G, I, L, S, M, or V: G195 replaced with A, I, L, S, T, M, or V: Y196 replaced with F, or W; F197 replaced with W, or Y; F198 replaced with W, or Y; I199 replaced with A, G, I, S, T, M, or V: Y200 replaced with F, or W; S201 replaced with A, G, I, L, T, M, or V: Q202 replaced with N; V203 replaced with A, G, I, L, S, T, or M; I:204 replaced with A, G, I, S, T, M, or V: Y205 replaced with F, or W; T206 replaced with A, G, I, L, S, M, or V: D207 replaced with E; I209 replaced with A, G, I, S, T, M, or V: F210 replaced with W, or Y; A211 replaced with G, I, L, S, T, M, or V: M212 replaced with A, G, I, L, S, T, or V: G213 replaced with A, I, L, S, T, M, or V: I214 replaced with K, or R; V215 replaced with A, G, I, L, S, T, or M; I216 replaced with A, G, I, L, S, T, M, or V: Q217 replaced with N; R218 replaced with H, or K; K219 replaced with H, or R; K220 replaced with H, or R; V221 replaced with A, G, I, L, S, T, or M; I222 replaced with K, or R; V223 replaced with A, G, I, L, S, T, or M; F224 replaced with W, or Y; G225 replaced with A, I, L, S, T, M, or V: D226 replaced with E; E227 replaced with D; I228 replaced with A, G, I, S, T, M, or V: S229 replaced with A, G, I, L, T, M, or V: I230 replaced with A, G, I, S, T, M, or V: V231 replaced with A, G, I, L, S, T, or M; T232 replaced with A, G, I, L, S, M, or V: I233 replaced with A, G, I, S, T, M, or V: F234 replaced with W, or Y; R235 replaced with H, or K; I237 replaced with A, G, I, S, T, M, or V: Q238 replaced with N; N239 replaced with Q; M240 replaced with A, G, I, L, S, T, or V: K242 replaced with H, or R; T243 replaced with A, G, I, L, S, M, or V: I244 replaced with A, G, I, S, T, M, or V: N246 replaced with Q; N247 replaced with Q; S248 replaced with A, G, I, L, T, M, or V: Y250 replaced with F, or W; S251 replaced with A, G, I, L, T, M, or V: A252 replaced with G, I, L, S, T, M, or V: G253 replaced with A, I, L, S, T, M, or V: I254 replaced with A, G, I, L, S, T, M, or V: A255 replaced with G, I, L, S, T, M, or V: R256 replaced with H, or K; I257 replaced with A, G, I, S, T, M, or V: I258 replaced with D; E259 replaced with D; G260 replaced with A, I, L, S, T, M, or V: D261 replaced with F; F262 replaced with D; I263 replaced with A, G, I, L, S, T, M, or V: Q264 replaced with N; L265 replaced with A, G, I, S, T, M, or V: A266 replaced with G, I, L, S, T, M, or V: I267 replaced with A, G, I, L, S, T, M, or V: R269 replaced with H, or K; F270 replaced with D; N271 replaced with Q; A272 replaced with G, I, L, S, T, M, or V: Q273 replaced with N; I274 replaced with A, G, I, L, S, T, M, or V: S275 replaced with A, G, I, L, T, M, or V: R276 replaced with H, or K; N277 replaced with Q; G278 replaced with A, I, L, S, T, M, or V: D279 replaced with E; D280 replaced with E; T281 replaced with A, G, I, L, S, M, or V: F282 replaced with W, or Y; F283 replaced with W, or Y; G284 replaced with A, I, L, S, T, M, or V: A285 replaced with G, I, L, S, T, M, or V: I286 replaced with A, G, I, S, T, M, or V: K287 replaced with H, or R; I288 replaced with A, G, I, S, T, M, or V: and/or L289 replaced with A, G, I, L, S, T, M, or V. Polynucleotides encoding these polypeptides are also encompassed by the invention. The resulting Neurotrophin- α proteins of the invention may be routinely screened for Neurotrophin- α and/or Neurotrophin- α SV functional activity

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and/or physical properties (such as, for example, enhanced or reduced stability and/or solubility). Preferably, the resulting proteins of the invention have an increased and/or a decreased Neurotrophin- α and/or Neurotrophin- α SV functional activity. More preferably, the resulting Neurotrophin- α and/or Neurotrophin- α SV proteins of the invention have more than one increased and/or decreased Neurotrophin- α and/or Neurotrophin- α SV functional activity and/or physical property.

Amino acids in the Neurotrophin- α and/or Neurotrophin- α SV polypeptides of the present invention that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham and Wells, *Science* 244:1081-1085 (1989)). The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for functional activity, such as ligand binding and the ability to stimulate lymphocyte (e.g., B cell) as, for example, proliferation, differentiation, and/or activation.

Of special interest are substitutions of charged amino acids with other charged or neutral amino acids which may produce proteins with highly desirable improved characteristics, such as less aggregation. Aggregation may not only reduce activity but also be problematic when preparing pharmaceutical formulations, because aggregates can be immunogenic (Pinckard et al., *Clin. Exp. Immunol.* 2:331-340 (1967); Robbins et al., *Diabetes* 36: 838-845 (1987); Cleland et al., *Crit. Rev. Therapeutic Drug Carrier Systems* 10:307-377 (1993)).

In another embodiment, the invention provides for polypeptides having amino acid sequences containing non-conservative substitutions of the amino acid sequence provided in SEQ ID NO:2. For example, non-conservative substitutions of the Neurotrophin- α protein sequence provided in SEQ ID NO:2 include: M1 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; D2 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; D3 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; S4 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; T5 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I6 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; R7 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; F8 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; Q9 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; S10 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; R11 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; I12 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; T13 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; S14 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; C15 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, or P; I16 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; K17 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; K18 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; R19 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; E20 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; E21 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; M22 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; K23 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; I24 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; K25 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; E26 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; C27 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, or P; V28 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; S29 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I30 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I31 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; P32

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Neutrokin- α and/or Neutrokin- α SV functional activities and/or physical properties (such as, for example, enhanced or reduced stability and/or solubility) described throughout the specification and known in the art. Preferably, the resulting proteins of the invention have an increased and/or a decreased Neutrokin- α and/or Neutrokin- α SV functional activity. More preferably, the resulting Neutrokin- α and/or Neutrokin- α SV proteins of the invention have more than one increased and/or decreased Neutrokin- α and/or Neutrokin- α SV functional activity and/or physical property.

In an additional embodiment, Neutrokin- α polypeptides of the invention comprise, or alternatively consist of, more than one amino acid (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30 and 50) replaced with the substituted amino acids as described above (either conservative or nonconservative).

In another embodiment of the invention, non-conservative substitutions of the Neutrokin- α SV protein sequence provided in SEQ ID NO:19 include: M1 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; D2 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; D3 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; S4 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; T5 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; E6 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; R7 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; E8 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; Q9 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; S10 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; R11 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I12 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; T13 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; S14 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; C15 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I16 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; K17 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; K18 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; R19 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; E20 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; E21 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; M22 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; K23 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; L24 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; K25 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; E26 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; C27 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, or P; V28 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; S29 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I30 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I31 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; P32 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, or C; R33 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; K34 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; E35 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; S36 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; P37 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, or C; S38 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; V39 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; R40 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; S41 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; S42 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; K43 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; D44 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; G45 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; K46 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; I47 replaced with

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D, E, H, K, R, N, Q, F, W, Y, P, or C; I48 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; A49 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; A50 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; T51 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; L52 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; L53 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; L54 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; A55 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; L56 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; L57 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; S58 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; C59 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, or P; C60 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, or P; I61 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; T62 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; V63 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; V64 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; S65 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; F66 replaced with D, E, H, K, R, N, Q, A, G, I, L, S, T, M, V, P, or C; Y67 replaced with D, E, H, K, R, N, Q, A, G, I, L, S, T, M, V, P, or C; Q68 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, F, W, Y, P, or C; V69 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; A70 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; A71 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I72 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; Q73 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, F, W, Y, P, or C; G74 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I75 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; I76 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; A77 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; S78 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I79 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; R80 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; A81 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; E82 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; I83 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; Q84 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, F, W, Y, P, or C; G85 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; H86 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; H87 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; A88 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; E89 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; K90 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; I91 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; P92 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, or C; A93 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; G94 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; A95 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; G96 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; A97 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; P98 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, or C; K99 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; A100 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; G101 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I102 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; E103 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; E104 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; A105 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; P106 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, or C; A107 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; V108 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; T109 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; A110 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; G111 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; L112 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; K113 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or

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or C: I.240 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; Q241 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, F, W, Y, P, or C; I.242 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; A243 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I244 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; P245 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; R246 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; I247 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; N248 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, F, W, Y, P, or C; A249 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; Q250 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, F, W, Y, P, or C; I251 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; S252 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I.253 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; D254 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; G255 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; D256 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; V257 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; T258 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; F259 replaced with D, E, H, K, R, N, Q, A, G, I, L, S, T, M, V, P, or C; F260 replaced with D, E, H, K, R, N, Q, A, G, I, L, S, T, M, V, P, or C; G261 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; A262 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I.263 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; K264 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; I.265 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; and/or I.266 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C. Polynucleotides encoding these polypeptides are also encompassed by the invention. The resulting Neurotrophin- α proteins of the invention may be routinely screened for Neurotrophin- α and/or Neurotrophin- α SV functional activities and/or physical properties (such as, for example, enhanced or reduced stability and/or solubility) described throughout the specification and known in the art. Preferably, the resulting proteins of the invention have an increased and/or a decreased Neurotrophin- α and/or Neurotrophin- α SV functional activity. More preferably, the resulting Neurotrophin- α and/or Neurotrophin- α SV proteins of the invention have more than one increased and/or decreased Neurotrophin- α and/or Neurotrophin- α SV functional activity and/or physical property.

In an additional embodiment, Neurotrophin- α polypeptides of the invention comprise, or alternatively consist of, more than one amino acid (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30 and 50) replaced with the substituted amino acids as described above (either conservative or nonconservative).

For example, preferred non-conservative substitutions of the Neurotrophin- α protein sequence provided in SEQ ID NO:23 include: R1 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; V2 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; V3 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I24 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; I.5 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; S6 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; A7 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; P8 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; P9 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; A10 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; P11 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; C12 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; P13 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; P14 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; G15 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; C16 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; P17 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or

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C; H18 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; S19 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; Q20 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, F, W, Y, P, or C; H21 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; D22 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; D23 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; N24 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, F, W, Y, P, or C; G25 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; M26 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; N27 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, F, W, Y, P, or C; L28 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; R29 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; N30 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, F, W, Y, P, or C; R31 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; T32 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; Y33 replaced with D, E, H, K, R, N, Q, A, G, I, L, S, T, M, V, P, or C; T34 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; F35 replaced with D, E, H, K, R, N, Q, A, G, I, L, S, T, M, V, P, or C; V36 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; P37 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; W38 replaced with D, E, H, K, R, N, Q, A, G, I, L, S, T, M, V, P, or C; I.39 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I.40 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; S41 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; F42 replaced with D, E, H, K, R, N, Q, A, G, I, L, S, T, M, V, P, or C; K43 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; R44 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; G45 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; N46 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, F, W, Y, P, or C; A47 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I.48 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I.49 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; E50 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; K51 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; I52 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; N53 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, F, W, Y, P, or C; K54 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; I55 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; V56 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; V57 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; R58 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; Q59 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, F, W, Y, P, or C; T60 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; G61 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; Y62 replaced with D, E, H, K, R, N, Q, A, G, I, L, S, T, M, V, P, or C; F63 replaced with D, E, H, K, R, N, Q, A, G, I, L, S, T, M, V, P, or C; F64 replaced with D, E, H, K, R, N, Q, A, G, I, L, S, T, M, V, P, or C; I65 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; Y66 replaced with D, E, H, K, R, N, Q, A, G, I, L, S, T, M, V, P, or C; S67 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; Q68 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, F, W, Y, P, or C; V69 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I.70 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; Y71 replaced with D, E, H, K, R, N, Q, A, G, I, L, S, T, M, V, P, or C; T72 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; I73 replaced with H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; P74 replaced with D, E, H, K, R, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; I75 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; F76 replaced with D, E, H, K, R, N, Q, A, G, I, L, S, T, M, V, P, or C; A77 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; M78 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; G79 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C; H80 replaced with D, E, A, G, I, L, S, T, M, V, N, Q, F, W, Y, P, or C; V81 replaced with D, E,

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H. K. R. N. Q. F. W. Y. P. or C: I82 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: Q83 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: R84 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: K85 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: K86 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: V87 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: I188 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: V89 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: F90 replaced with D. E. H. K. R. N. Q. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: G91 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: D92 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: F93 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: I194 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: S95 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: I196 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: V97 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: T98 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: I199 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: F100 replaced with D. E. H. K. R. N. Q. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: R101 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: C102 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: Q103 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: Q104 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: N105 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: M106 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: P107 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: K108 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: T109 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: I110 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: P111 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: N112 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: N113 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: S114 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: C115 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: P116 replaced with D. E. H. K. R. N. Q. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: S117 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: A118 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: G119 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: I120 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: A121 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: R122 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: I123 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: F124 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: F125 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: G126 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: D127 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: F128 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: I129 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: Q130 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: I131 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: A132 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: I133 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: P134 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: R135 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: E136 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: N137 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: A138 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: Q139 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: I140 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: S141 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: R142 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: N143 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: G144 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: D145

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replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: D146 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: T147 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: F148 replaced with D. E. H. K. R. N. Q. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: F149 replaced with D. E. H. K. R. N. Q. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: G150 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: A151 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: I152 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: K153 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: I154 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: and/or I155 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C. Polynucleotides encoding these polypeptides are also encompassed by the invention. The resulting Neurokinine-alpha proteins of the invention may be routinely screened for Neurokinine-alpha and/or Neurokinine-alphaSV functional activities and/or physical properties (such as, for example, enhanced or reduced stability and/or solubility) described throughout the specification and known in the art. Preferably, the resulting proteins of the invention have an increased and/or a decreased Neurokinine-alpha and/or Neurokinine-alphaSV functional activity. More preferably, the resulting Neurokinine-alpha and/or Neurokinine-alphaSV proteins of the invention have more than one increased and/or decreased Neurokinine-alpha and/or Neurokinine-alphaSV functional activity and/or physical property.

In an additional embodiment, Neurokinine-alpha polypeptides of the invention comprise, or alternatively consist of, more than one amino acid (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30 and 50) replaced with the substituted amino acids as described above (either conservative or nonconservative).

For example, preferred non-conservative substitutions of the Neurokinine-alpha protein sequence provided in SEQ ID NO:38 include: M1 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: D2 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: I3 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: S4 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: A5 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: K6 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: T7 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: I8 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: P9 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: P10 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: P11 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: C12 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: I13 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: C14 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: F15 replaced with D. E. H. K. R. N. Q. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: C16 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: S17 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: E18 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: K19 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: G20 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: E21 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: D22 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: M23 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: K24 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: V25 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: G26 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: Y27 replaced with D. E. H. K. R. N. Q. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: D28 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: P29 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: I30 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: T31 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: P32 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: Q33 replaced with D. E. H. K.

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R.A.G. I.L.S.T.M.V.F.W.Y.P. or C: K34 replaced with D.E.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: F35 replaced with H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: F36 replaced with H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: G37 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: A38 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: W39 replaced with D.E.H.K.R.N.Q.A.G. I.L.S.T.M.V.P. or C: F40 replaced with D.E.H.K.R.N.Q.A.G. I.L.S.T.M.V.P. or C: G41 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: I42 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: C43 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: R44 replaced with D.E.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: I45 replaced with H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: G46 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: R47 replaced with D.E.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: I48 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: L49 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: A50 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: A51 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: T52 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: L53 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: I54 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: L55 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: A56 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: L57 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: L58 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: S59 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: S60 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: S61 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: F62 replaced with D.E.H.K.R.N.Q.A.G. I.L.S.T.M.V.P. or C: T63 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: A64 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: M65 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: S66 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: I67 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: Y68 replaced with D.E.H.K.R.N.Q.A.G. I.L.S.T.M.V.P. or C: Q69 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.F.W.Y.P. or C: I70 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: A71 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: A72 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: I73 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: Q74 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.F.W.Y.P. or C: A75 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: D76 replaced with H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: I77 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: M78 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: N79 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.F.W.Y.P. or C: L80 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: R81 replaced with D.E.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: M82 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: E83 replaced with H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: I84 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: Q85 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.F.W.Y.P. or C: S86 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: Y87 replaced with D.E.H.K.R.N.Q.A.G. I.L.S.T.M.V.P. or C: R88 replaced with D.E.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: G89 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: S90 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: A91 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: T92 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: P93 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: A94 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: A95 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: A96 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: G97 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: A98 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: P99 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.

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Y. or C: F100 replaced with H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: I101 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: T102 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: A103 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: G104 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: V105 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: K106 replaced with D.E.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: I107 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: I108 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: T109 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: P110 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: A111 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: A112 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: P113 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: R114 replaced with D.E.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: P115 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: I116 replaced with D.E.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: N117 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.F.W.Y.P. or C: S118 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: S119 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: R120 replaced with D.E.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: G121 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: I122 replaced with D.E.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: R123 replaced with D.E.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: N124 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.F.W.Y.P. or C: R125 replaced with D.E.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: R126 replaced with D.E.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: A127 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: F128 replaced with D.E.H.K.R.N.Q.A.G. I.L.S.T.M.V.P. or C: Q129 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.F.W.Y.P. or C: G130 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: P131 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: E132 replaced with H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: E133 replaced with H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: T134 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: E135 replaced with H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: Q136 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.F.W.Y.P. or C: D137 replaced with H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: P138 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: D139 replaced with H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: L140 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: S141 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: A142 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: P143 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: P144 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: A145 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: P146 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: C147 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: P148 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: P149 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: G150 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: C151 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: R152 replaced with D.E.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: H153 replaced with D.E.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: S154 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: Q155 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.F.W.Y.P. or C: H156 replaced with D.E.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: D157 replaced with H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: D158 replaced with H.K.R.A.G. I.L.S.T.M.V.N.Q.F.W.Y.P. or C: N159 replaced with D.E.H.K.R.A.G. I.L.S.T.M.V.F.W.Y.P. or C: G160 replaced with D.E.H.K.R.N.Q.F.W.Y.P. or C: M161 replaced with D.E.H.K.R.N.Q.F.W.Y.

H. K. R. N. Q. F. W. Y. P. or C: D226 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: I227 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: I228 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: S229 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: I230 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: V231 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: T232 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: I233 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: I234 replaced with D. E. H. K. R. N. Q. A. G. I. L. S. T. M. V. P. or C: R235 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: C236 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. or P: I237 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: Q238 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. F. W. Y. P. or C: N239 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. F. W. Y. P. or C: M240 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: P241 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. or C: K242 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: T243 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: I244 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: P245 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. or C: N246 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. F. W. Y. P. or C: N247 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. F. W. Y. P. or C: S248 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: C249 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. or P: Y250 replaced with D. E. H. K. R. N. Q. A. G. I. L. S. T. M. V. P. or C: S251 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: A252 replaced with D. E. H. K. R. R. N. Q. F. W. Y. P. or C: G253 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: I254 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: A255 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: R256 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: I257 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: E258 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: I259 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: G260 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: D261 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: I262 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: I263 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: Q264 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. F. W. Y. P. or C: I265 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: A266 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: I267 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: P268 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. or C: R269 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: I270 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: N271 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. F. W. Y. P. or C: A272 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: Q273 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. F. W. Y. P. or C: I274 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: S275 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: R276 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: N277 replaced with D. E. H. K. R. A. G. I. L. S. T. M. V. F. W. Y. P. or C: G278 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: D279 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: D280 replaced with H. K. R. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: T281 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: F282 replaced with D. E. H. K. R. N. Q. A. G. I. L. S. T. M. V. P. or C: F283 replaced with D. E. H. K. R. N. Q. A. G. I. L. S. T. M. V. P. or C: G284 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: A285 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: L286 replaced with D. E. H. K. R. N. Q. F. W. Y. P. or C: K287 replaced with D. E. A. G. I. L. S. T. M. V. N. Q. F. W. Y. P. or C: I288 replaced with D. E. H. K. R. N. Q. F.

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W, Y, P, or C; and/or 1289 replaced with D, E, H, K, R, N, Q, F, W, Y, P, or C. Polynucleotides encoding these polypeptides are also encompassed by the invention. The resulting Neurotrophin- α proteins of the invention may be routinely screened for Neurotrophin- α and/or Neurotrophin- α SV functional activities and/or physical properties (such as, for example, enhanced or reduced stability and/or solubility) described throughout the specification and known in the art. Preferably, the resulting proteins of the invention have an increased and/or a decreased Neurotrophin- α and/or Neurotrophin- α SV functional activity. More preferably, the resulting Neurotrophin- α and/or Neurotrophin- α SV proteins of the invention have more than one increased and/or decreased Neurotrophin- α and/or Neurotrophin- α SV functional activity and/or physical property.

In an additional embodiment, Neurotrophin- α polypeptides of the invention comprise, or alternatively consist of, more than one amino acid (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30 and 50) replaced with the substituted amino acids as described above (either conservative or nonconservative).

Replacement of amino acids can also change the selectivity of the binding of a ligand to cell surface receptors. For example, Ostade et al., *Nature* 361:266-268 (1993) describes certain mutations resulting in selective binding of TNF- α to only one of the two known types of TNF receptors. Since Neurotrophin- α and Neurotrophin- α SV are members of the TNF polypeptide family, mutations similar to those in TNF- α are likely to have similar effects in Neurotrophin- α and/or Neurotrophin- α SV.

Sites that are critical for ligand-receptor binding can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith et al., *J. Mol. Biol.* 224:899-904 (1992) and de Vos et al., *Science* 255:306-312 (1992)).

Since Neurotrophin- α is a member of the TNF-related protein family, to modulate rather than completely eliminate functional activities (e.g., biological activities) of Neurotrophin- α , mutations may be made in sequences encoding amino acids in the TNF conserved domain, i.e., in positions Gly-191 through Leu-284 of FIGS. 1A and 1B (SEQ ID NO:2), more preferably in residues within this region which are not conserved in all, most or several members of the TNF family (e.g., TNF- α , TNF- β , LT- β , and Fas Ligand) (see e.g., FIGS. 2A, 2B, 2C, and 2D). By making a specific mutation in Neurotrophin- α in the position where such a conserved amino acid is typically found in related TNFs, the Neurotrophin- α mutant will act as an antagonist, thus possessing activity for example, which inhibits lymphocyte (e.g., B cell) proliferation, differentiation, and/or activation. Accordingly, polypeptides of the present invention include Neurotrophin- α mutants. Such Neurotrophin- α mutants comprise, or alternatively consist of, fragments, variants or derivatives of the full-length or preferably the extracellular domain of the Neurotrophin- α amino acid sequence shown in FIGS. 1A and 1B (SEQ ID NO:2). Polynucleotides encoding the above Neurotrophin- α mutants are also encompassed by the invention.

Since Neurotrophin- α SV is a member of the TNF-related protein family, to modulate rather than completely eliminate functional activities (e.g., biological activities) of Neurotrophin- α SV, mutations may be made in sequences encoding amino acids in the TNF conserved domain, i.e., in positions Gly-172 through Leu-265 of FIGS. 5A and 5B (SEQ ID NO:19), more preferably in residues within this region which are not conserved in all, most or several members of the TNF family (e.g., TNF- α , TNF- β , LT- β , and Fas Ligand) (see e.g., FIGS. 2A, 2B, 2C and 2D). By

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making a specific mutation in Neurotrophin- α SV in the position where such a conserved amino acid is typically found in related TNFs, the Neurotrophin- α SV mutant will act as an antagonist, thus possessing activity for example, which inhibits lymphocyte (e.g., B cell) proliferation, differentiation, and/or activation. Accordingly, polypeptides of the present invention include Neurotrophin- α SV mutants. Such Neurotrophin- α SV mutants comprise, or alternatively consist of, fragments, variants or derivatives of the full-length or preferably the extracellular domain of the Neurotrophin- α SV amino acid sequence shown in FIGS. 5A and 5B (SEQ ID NO:19). Polynucleotides encoding the above Neurotrophin- α SV mutants are also encompassed by the invention.

In addition, it will be recognized by one of ordinary skill in the art that mutations targeted to regions of a Neurotrophin- α polypeptide of the invention which encompass the nineteen amino acid residue insertion which is not found in the Neurotrophin- α SV polypeptide sequence (i.e., amino acid residues Val-142 through Lys-160 of the sequence presented in FIGS. 1A and 1B and in SEQ ID NO:2) may affect the observed functional activities (e.g., biological activity) of the Neurotrophin- α polypeptide. More specifically, a partial, non-limiting and non-exclusive list of such residues of the Neurotrophin- α polypeptide sequence which may be targeted for mutation includes the following amino acid residues of the Neurotrophin- α polypeptide sequence as shown in SEQ ID NO:2: V-142; T-143; Q-144; D-145; C-146; L-147; Q-148; L-149; I-150; A-151; D-152; S-153; E-154; T-155; P-156; T-157; I-158; Q-159; and K-160.

Recombinant DNA technology known to those skilled in the art (see, for instance, DNA shuffling supra) can be used to create novel mutant proteins or mutants including single or multiple amino acid substitutions, deletions, additions or fusion proteins. Such modified polypeptides can show, e.g., enhanced activity or increased stability. In addition, they may be purified in higher yields and show better solubility than the corresponding natural polypeptide, at least under certain purification and storage conditions.

Thus, the invention also encompasses Neurotrophin- α and/or Neurotrophin- α SV derivatives and analogs that have one or more amino acid residues deleted, added, or substituted to generate Neurotrophin- α and/or Neurotrophin- α SV polypeptides that are better suited for expression, scale up, etc., in the host cells chosen. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges; N-linked glycosylation sites can be altered or eliminated to achieve, for example, expression of a homogeneous product that is more easily recovered and purified from yeast hosts which are known to hyperglycosylate N-linked sites. To this end, a variety of amino acid substitutions at one or both of the first or third amino acid positions on any one or more of the glycosylation recognition sequences in the Neurotrophin- α and/or Neurotrophin- α SV polypeptides of the invention, and/or an amino acid deletion at the second position of any one or more such recognition sequences will prevent glycosylation of the Neurotrophin- α and/or Neurotrophin- α SV at the modified tripeptide sequence (see, e.g., Miyajima et al., *J. MBO J.* 5(6):1193-1197).

Additionally, one or more of the amino acid residues of the polypeptides of the invention (e.g., arginine and lysine residues) may be deleted or substituted with another residue to eliminate undesired processing by proteases such as, for example, furins or kexins. One possible result of such a mutation is that Neurotrophin- α polypeptide of the invention is not cleaved and released from the cell surface.

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In a specific embodiment, Lys-132 and/or Arg-133 of the Neutrokin- α sequence shown in SEQ ID NO:2 is mutated to another amino acid residue, or deleted altogether, to prevent or diminish release of the soluble form of Neutrokin- α from cells expressing Neutrokin- α . In a more specific embodiment, Lys-132 of the Neutrokin- α sequence shown in SEQ ID NO:2 is mutated to Ala-132. In another, nonexclusive specific embodiment, Arg-133 of the Neutrokin- α sequence shown in SEQ ID NO:2 is mutated to Ala-133. These mutated proteins, and/or polynucleotides encoding these proteins have uses such as, for example, in ex vivo therapy or gene therapy, to engineer cells expressing a Neutrokin- α polypeptide that is retained on the surface of the engineered cells.

In a specific embodiment, Cys-146 of the Neutrokin- α sequence shown in SEQ ID NO:2 is mutated to another amino acid residue, or deleted altogether, for example, to aid preventing or diminishing oligomerization of the mutant Neutrokin- α polypeptide when expressed in an expression system (essentially as described in Example 1). In a specific embodiment, Cys-146 is replaced with a Serine amino acid residue. Polypeptides encoding these polypeptides are also encompassed by the invention.

In another specific embodiment, Cys-232 of the Neutrokin- α sequence shown in SEQ ID NO:2 is mutated to another amino acid residue, or deleted altogether, for example, to aid preventing or diminishing oligomerization of the mutant Neutrokin- α polypeptide when expressed in an expression system (essentially as described in Example 1). In a specific embodiment, Cys-232 is replaced with a Serine amino acid residue. Polypeptides encoding these polypeptides are also encompassed by the invention.

In yet another specific embodiment, Cys-245 of the Neutrokin- α sequence shown in SEQ ID NO:2 is mutated to another amino acid residue, or deleted altogether, for example, to aid preventing or diminishing oligomerization of the mutant Neutrokin- α polypeptide when expressed in an expression system (essentially as described in Example 1). In a specific embodiment, Cys-245 is replaced with a Serine amino acid residue. Polypeptides encoding these polypeptides are also encompassed by the invention.

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of the Neutrokin- α and/or Neutrokin- α SV polypeptides can be substantially purified by the one-step method described in Smith and Johnson, *Gene* 67:31-40 (1988).

The polypeptides of the present invention include the complete polypeptide encoded by the deposited cDNA (ATCC Deposit No. 97768) including the intracellular, transmembrane and extracellular domains of the polypeptide encoded by the deposited cDNA, the mature soluble polypeptide encoded by the deposited cDNA, the extracellular domain minus the intracellular and transmembrane domains of the protein, the complete polypeptide of FIGS. 1A and 1B (amino acid residues 1-285 of SEQ ID NO:2), the mature soluble polypeptide of FIGS. 1A and 1B (amino acids 134-285 of SEQ ID NO:2), the extracellular domain of FIGS. 1A and 1B (amino acid residues 73-285 of SEQ ID NO:2) minus the intracellular and transmembrane domains, as well as polypeptides which have at least 80%, 85%, 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98% or 99% similarity to those described above. Polynucleotides encoding these polypeptides are also encompassed by the invention.

The polypeptides of the present invention also include the complete polypeptide encoded by the deposited cDNA

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including the intracellular, transmembrane and extracellular domains of the polypeptide encoded by the deposited cDNA (ATCC Deposit No. 203518), the mature soluble polypeptide encoded by the deposited cDNA, the extracellular domain minus the intracellular and transmembrane domains of the protein, the complete polypeptide of FIGS. 5A and 5B (amino acid residues 1-266 of SEQ ID NO:19), the extracellular domain of FIGS. 5A and 5B (amino acid residues 73-266 of SEQ ID NO:19) minus the intracellular and transmembrane domains, as well as polypeptides which have at least 80%, 85%, 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98% or 99% similarity to those described above. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Further polypeptides of the present invention include polypeptides at least 80%, or at least 85% identical, more preferably at least 90% or 95% identical, still more preferably at least 96%, 97%, 98% or 99% identical to the polypeptide encoded by the deposited cDNA (ATCC Deposit No. 97768) or to the polypeptide of FIGS. 1A and 1B (SEQ ID NO:2), and also include portions of such polypeptides with at least 30 amino acids and more preferably at least 50 amino acids. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Further polypeptides of the present invention include polypeptides at least 80%, or at least 85% identical, more preferably at least 90% or 95% identical, still more preferably at least 96%, 97%, 98% or 99% identical to the polypeptide encoded by the deposited cDNA (ATCC Deposit No. 203518) or to the polypeptide of FIGS. 5A and 5B (SEQ ID NO:19), and also include portions of such polypeptides with at least 30 amino acids and more preferably at least 50 amino acids. Polynucleotides encoding these polypeptides are also encompassed by the invention.

By "% similarity" for two polypeptides is intended a similarity score produced by comparing the amino acid sequences of the two polypeptides using the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, Wis. 53711) and the default settings for determining similarity. Bestfit uses the local homology algorithm of Smith and Waterman (*Advances in Applied Mathematics* 2:482-489, 1981) to find the best segment of similarity between two sequences.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a reference amino acid sequence of a Neutrokin- α and/or Neutrokin- α SV polypeptide is intended that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid of the Neutrokin- α and/or Neutrokin- α SV polypeptide. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99%

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identical to, for instance, the amino acid sequence shown in FIGS. 1A and 1B (SEQ ID NO:2), the amino acid sequence encoded by the deposited cDNA clone HNEIDU15 (ATCC Accession No. 97768), or fragments thereof, or, for instance, to the amino acid sequence shown in FIGS. 5A and 5B (SEQ ID NO:19), the amino acid sequence encoded by the deposited cDNA clone HNDPMC52 (ATCC Accession No. 203518), or fragments thereof, can be determined conventionally using known computer programs such as the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, Wis. 53711). When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference amino acid sequence and that gaps in homology of up to 5% of the total number of amino acid residues in the reference sequence are allowed.

In a specific embodiment, the identity between a reference (query) sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, is determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245 (1990)). Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter. According to this embodiment, if the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction is made to the results to take into consideration the fact that the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. A determination of whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of this embodiment. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C-terminal residues of the subject sequence. For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C-termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject

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sequence is compared with a 100 residue query sequence. This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are made for the purposes of this embodiment.

The polypeptides of the present invention have uses that include, but are not limited to, as a molecular weight marker on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those skilled in the art. Additionally, as described in detail below, the polypeptides of the present invention have uses that include, but are not limited to, to raise polyclonal and monoclonal antibodies, which are useful in assays for detecting Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide expression as described below or as agonists and antagonists capable of enhancing or inhibiting Neurokinine-alpha and/or Neurokinine-alphaSV function. The polypeptides of the invention also have therapeutic uses as described herein. Further, such polypeptides can be used in the yeast two-hybrid system to "capture" Neurokinine-alpha and/or Neurokinine-alphaSV binding proteins which are also candidate agonists and antagonists according to the present invention. The yeast two hybrid system is described in Fields and Song, Nature 340:245-246 (1989).

Transgenics and "Knock-Outs"

The polypeptides of the invention can also be expressed in transgenic animals. Animals of any species, including, but not limited to, mice, rats, rabbits, hamsters, guinea pigs, pigs, micro-pigs, goats, sheep, cows and non-human primates, e.g., baboons, monkeys, and chimpanzees may be used to generate transgenic animals. In a specific embodiment, techniques described herein or otherwise known in the art, are used to express polypeptides of the invention in humans, as part of a gene therapy protocol.

Any technique known in the art may be used to introduce the transgene (i.e., polynucleotides of the invention) into animals to produce the founder lines of transgenic animals. Such techniques include, but are not limited to, pronuclear microinjection (Paterson, et al., *Appl. Microbiol. Biotechnol.* 40:691-698 (1994); Carver et al., *Biotechnology* (NY) 11:1263-1270 (1993); Wright et al., *Biotechnology* (NY) 9:830-834 (1991); and Hoppe et al., U.S. Pat. No. 4,873,191 (1989)); retrovirus mediated gene transfer into germ lines (Van der Putten et al., *Proc. Natl. Acad. Sci., USA* 82:6148-6152 (1985)); blastocysts or embryos; gene targeting in embryonic stem cells (Thompson et al., *Cell* 56:313-321 (1989)); electroporation of cells or embryos (I. o. 1983, *Mol. Cell. Biol.* 3:1803-1814 (1983)); introduction of the polynucleotides of the invention using a gene gun (see, e.g., Ullmer et al., *Science* 259:1745 (1993)); introducing nucleic acid constructs into embryonic pluripotent stem cells and transferring the stem cells back into the blastocyst; and sperm-mediated gene transfer (Laviurano et al., *Cell* 57:717-723 (1989); etc. For a review of such techniques, see Gordon, "Transgenic Animals," *Intl. Rev. Cytol.* 115:171-229 (1989), which is incorporated by reference herein in its entirety. See also, U.S. Pat. No. 5,464,764 (Capecchi, et al., Positive-Negative Selection Methods and Vectors); U.S. Pat. No. 5,631,153 (Capecchi, et al., Cells and Non-Human Organisms Containing Predetermined Genomic Modifications and Positive-Negative Selection Methods and Vectors for Making Same); U.S. Pat. No. 4,736,866 (Leder, et al., Transgenic

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Non-human Animals); and U.S. Pat. No. 4,873,191 (Wagner, et al., Genetic Transformation of Zygotes); each of which is hereby incorporated by reference in its entirety.

Any technique known in the art may be used to produce transgenic clones containing polynucleotides of the invention, for example, nuclear transfer into enucleated oocytes of nuclei from cultured embryonic, fetal, or adult cells induced to quiescence (Campbell et al., *Nature* 380:64-66 (1996); Wilmut et al., *Nature* 385:810-813 (1997)).

The present invention provides for transgenic animals that carry the transgene in all their cells, as well as animals which carry the transgene in some, but not all their cells, i.e., mosaic or chimeric animals. The transgene may be integrated as a single transgene or as multiple copies such as in concatamers, e.g., head-to-head tandems or head-to-tail tandems. The transgene may also be selectively introduced into and activated in a particular cell type by following, for example, the teaching of Lasko et al. (Lasko et al., *Proc. Natl. Acad. Sci. USA* 89:6232-6236 (1992)). The regulatory sequences required for such a cell-type specific activation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art. When it is desired that the polynucleotide transgene be integrated into the chromosomal site of the endogenous gene, gene targeting is preferred. Briefly, when such a technique is to be utilized, vectors containing some nucleotide sequences homologous to the endogenous gene are designed for the purpose of integrating, via homologous recombination with chromosomal sequences, into and disrupting the function of the nucleotide sequence of the endogenous gene. The transgene may also be selectively introduced into a particular cell type, thus inactivating the endogenous gene in only that cell type, by following, for example, the teaching of Gu et al. (Gu et al., *Science* 265:103-106 (1994)). The regulatory sequences required for such a cell-type specific inactivation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art. In addition to expressing the polypeptide of the present invention in a ubiquitous or tissue specific manner in transgenic animals, it would also be routine for one skilled in the art to generate constructs which regulate expression of the polypeptide by a variety of other means (for example, developmentally or chemically regulated expression).

Once transgenic animals have been generated, the expression of the recombinant gene may be assayed utilizing standard techniques. Initial screening may be accomplished by Southern blot analysis or PCR techniques to analyze animal tissues to verify that integration of the transgene has taken place. The level of mRNA expression of the transgene in the tissues of the transgenic animals may also be assessed using techniques which include, but are not limited to, Northern blot analysis of tissue samples obtained from the animal, in situ hybridization analysis, reverse transcriptase-PCR (rt-PCR); and TaqMan PCR. Samples of transgenic gene-expressing tissue may also be evaluated immunocytochemically or immunohistochemically using antibodies specific for the transgene product.

Once the founder animals are produced, they may be bred, inbred, outbred, or crossbred to produce colonies of the particular animal. Examples of such breeding strategies include, but are not limited to: outbreeding of founder animals with more than one integration site in order to establish separate lines; inbreeding of separate lines in order to produce compound transgenics that express the transgene at higher levels because of the effects of additive expression of each transgene; crossing of heterozygous transgenic animals to produce animals homozygous for a given integration site in order to both augment expression and eliminate the need for screening

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of animals by DNA analysis; crossing of separate homozygous lines to produce compound heterozygous or homozygous lines; breeding to place the transgene on a distinct background that is appropriate for an experimental model of interest; and breeding of transgenic animals to other animals bearing a distinct transgene or knockout mutation.

Transgenic and "knock-out" animals of the invention have uses which include, but are not limited to, animal model systems useful in elaborating the biological function of Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides, studying conditions and/or disorders associated with aberrant Neutrokin-alpha and/or Neutrokin-alphaSV expression, and in screening for compounds effective in ameliorating such conditions and/or disorders.

In further embodiments of the invention, cells that are genetically engineered to express the polypeptides of the invention, or alternatively, that are genetically engineered not to express the polypeptides of the invention (e.g., knockouts) are administered to a patient in vivo. Such cells may be obtained from the patient (i.e., animal, including human) or an MHC compatible donor and can include, but are not limited to fibroblasts, bone marrow cells, blood cells (e.g., lymphocytes), adipocytes, muscle cells, endothelial cells etc. The cells are genetically engineered in vitro using recombinant DNA techniques to introduce the coding sequence of polypeptides of the invention into the cells, or alternatively, to disrupt the coding sequence and/or endogenous regulatory sequence associated with the polypeptides of the invention, e.g., by transduction (using viral vectors, and preferably vectors that integrate the transgene into the cell genome) or transfection procedures, including, but not limited to, the use of plasmids, cosmids, YACs, naked DNA, electroporation, liposomes, etc. The coding sequence of the polypeptides of the invention can be placed under the control of a strong constitutive or inducible promoter or promoter/enhancer to achieve expression, and preferably secretion, of the polypeptides of the invention. The engineered cells which express and preferably secrete the polypeptides of the invention can be introduced into the patient systemically, e.g., in the circulation, or intraperitoneally.

Alternatively, the cells can be incorporated into a matrix and implanted in the body, e.g., genetically engineered fibroblasts can be implanted as part of a skin graft; genetically engineered endothelial cells can be implanted as part of a lymphatic or vascular graft. (See, for example, Anderson et al. U.S. Pat. No. 5,399,349; and Mulligan & Wilson, U.S. Pat. No. 5,460,959 each of which is incorporated by reference herein in its entirety).

When the cells to be administered are non-autologous or non-MHC compatible cells, they can be administered using well known techniques which prevent the development of a host immune response against the introduced cells. For example, the cells may be introduced in an encapsulated form which, while allowing for an exchange of components with the immediate extracellular environment, does not allow the introduced cells to be recognized by the host immune system. Antibodies

Further polypeptides of the invention relate to antibodies and T-cell antigen receptors (TCR) which immunospecifically bind a polypeptide, polypeptide fragment, or variant of SEQ ID NO:2 and/or SEQ ID NO:19, and/or an epitope, of the present invention (as determined by immunoassays well known in the art for assaying specific antibody-antigen binding). Antibodies of the invention include, but are not limited to, polyclonal, monoclonal, multispecific, human, humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab') fragments, fragments produced by a Fab

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expression library, anti-idiotypic (anti-Id) antibodies (including, e.g., anti-Id antibodies to antibodies of the invention), and epitope-binding fragments of any of the above. The term "antibody," as used herein, refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that immunospecifically binds an antigen. The immunoglobulin molecules of the invention can be of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass of immunoglobulin molecule. Immunoglobulins may have both a heavy and light chain. An array of IgG, IgE, IgM, IgD, IgA, and IgY heavy chains may be paired with a light chain of the kappa or lambda forms.

Most preferably the antibodies are human antigen-binding antibody fragments of the present invention and include, but are not limited to, Fab, Fab' and F(ab')₂, Fd, single-chain Fvs (scFv), single-chain antibodies, disulfide-linked Fvs (sdFv) and fragments comprising either a VL or VH domain. Antigen-binding antibody fragments, including single-chain antibodies, may comprise the variable region(s) alone or in combination with the entirety or a portion of the following: hinge region, C1H1, C1H2, and C1H3 domains. Also included in the invention are antigen-binding fragments also comprising any combination of variable region(s) with a hinge region, C1H1, C1H2, and C1H3 domains. The antibodies of the invention may be from any animal origin including birds and mammals. Preferably, the antibodies are human, murine (e.g., mouse and rat), donkey, sheep, rabbit, goat, guinea pig, camel, horse, or chicken. As used herein, "human" antibodies include antibodies having the amino acid sequence of a human immunoglobulin and include antibodies isolated from human immunoglobulin libraries or from animals transgenic for one or more human immunoglobulin and that do not express endogenous immunoglobulins, as described *infra* and, for example, in U.S. Pat. No. 5,939,598 by Kucherlapati et al.

The antibodies of the present invention may be monospecific, bispecific, trispecific or of greater multispecificity. Multispecific antibodies may be specific for different epitopes of a polypeptide of the present invention or may be specific for both a polypeptide of the present invention as well as for a heterologous epitope, such as a heterologous polypeptide or solid support material. See, e.g., PCT publications WO 93/17715; WO 92/08802; WO 91/00360; WO 92/05793; Tutt, et al., J. Immunol., 147:60-69 (1991); U.S. Pat. Nos. 4,474, 893; 4,714,681; 4,925,648; 5,573,920; 5,601,819; Kostelny et al., J. Immunol., 148:1547-1553 (1992).

Antibodies of the present invention may be described or specified in terms of the epitope(s) or portion(s) of a polypeptide of the present invention which they recognize or specifically bind. The epitope(s) or polypeptide portion(s) may be specified as described herein, e.g., by N-terminal and C-terminal positions, by size in contiguous amino acid residues, or listed in the Tables and Figures. Antibodies which specifically bind any epitope or polypeptide of the present invention may also be excluded. Therefore, the present invention includes antibodies that specifically bind polypeptides of the present invention, and allows for the exclusion of the same.

In specific embodiments, antibodies of the invention bind to polypeptides comprising Phe-115 to Leu-147, Ile-150 to Tyr-163, Ser-171 to Phe-194, Glu-223 to Tyr-246, and Ser-271 to Phe-278 of the amino acid sequence of Sl:Q ID NO:2. In another specific embodiment, antibodies of the invention bind to polypeptides consisting of Phe-115 to Leu-147, Ile-150 to Tyr-163, Ser-171 to Phe-194, Glu-223 to Tyr-246, and Ser-271 to Phe-278 of the amino acid sequence of Sl:Q ID NO:2. In a preferred embodiment, antibodies of the invention

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bind to a polypeptide comprising Glu-223 to Tyr-246 of Sl:Q ID NO:2. In another preferred embodiment, antibodies of the invention bind to a polypeptide consisting of Glu-223 to Tyr-246 of Sl:Q ID NO:2. In a more preferred embodiment, antibodies of the invention bind to a polypeptide consisting of Phe-230 to Asn-242 of Sl:Q ID NO:2. In further preferred, nonexclusive embodiments, the antibodies of the invention inhibit one or more biological activities of Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides of the invention through specific binding. In more preferred embodiments, the antibody of the invention inhibits Neutrokin-alpha- and/or Neutrokin-alphaSV-mediated B cell proliferation.

Antibodies of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies that do not bind any other analog, ortholog, or homolog of a polypeptide of the present invention are included. Antibodies that bind polypeptides with at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55%, and at least 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. In specific embodiments, antibodies of the present invention cross-react with murine, rat and/or rabbit homologs of human proteins and the corresponding epitopes thereof. Antibodies that do not bind polypeptides with less than 95%, less than 90%, less than 85%, less than 80%, less than 75%, less than 70%, less than 65%, less than 60%, less than 55%, and less than 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. In a specific embodiment, the above-described cross-reactivity is with respect to any single specific antigenic or immunogenic polypeptide, or combination(s) of 2, 3, 4, 5, or more of the specific antigenic and/or immunogenic polypeptides disclosed herein. Further included in the present invention are antibodies which bind polypeptides encoded by polynucleotides which hybridize to a polynucleotide of the present invention under hybridization conditions (as described herein). Antibodies of the present invention may also be described or specified in terms of their binding affinity to a polypeptide of the invention. Preferred binding affinities include those with a dissociation constant or K_d less than 5×10⁻⁵ M, 10⁻⁵ M, 5×10⁻⁶ M, 10⁻⁶ M, 5×10⁻⁷ M, 10⁻⁷ M, 5×10⁻⁸ M, 10⁻⁸ M, 5×10⁻⁹ M, 10⁻⁹ M, 5×10⁻¹⁰ M, 10⁻¹⁰ M, 5×10⁻¹¹ M, 10⁻¹¹ M, 5×10⁻¹² M, 10⁻¹² M, 5×10⁻¹³ M, 5×10⁻¹⁴ M, 10⁻¹⁴ M, 5×10⁻¹⁵ M, or 10⁻⁵ M.

The invention also provides antibodies that competitively inhibit binding of an antibody to an epitope of the invention as determined by any method known in the art for determining competitive binding, for example, the immunoassays described herein. In preferred embodiments, the antibody competitively inhibits binding to the epitope by at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50%.

Antibodies of the present invention may act as agonists or antagonists of the polypeptides of the present invention. For example, the present invention includes antibodies which disrupt the receptor/ligand interactions with the polypeptides of the invention either partially or fully. Preferably, antibodies of the present invention bind an antigenic epitope disclosed herein, or a portion thereof. The invention features both receptor-specific antibodies and ligand-specific antibodies. The invention also features receptor-specific antibodies which do not prevent ligand binding but prevent receptor activation. Receptor activation (i.e., signaling) may be determined by techniques described herein or otherwise known in the art. For example, receptor activation can be determined by

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detecting the phosphorylation (e.g., tyrosine or serine/threonine) of the receptor or its substrate by immunoprecipitation followed by western blot analysis (for example, as described supra). In specific embodiments, antibodies are provided that inhibit ligand activity or receptor activity by at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50% of the activity in absence of the antibody.

The invention also features receptor-specific antibodies which both prevent ligand binding and receptor activation as well as antibodies that recognize the receptor-ligand complex, and, preferably, do not specifically recognize the unbound receptor or the unbound ligand. Likewise, included in the invention are neutralizing antibodies which bind the ligand and prevent binding of the ligand to the receptor, as well as antibodies which bind the ligand, thereby preventing receptor activation, but do not prevent the ligand from binding the receptor. Further included in the invention are antibodies which activate the receptor. These antibodies may act as receptor agonists, i.e., potentiate or activate either all or a subset of the biological activities of the ligand-mediated receptor activation, for example, by inducing dimerization of the receptor. The antibodies may be specified as agonists, antagonists or inverse agonists for biological activities comprising the specific biological activities of the peptides of the invention disclosed herein. The above antibody agonists can be made using methods known in the art. See, e.g., PCT publication WO 96/40281; U.S. Pat. No. 5,811,097; Deng et al., *Blood* 92(6):1981-1988 (1998); Chen et al., *Cancer Res.* 58(16):3668-3678 (1998); Harrop et al., *J. Immunol.* 161(4):1786-1794 (1998); Zhu et al., *Cancer Res.* 58(15):3209-3214 (1998); Yoon et al., *J. Immunol.* 160(7):3170-3179 (1998); Prat et al., *J. Cell. Sci.* 111(Pt2):237-247 (1998); Pitard et al., *J. Immunol. Methods* 205(2):177-190 (1997); Lautard et al., *Cytokine* 9(4):233-241 (1997); Carlson et al., *J. Biol. Chem.* 272(17):11295-11301 (1997); Taryman et al., *Neuron* 14(4):755-762 (1995); Muller et al., *Structure* 6(9):1153-1167 (1998); Bartunek et al., *Cytokine* 8(1):14-20 (1996) (which are all incorporated by reference herein in their entireties).

Antibodies of the present invention may be used, for example, but not limited to, to purify, detect, and target the polypeptides of the present invention, including both in vitro and in vivo diagnostic and therapeutic methods. For example, the antibodies have use in immunoassays for qualitatively and quantitatively measuring levels of the polypeptides of the present invention in biological samples. See, e.g., Harlow et al., *Antibodies: A Laboratory Manual*, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988) (incorporated by reference herein in its entirety).

As discussed in more detail below, the antibodies of the present invention may be used either alone or in combination with other compositions. The antibodies may further be recombinantly fused to a heterologous polypeptide at the N- or C-terminus or chemically conjugated (including covalent and non-covalent conjugations) to polypeptides or other compositions. For example, antibodies of the present invention may be recombinantly fused or conjugated to molecules useful as labels in detection assays and effector molecules such as heterologous polypeptides, drugs, radionuclides, or toxins. See, e.g., PCT publications WO 92/08495; WO 91/14438; WO 89/12624; U.S. Pat. No. 5,314,995; and EP 396,387.

The antibodies of the invention include derivatives that are modified, i.e., by the covalent attachment of any type of molecule to the antibody such that covalent attachment does not prevent the antibody from generating an anti-idiotypic response. For example, but not by way of limitation, the antibody derivatives include antibodies that have been modi-

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lied, e.g., by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, etc. Any of numerous chemical modifications may be carried out by known techniques, including, but not limited to specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, etc. Additionally, the derivative may contain one or more non-classical amino acids.

The antibodies of the present invention may be generated by any suitable method known in the art. Polyclonal antibodies to an antigen-of-interest can be produced by various procedures well known in the art. For example, a polypeptide of the invention can be administered to various host animals including, but not limited to, rabbits, mice, rats, etc. to induce the production of sera containing polyclonal antibodies specific for the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species, and include but are not limited to, Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lyssolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and *corynebacterium parvum*. Such adjuvants are also well known in the art.

Monoclonal antibodies can be prepared using a wide variety of techniques known in the art including the use of hybridoma, recombinant, and phage display technologies, or a combination thereof. For example, monoclonal antibodies can be produced using hybridoma techniques including those known in the art and taught, for example, in Harlow et al., *Antibodies: A Laboratory Manual*, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling, et al., in: *Monoclonal Antibodies and T-Cell Hybridomas* 563-681 (Elsevier, N.Y., 1981) (said references incorporated by reference in their entireties). The term "monoclonal antibody" as used herein is not limited to antibodies produced through hybridoma technology. The term "monoclonal antibody" refers to an antibody that is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced.

A "monoclonal antibody" may comprise, or alternatively consist of, two proteins, i.e., a heavy and a light chain.

Methods for producing and screening for specific antibodies using hybridoma technology are routine and well known in the art and are discussed in detail in the Examples (e.g., Example 9). In a non-limiting example, mice can be immunized with a polypeptide of the invention or a cell expressing such peptide. Once an immune response is detected, e.g., antibodies specific for the antigen are detected in the mouse serum, the mouse spleen is harvested and splenocytes isolated. The splenocytes are then fused by well-known techniques to any suitable myeloma cells, for example cells from cell line SP20 available from the ATCC. Hybridomas are selected and cloned by limited dilution. The hybridoma clones are then assayed by methods known in the art for cells that secrete antibodies capable of binding a polypeptide of the invention. Ascites fluid, which generally contains high levels of antibodies, can be generated by immunizing mice with positive hybridoma clones.

Accordingly, the present invention provides methods of generating monoclonal antibodies as well as antibodies produced by the method comprising culturing a hybridoma cell secreting an antibody of the invention wherein, preferably, the hybridoma is generated by fusing splenocytes isolated from a mouse immunized with an antigen of the invention

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with myeloma cells and then screening the hybridomas resulting from the fusion for hybridoma clones that secrete an antibody able to bind a polypeptide of the invention.

Antibody fragments which recognize specific epitopes may be generated by known techniques. For example, Fab and F(ab')₂ fragments of the invention may be produced by proteolytic cleavage of immunoglobulin molecules, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). F(ab')₂ fragments contain the variable region, the light chain constant region and the CH1 domain of the heavy chain.

For example, the antibodies of the present invention can also be generated using various phage display methods known in the art. In phage display methods, functional antibody domains are displayed on the surface of phage particles which carry the polynucleotide sequences encoding them. In a particular embodiment, such phage can be utilized to display antigen-binding domains expressed from a repertoire or combinatorial antibody library (e.g., human or murine). Phage expressing an antigen binding domain that binds the antigen of interest can be selected or identified with antigen, e.g., using labeled antigen or antigen bound or captured to a solid surface or bead. Phage used in these methods are typically filamentous phage including fd and M13 binding domains expressed from phage with Fab, Fv or disulfide stabilized Fv antibody domains recombinantly fused to either the phage gene III or gene VIII protein. Examples of phage display methods that can be used to make the antibodies of the present invention include those disclosed in Brinkman et al., *J. Immunol. Methods* 182:41-50 (1995); Ames et al., *J. Immunol. Methods* 184:177-186 (1995); Kettleborough et al., *Eur. J. Immunol.* 24:952-958 (1994); Persic et al., *Gene* 187 9-18 (1997); Burton et al., *Advances in Immunology* 57:191-280 (1994); PCT application No. PCT/GB91/01134; PCT publications WO 90/02809; WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20401; and U.S. Pat. Nos. 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743 and 5,969,108; each of which is incorporated herein by reference in its entirety.

As described in the above references, after phage selection, the antibody coding regions from the phage can be isolated and used to generate whole antibodies, including human antibodies, or any other desired antigen binding fragment, and expressed in any desired host, including mammalian cells, insect cells, plant cells, yeast, and bacteria, e.g., as described in detail below. For example, techniques to recombinantly produce Fab, Fab' and F(ab')₂ fragments can also be employed using methods known in the art such as those disclosed in PCT publication WO 92/22324; Mullinax et al., *BioTechniques* 12(6):864-869 (1992); and Sawai et al., *AJRI* 34:26-34 (1995); and Betler et al., *Science* 240:1041-1043 (1988) (said references incorporated by reference in their entireties).

Examples of techniques which can be used to produce single-chain Fvs and antibodies include those described in U.S. Pat. Nos. 4,946,778 and 5,258,498; Huston et al., *Methods in Enzymology* 203:46-88 (1991); Shu et al., *PNAS* 90:7995-7999 (1993); and Skerra et al., *Science* 240:1038-1040 (1988). For some uses, including in vivo use of antibodies in humans and in vitro detection assays, it may be preferable to use chimeric, humanized, or human antibodies. A chimeric antibody is a molecule in which different portions of the antibody are derived from different animal species, such as antibodies having a variable region derived from a murine monoclonal antibody and a human immunoglobulin constant

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region. Methods for producing chimeric antibodies are known in the art. See e.g., Morrison, *Science* 229:1202 (1985); Oi et al., *BioTechniques* 4:214 (1986); Gillies et al., (1989) *J. Immunol. Methods* 125:191-202; U.S. Pat. Nos. 5,807,715; 4,816,567; and 4,816,397, which are incorporated herein by reference in their entirety. Humanized antibodies are antibody molecules from non-human species antibody that binds the desired antigen having one or more complementarity determining regions (CDRs) from the non-human species and a framework region from a human immunoglobulin molecule. Often, framework residues in the human framework regions will be substituted with the corresponding residue from the CDR donor antibody to alter, preferably improve, antigen binding. These framework substitutions are identified by methods well known in the art, e.g., by modeling of the interactions of the CDR and framework residues to identify framework residues important for antigen binding and sequence comparison to identify unusual framework residues at particular positions. (See, e.g., Queen et al., U.S. Pat. No. 5,585,089; Riechmann et al., *Nature* 332:323 (1988), which are incorporated herein by reference in their entireties.) Antibodies can be humanized using a variety of techniques known in the art including, for example, CDR-grafting (EP 239,400; PCT publication WO 91/09967; U.S. Pat. Nos. 5,225,539; 5,530,101; and 5,585,089), veneering or resurfacing (EP 592,106; EP 519,596; Padlan, *Molecular Immunology* 28(4/5):489-498 (1991); Studnicka et al., *Protein Engineering* 7(6):805-814 (1994); Roguska et al., *PNAS* 91:969-973 (1994)), and chain shuffling (U.S. Pat. No. 5,565,332).

Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Human antibodies can be made by a variety of methods known in the art including phage display methods described above using antibody libraries derived from human immunoglobulin sequences. See also, U.S. Pat. Nos. 4,444,887 and 4,716,111; and PCT publications WO 98/46645, WO 98/50433, WO 98/24893, WO 98/16654, WO 96/34096, WO 96/33735, and WO 91/10741; each of which is incorporated herein by reference in its entirety.

Human antibodies can also be produced using transgenic mice which are incapable of expressing functional endogenous immunoglobulins, but which can express human immunoglobulin genes. For example, the human heavy and light chain immunoglobulin gene complexes may be introduced randomly or by homologous recombination into mouse embryonic stem cells. Alternatively, the human variable region, constant region, and diversity region may be introduced into mouse embryonic stem cells in addition to the human heavy and light chain genes. The mouse heavy and light chain immunoglobulin genes may be rendered non-functional separately or simultaneously with the introduction of human immunoglobulin loci by homologous recombination. In particular, homozygous deletion of the JH region prevents endogenous antibody production. The modified embryonic stem cells are expanded and microinjected into blastocysts to produce chimeric mice. The chimeric mice are then bred to produce homozygous offspring which express human antibodies. The transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of a polypeptide of the invention. Monoclonal antibodies directed against the antigen can be obtained from the immunized, transgenic mice using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA, IgM and IgE antibodies. For

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an overview of this technology for producing human antibodies. see Lonberg and Huszar, *Int. Rev. Immunol.* 13:65-93 (1995). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies. see, e.g., PCT publications WO 98/24893; WO 92/01047; WO 96/34096; WO 96/33735; European Patent No. 0 598 877; U.S. Pat. Nos. 5,413,923; 5,625,126; 5,633,425; 5,569,825; 5,661,016; 5,545,806; 5,814,318; 5,885,793; 5,916,771; and 5,939,598, which are incorporated by reference herein in their entirety. In addition, companies such as Abgenix, Inc. (Freemont, Calif.) and Genpharm (San Jose, Calif.) can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a mouse antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. (Jespersen et al., *Bio/technology* 12:899-903 (1988)).

Further, antibodies to the polypeptides of the invention can, in turn, be utilized to generate anti-idiotype antibodies that "mimic" polypeptides of the invention using techniques well known to those skilled in the art. (See, e.g., Greenspan & Bona, *FASEB J.* 7(5):437-444; (1989) and Nissinoff, *J. Immunol.* 147(8):2429-2438 (1991)). For example, antibodies which bind to and competitively inhibit polypeptide multimerization and/or binding of a polypeptide of the invention to a ligand can be used to generate anti-idiotypes that "mimic" the polypeptide multimerization and/or binding domain and, as a consequence, bind to and neutralize polypeptide and/or its ligand. Such neutralizing anti-idiotypes or Fab fragments of such anti-idiotypes can be used in therapeutic regimens to neutralize polypeptide ligand. For example, such anti-idiotypic antibodies can be used to bind a polypeptide of the invention and/or to bind its ligands/receptors, and thereby block its biological activity.

Polynucleotides Encoding Antibodies

The invention further provides polynucleotides comprising a nucleotide sequence encoding an antibody of the invention and fragments thereof. The invention also encompasses polynucleotides that hybridize under stringent or lower stringency hybridization conditions, e.g., as defined supra, to polynucleotides that encode an antibody, preferably, that specifically binds to a polypeptide of the invention, preferably, an antibody that binds to a polypeptide having the amino acid sequence of SEQ ID NO:2. In another preferred embodiment, the antibody binds specifically to a polypeptide having the amino acid sequence of SEQ ID NO:19. In another preferred embodiment, the antibody binds specifically to a polypeptide having the amino acid sequence of SEQ ID NO:23. In another preferred embodiment, the antibody binds specifically to a polypeptide having the amino acid sequence of SEQ ID NO:28. In another preferred embodiment, the antibody binds specifically to a polypeptide having the amino acid sequence of SEQ ID NO:30.

The polynucleotides may be obtained, and the nucleotide sequence of the polynucleotides determined, by any method known in the art. For example, if the nucleotide sequence of the antibody is known, a polynucleotide encoding the antibody may be assembled from chemically synthesized oligonucleotides (e.g., as described in Kutmeier et al., *Bio/Techniques* 17:242 (1994)), which, briefly, involves the synthesis of overlapping oligonucleotides containing portions of the

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sequence encoding the antibody, annealing and ligating of those oligonucleotides, and then amplification of the ligated oligonucleotides by PCR.

Alternatively, a polynucleotide encoding an antibody may be generated from nucleic acid from a suitable source. If a clone containing a nucleic acid encoding a particular antibody is not available, but the sequence of the antibody molecule is known, a nucleic acid encoding the immunoglobulin may be chemically synthesized or obtained from a suitable source (e.g., an antibody cDNA library, or a cDNA library generated from, or nucleic acid, preferably poly A+ RNA, isolated from, any tissue or cells expressing the antibody, such as hybridoma cells selected to express an antibody of the invention) by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of the sequence or by cloning using an oligonucleotide probe specific for the particular gene sequence to identify, e.g., a cDNA clone from a cDNA library that encodes the antibody. Amplified nucleic acids generated by PCR may then be cloned into replicable cloning vectors using any method well known in the art.

Once the nucleotide sequence and corresponding amino acid sequence of the antibody is determined, the nucleotide sequence of the antibody may be manipulated using methods well known in the art for the manipulation of nucleotide sequences, e.g., recombinant DNA techniques, site directed mutagenesis, PCR, etc. (see, for example, the techniques described in Sambrook et al., 1990, *Molecular Cloning, A Laboratory Manual*, 2d Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y. and Ausubel et al., eds., 1998, *Current Protocols in Molecular Biology*, John Wiley & Sons, NY, which are both incorporated by reference herein in their entirety), to generate antibodies having a different amino acid sequence, for example to create amino acid substitutions, deletions, and/or insertions.

In a specific embodiment, the amino acid sequence of the heavy and/or light chain variable domains may be inspected to identify the sequences of the complementarity determining regions (CDRs) by methods that are well known in the art, e.g., by comparison to known amino acid sequences of other heavy and light chain variable regions to determine the regions of sequence hypervariability. Using routine recombinant DNA techniques, one or more of the CDRs may be inserted within framework regions, e.g., into human framework regions to humanize a non-human antibody, as described supra. The framework regions may be naturally occurring or consensus framework regions, and preferably human framework regions (see, e.g., Chothia et al., *J. Mol. Biol.* 278: 457-479 (1998) for a listing of human framework regions). Preferably, the polynucleotide generated by the combination of the framework regions and CDRs encodes an antibody that specifically binds a polypeptide of the invention. Preferably, as discussed supra, one or more amino acid substitutions may be made within the framework regions, and, preferably, the amino acid substitutions improve binding of the antibody to its antigen. Additionally, such methods may be used to make amino acid substitutions or deletions of one or more variable region cysteine residues participating in an intrachain disulfide bond to generate antibody molecules lacking one or more intrachain disulfide bonds. Other alterations to the polynucleotide are encompassed by the present invention and within the skill of the art.

In addition, techniques developed for the production of "chimeric antibodies" (Morrison et al., *Proc. Natl. Acad. Sci.* 81:851-855 (1984); Neuberger et al., *Nature* 312:604-608 (1984); Takeda et al., *Nature* 314:452-454 (1985)) by splicing genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody mol-

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ecule of appropriate biological activity can be used. As described supra, a chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region, e.g., humanized antibodies.

Alternatively, techniques described for the production of single chain antibodies (U.S. Pat. No. 4,946,778; Bird, Science 242:423-42 (1988); Huston et al., Proc. Natl. Acad. Sci. USA 85:5879-5883 (1988); and Ward et al., Nature 334:544-54 (1989)) can be adapted to produce single chain antibodies. Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide. Techniques for the assembly of functional Fv fragments in *E. coli* may also be used (Skerra et al., Science 242:1038-1041 (1988)).

Methods of Producing Antibodies

The antibodies of the invention can be produced by any method known in the art for the synthesis of antibodies, in particular, by chemical synthesis or preferably, by recombinant expression techniques.

Recombinant expression of an antibody of the invention, or fragment, derivative or analog thereof, (e.g., a heavy or light chain of an antibody of the invention or a single chain antibody of the invention), requires construction of an expression vector containing a polynucleotide that encodes the antibody. Once a polynucleotide encoding an antibody molecule or a heavy or light chain of an antibody, or portion thereof (preferably containing the heavy or light chain variable domain), of the invention has been obtained, the vector for the production of the antibody molecule may be produced by recombinant DNA technology using techniques well known in the art. Thus, methods for preparing a protein by expressing a polynucleotide containing an antibody encoding nucleotide sequence are described herein. Methods which are well known to those skilled in the art can be used to construct expression vectors containing antibody coding sequences and appropriate transcriptional and translational control signals. These methods include, for example, in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. The invention, thus, provides replicable vectors comprising a nucleotide sequence encoding an antibody molecule of the invention, or a heavy or light chain thereof, or a heavy or light chain variable domain, operably linked to a promoter. Such vectors may include the nucleotide sequence encoding the constant region of the antibody molecule (see, e.g., PCT Publication WO 86/05807; PCT Publication WO 89/01036; and U.S. Pat. No. 5,122,464) and the variable domain of the antibody may be cloned into such a vector for expression of the entire heavy or light chain.

The expression vector is transferred to a host cell by conventional techniques and the transfected cells are then cultured by conventional techniques to produce an antibody of the invention. Thus, the invention includes host cells containing a polynucleotide encoding an antibody of the invention, or a heavy or light chain thereof, or a single chain antibody of the invention, operably linked to a heterologous promoter. In preferred embodiments for the expression of double-chained antibodies, vectors encoding both the heavy and light chains may be co-expressed in the host cell for expression of the entire immunoglobulin molecule, as detailed below.

A variety of host-expression vector systems may be utilized to express the antibody molecules of the invention. Such host-expression systems represent vehicles by which the coding sequences of interest may be produced and subsequently purified, but also represent cells which may, when transformed or transfected with the appropriate nucleotide coding

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sequences, express an antibody molecule of the invention in situ. These include but are not limited to microorganisms such as bacteria (e.g., *E. coli*, *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing antibody coding sequences; yeast (e.g., *Saccharomyces*, *Pichia*) transformed with recombinant yeast expression vectors containing antibody coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing antibody coding sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing antibody coding sequences; or mammalian cell systems (e.g., COS, CHO, BHK, 293, 3T3 cells) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter). Preferably, bacterial cells such as *Escherichia coli*, and more preferably, eukaryotic cells, especially for the expression of whole recombinant antibody molecule, are used for the expression of a recombinant antibody molecule. For example, mammalian cells such as Chinese hamster ovary cells (CHO), in conjunction with a vector such as the major intermediate early gene promoter element from human cytomegalovirus is an effective expression system for antibodies (Foecking et al., Gene 45:101 (1986); Cockett et al., BioTechnology 8:2 (1990)).

In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the antibody molecule being expressed. For example, when a large quantity of such a protein is to be produced, for the generation of pharmaceutical compositions of an antibody molecule, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited, to the *E. coli* expression vector pUR278 (Ruther et al., EMBO J. 2:1791 (1983)), in which the antibody coding sequence may be ligated individually into the vector in frame with the lac Z coding region so that a fusion protein is produced; pIN vectors (Inouye & Inouye, Nucleic Acids Res. 13:3101-3109 (1985); Van Hecke & Schuster, J. Biol. Chem. 24:5503-5509 (1989)); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption and binding to matrix glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

In an insect system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. The antibody coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter).

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the antibody coding sequence of interest may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by in vitro or in vivo recombination. Insertion in a non-essential region of the viral genome (e.g.,

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region E1 or E3) will result in a recombinant virus that is viable and capable of expressing the antibody molecule in infected hosts. (E.g., see Logan & Shenk, *Proc. Natl. Acad. Sci. USA* 81:355-359 (1984)). Specific initiation signals may also be required for efficient translation of inserted antibody coding sequences. These signals include the ATG initiation codon and adjacent sequences. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see Bittner et al., *Methods in Enzymol.* 153:51-544 (1987)).

In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins and gene products. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be used. Such mammalian host cells include but are not limited to CHO, VERO, BHK, Hela, COS, MDCK, 293, 3T3, WI38, and in particular, breast cancer cell lines such as, for example, BT483, Hs5781, T1B2, BT20 and T47D, and normal mammary gland cell lines such as, for example, CRL7030 and Hs5783st.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express the antibody molecule may be engineered. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of the foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines which express the antibody molecule. Such engineered cell lines may be particularly useful in screening and evaluation of compounds that interact directly or indirectly with the antibody molecule.

A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler et al., *Cell* 11:223 (1977)), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, *Proc. Natl. Acad. Sci. USA* 48:202 (1992)), and adenine phosphoribosyltransferase (Lowy et al., *Cell* 22:817 (1980)) genes can be employed in tk-, hprt- or aprt-cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for the following genes: dhfr, which confers resistance to methotrexate (Wigler et al., *Natl. Acad. Sci. USA* 77:357 (1980)); O'Hare et al., *Proc. Natl. Acad. Sci. USA* 78:1527 (1981)); gpt, which confers resistance to mycophenolic acid (Mulligan & Berg, *Proc. Natl. Acad. Sci. USA* 78:2072 (1981)); neo, which confers resistance to the aminoglycoside

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Gi-418 (*Clinical Pharmacy* 12:488-505; Wu and Wu, *Biotherapy* 3:87-95 (1991); Tolstoshev, *Ann. Rev. Pharmacol. Toxicol.* 32:573-596 (1993); Mulligan, *Science* 260:926-932 (1993); and Morgan and Anderson, *Ann. Rev. Biochem.* 62:191-217 (1993); May, 1993, *TIB TECH* 11(5):155-215); and hygromycin, which confers resistance to hygromycin (Santerre et al., *Gene* 30:147 (1984)). Methods commonly known in the art of recombinant DNA technology may be routinely applied to select the desired recombinant clone, and such methods are described, for example, in Ausubel et al. (eds.), *Current Protocols in Molecular Biology*, John Wiley & Sons, NY (1993); Kriegler, *Gene Transfer and Expression, A Laboratory Manual*, Stockton Press, NY (1990); and in Chapters 12 and 13, Dracopoli et al. (eds.), *Current Protocols in Human Genetics*, John Wiley & Sons, NY (1994); Colberre-Garapin et al., *J. Mol. Biol.* 150:1 (1981), which are incorporated by reference herein in their entireties.

The expression levels of an antibody molecule can be increased by vector amplification (for a review, see Bebbington and Hentschel, *The use of vectors based on gene amplification for the expression of cloned genes in mammalian cells in DNA cloning*, Vol. 3, (Academic Press, New York, 1987)). When a marker in the vector system expressing antibody is amplifiable, increase in the level of inhibitor present in culture of host cell will increase the number of copies of the marker gene. Since the amplified region is associated with the antibody gene, production of the antibody will also increase (Crouse et al., *Mol. Cell. Biol.* 3:257 (1983)).

The host cell may be co-transfected with two expression vectors of the invention, the first vector encoding a heavy chain derived polypeptide and the second vector encoding a light chain derived polypeptide. The two vectors may contain identical selectable markers which enable equal expression of heavy and light chain polypeptides. Alternatively, a single vector may be used which encodes, and is capable of expressing, both heavy and light chain polypeptides. In such situations, the light chain should be placed before the heavy chain to avoid an excess of toxic free heavy chain (Proudfoot, *Nature* 322:52 (1986); Kohler, *Proc. Natl. Acad. Sci. USA* 77:2197 (1980)). The coding sequences for the heavy and light chains may comprise cDNA or genomic DNA.

Once an antibody molecule of the invention has been produced by an animal, chemically synthesized, or recombinantly expressed, it may be purified by any method known in the art for purification of an immunoglobulin molecule, for example, by chromatography (e.g., ion exchange, affinity, particularly by affinity for the specific antigen after Protein A, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. In addition, the antibodies of the present invention or fragments thereof can be fused to heterologous polypeptide sequences described herein or otherwise known in the art, to facilitate purification.

The present invention encompasses antibodies recombinantly fused or chemically conjugated (including both covalent and non-covalent conjugations) to a polypeptide (or portion thereof, preferably at least 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 amino acids of the polypeptide) of the present invention to generate fusion proteins. The fusion does not necessarily need to be direct, but may occur through linker sequences. The antibodies may be specific for antigens other than polypeptides (or portion thereof, preferably at least 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 amino acids of the polypeptide) of the present invention. For example, antibodies may be used to target the polypeptides of the present invention to particular cell types, either in vitro or in vivo, by fusing or conjugating the polypeptides of the present inven-

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tion to antibodies specific for particular cell surface receptors. Antibodies fused or conjugated to the polypeptides of the present invention may also be used in *in vitro* immunoassays and purification methods using methods known in the art. See e.g., Harbor et al., *supra*, and PCT publication WO 93/21232; EP 439,095; Naramura et al., *Immunol. Lett.* 39:91-99 (1994); U.S. Pat. No. 5,474,981; Gillies et al., *PNAS* 89:1428-1432 (1992); Fell et al., *J. Immunol.* 146:2446-2452 (1991), which are incorporated by reference in their entireties.

The present invention further includes compositions comprising the polypeptides of the present invention fused or conjugated to antibody domains other than the variable regions. For example, the polypeptides of the present invention may be fused or conjugated to an antibody Fc region, or portion thereof. The antibody portion fused to a polypeptide of the present invention may comprise the constant region, hinge region, CH1 domain, CH2 domain, and CH3 domain or any combination of whole domains or portions thereof. The polypeptides may also be fused or conjugated to the above antibody portions to form multimers. For example, Fc portions fused to the polypeptides of the present invention can form dimers through disulfide bonding between the Fc portions. Higher multimeric forms can be made by fusing the polypeptides to portions of IgA and IgM. Methods for fusing or conjugating the polypeptides of the present invention to antibody portions are known in the art. See, e.g., U.S. Pat. Nos. 5,336,603; 5,622,929; 5,359,046; 5,349,053; 5,447,851; 5,112,946; EP 307,434; EP 367,166; PCT publications WO 96/04388; WO 91/06570; Ashkenazi et al., *Proc. Natl. Acad. Sci. USA* 88:10535-10539 (1991); Zheng et al., *J. Immunol.* 154:5590-5600 (1995); and Vil et al., *Proc. Natl. Acad. Sci. USA* 89:11337-11341 (1992) (said references incorporated by reference in their entireties).

As discussed, *supra*, the polypeptides corresponding to a polypeptide, polypeptide fragment, or a variant of SEQ ID NO:2 may be fused or conjugated to the above antibody portions to increase the *in vivo* half life of the polypeptides or for use in immunoassays using methods known in the art. Further, the polypeptides corresponding to SEQ ID NO:2 may be fused or conjugated to the above antibody portions to facilitate purification. Also as discussed, *supra*, the polypeptides corresponding to a polypeptide, polypeptide fragment, or a variant of SEQ ID NO:19 may be fused or conjugated to the above antibody portions to increase the *in vivo* half life of the polypeptides or for use in immunoassays using methods known in the art. Moreover, the polypeptides corresponding to SEQ ID NO:19 may be fused or conjugated to the above antibody portions to facilitate purification. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP 394,827; Trautwein et al., *Nature* 331:84-86 (1988)). The polypeptides of the present invention fused or conjugated to an antibody having disulfide-linked dimeric structures (due to the IgG) may also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., *J. Biochem.* 270:3958-3964 (1995)). In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (JP A 232, 262). Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins,

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such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, Bennett et al., *J. Molecular Recognition* 8:52-58 (1995); Johanson et al., *J. Biol. Chem.* 270: 9459-9471 (1995)).

Moreover, the antibodies or fragments thereof of the present invention can be fused to marker sequences, such as a peptide to facilitate purification. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Edison Avenue, Chatsworth, Calif. 91311), among others, many of which are commercially available. As described in Gentz et al., *Proc. Natl. Acad. Sci. USA* 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Other peptide tags useful for purification include, but are not limited to, the "HA" tag, which corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson et al., *Cell* 37:767 (1984)) and the "flag" tag.

The present invention further encompasses antibodies or fragments thereof conjugated to a diagnostic or therapeutic agent. The antibodies can be used diagnostically to, for example, monitor the development or progression of a tumor as part of a clinical testing procedure to, e.g., determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, radioactive materials, positron emitting metals using various positron emission tomographies, and nonradioactive paramagnetic metal ions. The detectable substance may be coupled or conjugated either directly to the antibody (or fragment thereof) or indirectly, through an intermediate (such as, for example, a linker known in the art) using techniques known in the art. See, for example, U.S. Pat. No. 4,741,900 for metal ions which can be conjugated to antibodies for use as diagnostics according to the present invention. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin; and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{111}In or $^{99\text{Tc}}$.

Further, an antibody or fragment thereof may be conjugated to a therapeutic moiety such as a cytotoxin, e.g., a cytostatic or cytotoxic agent, a therapeutic agent or a radioactive metal ion, e.g., alpha-emitters such as, for example, ^{213}Bi . A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include paclitaxel, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, teniposide, vincristine, vinblastine, colchicine, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (e.g., methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclophosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II)

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(DDP) cisplatin), anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (e.g., vincristine and vinblastine).

The conjugates of the invention can be used for modifying a given biological response, the therapeutic agent or drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a protein such as tumor necrosis factor, alpha-interferon, beta-interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator, an apoptotic agent, e.g., TNF-alpha, TNF-beta, AIM I (See, International Publication No. WO 97/33899), AIM II (See, International Publication No. WO 97/34911), Fas ligand (Takahashi et al., *Int. Immunol.*, 6:1567-1574 (1994)), VEGF (See, International Publication No. WO 99/23105), CD40 ligand, a thrombotic agent or an anti-angiogenic agent, e.g., angiostatin or endostatin; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophage colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

Antibodies may also be attached to solid supports, which are particularly useful for immunoassays or purification of the target antigen. Such solid supports include, but are not limited to, glass, cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene.

Techniques for conjugating such therapeutic moiety to antibodies are well known, see, e.g., Anon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in *Monoclonal Antibodies And Cancer Therapy*, Reisfeld et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For Drug Delivery", in *Controlled Drug Delivery* (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in *Monoclonal Antibodies '84: Biological And Clinical Applications*, Pinchera et al. (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in *Monoclonal Antibodies For Cancer Detection And Therapy*, Baldwin et al. (eds.), pp. 303-16 (Academic Press 1985), and Thorpe et al., "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", *Immunol. Rev.* 62:119-58 (1982).

Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate as described by Segal in U.S. Pat. No. 4,676,980, which is incorporated herein by reference in its entirety.

An antibody, with or without a therapeutic moiety conjugated to it, administered alone or in combination with cytotoxic factor(s) and/or cytokine(s) can be used as a therapeutic. Immunophenotyping

The antibodies of the invention may be utilized for immunophenotyping of cell lines and biological samples. The translation product of the gene of the present invention may be useful as a cell specific marker, or more specifically as a cellular marker that is differentially expressed at various stages of differentiation and/or maturation of particular cell types. Monoclonal antibodies directed against a specific epitope, or combination of epitopes, will allow for the screening of cellular populations expressing the marker. Various techniques can be utilized using monoclonal antibodies to screen for cellular populations expressing the marker(s), and

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include magnetic separation using antibody-coated magnetic beads, "panning" with antibody attached to a solid matrix (i.e., plate), and flow cytometry (See, e.g., U.S. Pat. No. 5,985,660; and Morrison et al., *Cell*, 96:737-49 (1999)).

These techniques allow for the screening of particular populations of cells, such as might be found with hematological malignancies (i.e. minimal residual disease (MRD) in acute leukemic patients) and "non-self" cells in transplantations to prevent Graft-versus-Host Disease (GVHD). Alternatively, these techniques allow for the screening of hematopoietic stem and progenitor cells capable of undergoing proliferation and/or differentiation, as might be found in human umbilical cord blood.

Assays For Antibody Binding

The antibodies of the invention may be assayed for immunospecific binding by any method known in the art. The immunoassays which can be used, include but are not limited to, competitive and non-competitive assay systems using techniques such as western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays, to name but a few. Such assays are routine and well known in the art (see, e.g., Ausubel et al. eds., 1994, *Current Protocols in Molecular Biology*, Vol. 1, John Wiley & Sons, Inc., New York, which is incorporated by reference herein in its entirety). Exemplary immunoassays are described briefly below (but are not intended by way of limitation).

Immunoprecipitation protocols generally comprise lysing a population of cells in a lysis buffer such as RIPA buffer (1% NP-40 or Triton X-100, 1% sodium deoxycholate, 0.1% SDS, 0.15 M NaCl, 0.01 M sodium phosphate at pH 7.2, 1% Triton) supplemented with protein phosphatase and/or protease inhibitors (e.g., EDTA, PMSE, aprotinin, sodium vanadate), adding the antibody of interest to the cell lysate, incubating for a period of time (e.g., 1-4 hours) at 4° C., adding protein A and/or protein G sepharose beads to the cell lysate, incubating for about an hour or more at 4° C., washing the beads in lysis buffer and resuspending the beads in SDS/sample buffer. The ability of the antibody of interest to immunoprecipitate a particular antigen can be assessed by, e.g., western blot analysis. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the binding of the antibody to an antigen and decrease the background (e.g., pre-clearing the cell lysate with sepharose beads). For further discussion regarding immunoprecipitation protocols see, e.g., Ausubel et al. eds., 1994, *Current Protocols in Molecular Biology*, Vol. 1, John Wiley & Sons, Inc., New York at 10.16.1.

Western blot analysis generally comprises preparing protein samples, electrophoresis of the protein samples in a polyacrylamide gel (e.g., 8%-20% SDS-PAGE; depending on the molecular weight of the antigen), transferring the protein sample from the polyacrylamide gel to a membrane such as nitrocellulose, PVDF or nylon, blocking the membrane in blocking solution (e.g., PBS with 3% BSA or non-fat milk), washing the membrane in washing buffer (e.g., PBS-Tween 20), blocking the membrane with primary antibody (the antibody of interest) diluted in blocking buffer, washing the membrane in washing buffer, blocking the membrane with a secondary antibody (which recognizes the primary antibody, e.g., an anti-human antibody) conjugated to an enzymatic substrate (e.g., horseradish peroxidase or alkaline phosphatase) or radioactive molecule (e.g., ³²P or ¹²⁵I) diluted in

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blocking buffer, washing the membrane in wash buffer, and detecting the presence of the antigen. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected and to reduce the background noise. For further discussion regarding western blot protocols see, e.g., Ausubel et al., eds. 1994, *Current Protocols in Molecular Biology*, Vol. 1, John Wiley & Sons, Inc., New York at 10.8.1.

ELISAs comprise preparing antigen, coating the well of a 96 well microtiter plate with the antigen, adding the antibody of interest conjugated to a detectable compound such as an enzymatic substrate (e.g., horseradish peroxidase or alkaline phosphatase) to the well and incubating for a period of time, and detecting the presence of the antigen. In ELISAs the antibody of interest does not have to be conjugated to a detectable compound; instead, a second antibody (which recognizes the antibody of interest) conjugated to a detectable compound may be added to the well. Further, instead of coating the well with the antigen, the antibody may be coated to the well. In this case, a second antibody conjugated to a detectable compound may be added following the addition of the antigen of interest to the coated well. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected as well as other variations of ELISAs known in the art. For further discussion regarding ELISAs see, e.g., Ausubel et al., eds. 1994, *Current Protocols in Molecular Biology*, Vol. 1, John Wiley & Sons, Inc., New York at 11.2.1.

The binding affinity of an antibody to an antigen and the off-rate of an antibody-antigen interaction can be determined by competitive binding assays. One example of a competitive binding assay is a radioimmunoassay comprising the incubation of labeled antigen (e.g., ^{31}I or ^{125}I) with the antibody of interest in the presence of increasing amounts of unlabeled antigen, and the detection of the antibody bound to the labeled antigen. The affinity of the antibody of interest for a particular antigen and the binding off-rates can be determined from the data by scatchard plot analysis. Competition with a second antibody can also be determined using radioimmunoassays. In this case, the antigen is incubated with antibody of interest conjugated to a labeled compound (e.g., ^{31}I or ^{125}I) in the presence of increasing amounts of an unlabeled second antibody.

Therapeutic Uses

The present invention is further directed to antibody-based therapies which involve administering antibodies of the invention to an animal, preferably a mammal, and most preferably a human, patient for treating one or more of the disclosed diseases, disorders, or conditions. Therapeutic compounds of the invention include, but are not limited to, antibodies of the invention (including fragments, analogs and derivatives thereof as described herein) and nucleic acids encoding antibodies of the invention (including fragments, analogs and derivatives thereof and anti-idiotypic antibodies as described herein). The antibodies of the invention can be used to treat, inhibit or prevent diseases, disorders or conditions associated with aberrant expression and/or activity of a polypeptide of the invention, including, but not limited to, any one or more of the diseases, disorders, or conditions described herein (e.g., autoimmune diseases, disorders, or conditions associated with such diseases or disorders, including, but not limited to, autoimmune hemolytic anemia, autoimmune neonatal thrombocytopenia, idiopathic thrombocytopenia purpura, autoimmune cytopenia, hemolytic anemia, antiphospholipid syndrome, dermatitis, allergic encephalomyelitis, myocarditis, relapsing polychondritis, rheumatic heart disease, glomerulonephritis (e.g., IgA neph-

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ropathy), Multiple Sclerosis, Neuritis, Uveitis Ophthalmia, Polyendocrinopathies, Purpura (e.g., Henoch-Schoenlein purpura), Reiter's Disease, Still-Man Syndrome, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune inflammatory eye, autoimmune thyroiditis, hypothyroidism (i.e., Hashimoto's thyroiditis, systemic lupus erythematosus, Goodpasture's syndrome, Pemphigus, Receptor autoimmunities such as, for example, (a) Graves' Disease, (b) Myasthenia Gravis, and (c) insulin resistance, autoimmune hemolytic anemia, autoimmune thrombocytopenic purpura rheumatoid arthritis, scleroderma with anti-collagen antibodies, mixed connective tissue disease, polymyositis/dermatomyositis, pernicious anemia, idiopathic Addison's disease, infertility, glomerulonephritis such as primary glomerulonephritis and IgA nephropathy, bullous pemphigoid, Sjogren's syndrome, diabetes mellitus, and adrenergic drug resistance (including adrenergic drug resistance with asthma or cystic fibrosis), chronic active hepatitis, primary biliary cirrhosis, other endocrine gland failure, vitiligo, vasculitis, post-MI, cardiomyopathy syndrome, urticaria, atopic dermatitis, asthma, inflammatory myopathies, and other inflammatory, granulomatous, degenerative, and atrophic disorders).

In a specific embodiment, antibodies of the invention are used to treat, inhibit, prognose, diagnose or prevent rheumatoid arthritis.

In another specific embodiment, antibodies of the invention are used to treat, inhibit, prognose, diagnose or prevent systemic lupus erythematosus.

The treatment and/or prevention of diseases, disorders, or conditions associated with aberrant expression and/or activity of a polypeptide of the invention includes, but is not limited to, alleviating symptoms associated with those diseases, disorders or conditions. The antibodies of the invention may also be used to target and kill cells expressing Neurokinine-alpha on their surface and/or cells having Neurokinine-alpha bound to their surface. Antibodies of the invention may be provided in pharmaceutically acceptable compositions as known in the art or as described herein.

A summary of the ways in which the antibodies of the present invention may be used therapeutically includes binding polynucleotides or polypeptides of the present invention locally or systemically in the body or by direct cytotoxicity of the antibody, e.g. as mediated by complement (CDC) or by effector cells (ADCC). Some of these approaches are described in more detail below. Armed with the teachings provided herein, one of ordinary skill in the art will know how to use the antibodies of the present invention for diagnostic, monitoring or therapeutic purposes without undue experimentation.

The antibodies of this invention may be advantageously utilized in combination with other monoclonal or chimeric antibodies, or with lymphokines or hematopoietic growth factors (such as, e.g., IL-2, IL-3 and IL-7), for example, which serve to increase the number or activity of effector cells which interact with the antibodies.

The antibodies of the invention may be administered alone or in combination with other types of treatments (e.g., radiation therapy, chemotherapy, hormonal therapy, immunotherapy, anti-tumor agents, antibiotics, and immunoglobulin). Generally, administration of products of a species origin or species reactivity (in the case of antibodies) that is the same species as that of the patient is preferred. Thus, in a preferred embodiment, human antibodies, fragments derivatives, analogs, or nucleic acids, are administered to a human patient for therapy or prophylaxis.

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It is preferred to use high affinity and/or potent in vivo inhibiting and/or neutralizing antibodies against polypeptides or polynucleotides of the present invention, fragments or regions thereof, for both immunoassays directed to and therapy of disorders related to polynucleotides or polypeptides, including fragments thereof, of the present invention. Such antibodies, fragments, or regions, will preferably have an affinity for polynucleotides or polypeptides of the invention, including fragments thereof. Preferred binding affinities include those with a dissociation constant or K_d less than 5×10^{-5} M, 10^{-5} M, 5×10^{-6} M, 10^{-6} M, 5×10^{-7} M, 10^{-7} M, 5×10^{-8} M, 10^{-8} M, 5×10^{-9} M, 10^{-9} M, 5×10^{-10} M, 10^{-10} M, 5×10^{-11} M, 10^{-11} M, 5×10^{-12} M, 10^{-12} M, 5×10^{-13} M, 10^{-13} M, 5×10^{-14} M, 10^{-14} M, 5×10^{-15} M, and 10^{-15} M.

Gene Therapy

In a specific embodiment, nucleic acids comprising sequences encoding antibodies or functional derivatives thereof, are administered to treat, inhibit or prevent a disease or disorder associated with aberrant expression and/or activity of a polypeptide of the invention, by way of gene therapy. Gene therapy refers to therapy performed by the administration to a subject of an expressed or expressible nucleic acid. In this embodiment of the invention, the nucleic acids produce their encoded protein that mediates a therapeutic effect.

Any of the methods for gene therapy available in the art can be used according to the present invention. Exemplary methods are described below.

For general reviews of the methods of gene therapy, see Goldspiel et al., *Clinical Pharmacy* 12:488-505 (1993); Wu and Wu, *Biotherapy* 3:87-95 (1991); Tolstoshev, *Ann. Rev. Pharmacol. Toxicol.* 32:573-596 (1993); Mulligan, *Science* 260:926-932 (1993); and Morgan and Anderson, *Ann. Rev. Biochem.* 62:191-217 (1993); May, *TECHNIQUES* 11(5):155-215 (1993). Methods commonly known in the art of recombinant DNA technology which can be used are described in Ausubel et al. (eds.), *Current Protocols in Molecular Biology*, John Wiley & Sons, NY (1993); and Kriegler, *Gene Transfer and Expression, A Laboratory Manual*, Stockton Press, NY (1990).

In a preferred embodiment, the compound comprises nucleic acid sequences encoding an antibody, said nucleic acid sequences being part of expression vectors that express the antibody or fragments or chimeric proteins or heavy or light chains thereof in a suitable host. In particular, such nucleic acid sequences have promoters operably linked to the antibody coding region, said promoter being inducible or constitutive, and, optionally, tissue-specific. In another particular embodiment, nucleic acid molecules are used in which the antibody coding sequences and any other desired sequences are flanked by regions that promote homologous recombination at a desired site in the genome, thus providing for intrachromosomal expression of the antibody encoding nucleic acids (Koller and Smithies, *Proc. Natl. Acad. Sci. USA* 86:8932-8935 (1989); Zijlstra et al., *Nature* 342:435-438 (1989)). In specific embodiments, the expressed antibody molecule is a single chain antibody; alternatively, the nucleic acid sequences include sequences encoding both the heavy and light chains, or fragments thereof, of the antibody.

Delivery of the nucleic acids into a patient may be either direct, in which case the patient is directly exposed to the nucleic acid or nucleic acid-carrying vectors, or indirect, in which case, cells are first transformed with the nucleic acids in vitro, then transplanted into the patient. These two approaches are known, respectively, as in vivo or ex vivo gene therapy.

In a specific embodiment, the nucleic acid sequences are directly administered in vivo, where it is expressed to produce

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the encoded product. This can be accomplished by any of numerous methods known in the art, e.g., by constructing them as part of an appropriate nucleic acid expression vector and administering it so that they become intracellular, e.g., by infection using defective or attenuated retrovirals or other viral vectors (see U.S. Pat. No. 4,980,286), or by direct injection of naked DNA, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, encapsulation in liposomes, microparticles, or microcapsules, or by administering them in linkage to a peptide which is known to enter the nucleus, by administering it in linkage to a ligand subject to receptor-mediated endocytosis (see, e.g., Wu and Wu, *J. Biol. Chem.* 262:4429-4432 (1987)) (which can be used to target cell types specifically expressing the receptors), etc. In another embodiment, nucleic acid-ligand complexes can be formed in which the ligand comprises a fusogenic viral peptide to disrupt endosomes, allowing the nucleic acid to avoid lysosomal degradation. In yet another embodiment, the nucleic acid can be targeted in vivo for cell specific uptake and expression, by targeting a specific receptor (see, e.g., PCT Publications WO 92/06180; WO 92/22635; WO92/20316; WO93/14188, WO 93/20221). Alternatively, the nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination (Koller and Smithies, *Proc. Natl. Acad. Sci. USA* 86:8932-8935 (1989); Zijlstra et al., *Nature* 342:435-438 (1989)).

In a specific embodiment, viral vectors that contain nucleic acid sequences encoding an antibody of the invention are used. For example, a retroviral vector can be used (see Miller et al., *Meth. Enzymol.* 217:581-599 (1993)). These retroviral vectors contain the components necessary for the correct packaging of the viral genome and integration into the host cell DNA. The nucleic acid sequences encoding the antibody to be used in gene therapy are cloned into one or more vectors, which facilitates delivery of the gene into a patient. More detail about retroviral vectors can be found in Boesen et al., *Biotherapy* 6:291-302 (1994), which describes the use of a retroviral vector to deliver the mdrl gene to hematopoietic stem cells in order to make the stem cells more resistant to chemotherapy. Other references illustrating the use of retroviral vectors in gene therapy are: Clowes et al., *J. Clin. Invest.* 93:644-651 (1994); Kiem et al., *Blood* 83:1467-1473 (1994); Salmons and Gunzberg, *Human Gene Therapy* 4:129-141 (1993); and Grossman and Wilson, *Curr. Opin. in Genetics and Devel.* 3:110-114 (1993).

Adenoviruses are other viral vectors that can be used in gene therapy. Adenoviruses are especially attractive vehicles for delivering genes to respiratory epithelia. Adenoviruses naturally infect respiratory epithelia where they cause a mild disease. Other targets for adenovirus-based delivery systems are liver, the central nervous system, endothelial cells, and muscle. Adenoviruses have the advantage of being capable of infecting non-dividing cells. Kozarsky and Wilson, *Current Opinion in Genetics and Development* 3:499-503 (1993) present a review of adenovirus-based gene therapy. Bout et al., *Human Gene Therapy* 5:3-10 (1994) demonstrated the use of adenovirus vectors to transfer genes to the respiratory epithelia of rhesus monkeys. Other instances of the use of adenoviruses in gene therapy can be found in Rosenfeld et al., *Science* 252:431-434 (1991); Rosenfeld et al., *Cell* 68:143-155 (1992); Mastrangeli et al., *J. Clin. Invest.* 91:225-234 (1993); PCT Publication WO94/12649; and Wang, et al., *Gene Therapy* 2:775-783 (1995). In a preferred embodiment, adenovirus vectors are used.

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Adeno-associated virus (AAV) has also been proposed for use in gene therapy (Walsh et al., *Proc. Soc. Exp. Biol. Med.* 204:289-300 (1993); U.S. Pat. No. 5,436,146).

Another approach to gene therapy involves transferring a gene to cells in tissue culture by such methods as electroporation, lipofection, calcium phosphate mediated transfection, or viral infection. Usually, the method of transfer includes the transfer of a selectable marker to the cells. The cells are then placed under selection to isolate those cells that have taken up and are expressing the transferred gene. Those cells are then delivered to a patient.

In this embodiment, the nucleic acid is introduced into a cell prior to administration in vivo of the resulting recombinant cell. Such introduction can be carried out by any method known in the art, including but not limited to transfection, electroporation, microinjection, infection with a viral or bacteriophage vector containing the nucleic acid sequences, cell fusion, chromosomal-mediated gene transfer, microcell-mediated gene transfer, spheroplast fusion, etc. Numerous techniques are known in the art for the introduction of foreign genes into cells (see, e.g., Loeffler and Behr, *Meth. Enzymol.* 217:599-618 (1993); Cohen et al., *Meth. Enzymol.* 217:618-644 (1993); *Clin. Pharmac. Ther.* 29:69-92m (1985) and may be used in accordance with the present invention, provided that the necessary developmental and physiological functions of the recipient cells are not disrupted. The technique should provide for the stable transfer of the nucleic acid to the cell, so that the nucleic acid is expressible by the cell and preferably heritable and expressible by its cell progeny.

The resulting recombinant cells can be delivered to a patient by various methods known in the art. Recombinant blood cells (e.g., hematopoietic stem or progenitor cells) are preferably administered intravenously. The amount of cells envisioned for use depends on the desired effect, patient state, etc., and can be determined by one skilled in the art.

Cells into which a nucleic acid can be introduced for purposes of gene therapy encompass any desired, available cell type, and include, but are not limited to, epithelial cells, endothelial cells, keratinocytes, fibroblasts, muscle cells, hepatocytes, blood cells such as T lymphocytes, B lymphocytes, monocytes, macrophages, neutrophils, eosinophils, megakaryocytes, granulocytes, various stem or progenitor cells, in particular hematopoietic stem or progenitor cells, e.g., as obtained from bone marrow, umbilical cord blood, peripheral blood, fetal liver, etc.

In a preferred embodiment, the cell used for gene therapy is autologous to the patient.

In an embodiment in which recombinant cells are used in gene therapy, nucleic acid sequences encoding an antibody are introduced into the cells such that they are expressible by the cells or their progeny, and the recombinant cells are then administered in vivo for therapeutic effect. In a specific embodiment, stem or progenitor cells are used. Any stem and/or progenitor cells which can be isolated and maintained in vitro can potentially be used in accordance with this embodiment of the present invention (see e.g. PCT Publication WO 94/08598; Stemple and Anderson, *Cell* 71:973-985 (1992); Rheinwald, *Meth. Cell Bio.* 21A:229 (1980); and Pittelkow and Scott, *Mayo Clinic Proc.* 61:771 (1986)).

In a specific embodiment, the nucleic acid to be introduced for purposes of gene therapy comprises an inducible promoter operably linked to the coding region, such that expression of the nucleic acid is controllable by controlling the presence or absence of the appropriate inducer of transcription.

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Demonstration of Therapeutic or Prophylactic Activity

The compounds or pharmaceutical compositions of the invention are preferably tested in vitro, and then in vivo for the desired therapeutic or prophylactic activity, prior to use in humans. For example, in vitro assays to demonstrate the therapeutic or prophylactic utility of a compound or pharmaceutical composition include, the effect of a compound on a cell line or a patient tissue sample. The effect of the compound or composition on the cell line and/or tissue sample can be determined utilizing techniques known to those of skill in the art including, but not limited to, rosette formation assays and cell lysis assays. In accordance with the invention, in vitro assays which can be used to determine whether administration of a specific compound is indicated, include in vitro cell culture assays in which a patient tissue sample is grown in culture, and exposed to or otherwise administered a compound, and the effect of such compound upon the tissue sample is observed.

Therapeutic and/or Prophylactic Administration and Composition

The invention provides methods of treatment, inhibition and prophylaxis by administration to a subject of an effective amount of a compound or pharmaceutical composition of the invention, preferably an antibody of the invention. In a preferred embodiment, the compound is substantially purified (e.g., substantially free from substances that limit its effect or produce undesired side effects). The subject is preferably an animal, including but not limited to animals such as cows, pigs, horses, chickens, cats, dogs, etc., and is preferably a mammal, and most preferably human.

Formulations and methods of administration that can be employed when the compound comprises a nucleic acid or an immunoglobulin are described above; additional appropriate formulations and routes of administration can be selected from among those described herein below.

Various delivery systems are known and can be used to administer a compound of the invention, e.g., encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the compound, receptor-mediated endocytosis (see, e.g., Wu and Wu, *J. Biol. Chem.* 262:4429-4432 (1987)), construction of a nucleic acid as part of a retroviral or other vector, etc. Methods of introduction include but are not limited to intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The compounds or compositions may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other biologically active agents. Administration can be systemic or local. In addition, it may be desirable to introduce the pharmaceutical compounds or compositions of the invention into the central nervous system by any suitable route, including intraventricular and intrathecal injection; intraventricular injection may be facilitated by an intraventricular catheter, for example, attached to a reservoir, such as an Ommaya reservoir. Pulmonary administration can also be employed, e.g., by use of an inhaler or nebulizer, and formulation with an aerosolizing agent.

In a specific embodiment, it may be desirable to administer the pharmaceutical compounds or compositions of the invention locally to the area in need of treatment; this may be achieved by, for example, and not by way of limitation, local infusion during surgery, topical application, e.g., in conjunction with a wound dressing after surgery, by injection, by means of a catheter, by means of a suppository, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as silastic

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membranes, or fibers. Preferably, when administering a protein, including an antibody, of the invention, care must be taken to use materials to which the protein does not adsorb.

In another embodiment, the compound or composition can be delivered in a vesicle, in particular a liposome (see Langer, *Science* 249:1527-1533 (1990); Treat et al., in *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 353-365 (1989); Lopez-Berestein, *ibid.*, pp. 317-327; see generally *ibid.*)

In yet another embodiment, the compound or composition can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, *supra*; Seltzer, *CRC Crit. Rev. Biomed. Eng.* 14:201 (1987); Buchwald et al., *Surgery* 88:507 (1980); Saudek et al., *N. Engl. J. Med.* 321:574 (1989)). In another embodiment, polymeric materials can be used (see *Medical Applications of Controlled Release*, Langer and Wise (eds.), CRC Press, Boca Raton, Fla. (1974); *Controlled Drug Bioavailability, Drug Product Design and Performance*, Smolen and Ball (eds.), Wiley, New York (1984); Ranger and Peppas, *J. Macromol. Sci. Rev. Macromol. Chem.* 23:61 (1983); see also Levy et al., *Science* 228:190 (1985); During et al., *Ann. Neurol.* 25:351 (1989); Howard et al., *J. Neurosurg.* 71:105 (1989)). In yet another embodiment, a controlled release system can be placed in proximity of the therapeutic target, i.e., the brain, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, in *Medical Applications of Controlled Release*, *supra*, vol. 2, pp. 115-138 (1984)).

Other controlled release systems are discussed in the review by Langer (*Science* 249:1527-1533 (1990)).

In a specific embodiment where the compound of the invention is a nucleic acid encoding a protein, the nucleic acid can be administered in vivo to promote expression of its encoded protein, by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by use of a retroviral vector (see U.S. Pat. No. 4,980,286), or by direct injection, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, or by administering it in linkage to a homobox-like peptide which is known to enter the nucleus (see e.g., Joliet et al., *Proc. Natl. Acad. Sci. USA* 88:1864-1868 (1991)), etc. Alternatively, a nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination.

The present invention also provides pharmaceutical compositions. Such compositions comprise a therapeutically effective amount of a compound, and a pharmaceutically acceptable carrier. In a specific embodiment, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired,

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can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E. W. Martin. Such compositions will contain a therapeutically effective amount of the compound, preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the patient. The formulation should suit the mode of administration.

In a preferred embodiment, the composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic such as lignocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

The compounds of the invention can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with anions such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with cations such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

The amount of the compound of the invention which will be effective in the treatment, inhibition and prevention of a disease or disorder associated with aberrant expression and/or activity of a polypeptide of the invention can be determined by standard clinical techniques. In addition, in vitro assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from in vitro or animal model test systems.

For antibodies, the dosage administered to a patient is typically 0.1 mg/kg to 100 mg/kg of the patient's body weight. Preferably, the dosage administered to a patient is between 0.1 mg/kg and 20 mg/kg of the patient's body weight, more preferably 1 mg/kg to 10 mg/kg of the patient's body weight. Generally, human antibodies have a longer half-life within the human body than antibodies from other species due to the immune response to the foreign polypeptides. Thus, lower dosages of human antibodies and less frequent administration is often possible. Further, the dosage and frequency of administration of antibodies of the invention may

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be reduced by enhancing uptake and tissue penetration (e.g., into the brain) of the antibodies by modifications such as, for example, lipidation.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. Diagnosis and Imaging

Labeled antibodies, and derivatives and analogs thereof, which specifically bind to a polypeptide of interest can be used for diagnostic purposes to detect, diagnose, or monitor diseases and/or disorders associated with the aberrant expression and/or activity of a polypeptide of the invention. The invention provides for the detection of aberrant expression of a polypeptide of interest, comprising (a) assaying the expression of the polypeptide of interest in cells or body fluid of an individual using one or more antibodies specific to the polypeptide interest and (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of aberrant expression.

The invention provides a diagnostic assay for diagnosing a disorder, comprising (a) assaying the expression of the polypeptide of interest in cells or body fluid of an individual using one or more antibodies specific to the polypeptide interest and (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a particular disorder. With respect to cancer, the presence of a relatively high amount of transcript in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Antibodies of the invention can be used to assay protein levels in a biological sample using classical immunohistological methods known to those of skill in the art (e.g., see Jalkanen, et al., *J. Cell. Biol.* 101:976-985 (1985); Jalkanen, et al., *J. Cell. Biol.* 105:3087-3096 (1987)). Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase; radioisotopes, such as iodine (^{125}I , ^{123}I , ^{121}I), carbon (^{14}C), sulfur (^{35}S), tritium (^3H), indium ($^{115\text{m}}\text{In}$, $^{113\text{m}}\text{In}$, ^{112}In , ^{111}In), and technetium ($^{99\text{m}}\text{Tc}$, $^{99\text{m}}\text{Tc}$), thallium (^{201}Tl), gallium (^{67}Ga , ^{67}Ga), palladium (^{103}Pd), molybdenum (^{99}Mo), xenon (^{133}Xe), fluorine (^{18}F), ^{153}Sm , ^{177}Lu , ^{159}Gd , ^{149}Pm , ^{140}La , ^{175}Yb , ^{166}Ho , ^{90}Y , ^{47}Sc , ^{86}Re , ^{88}Re , ^{42}Pr , ^{105}Rh , ^{97}Ru ; luminescent labels, such as luminol; and fluorescent labels, such as fluorescein and rhodamine, and biotin.

Techniques known in the art may be applied to label antibodies of the invention. Such techniques include, but are not limited to, the use of bifunctional conjugating agents (see e.g., U.S. Pat. Nos. 5,756,065; 5,714,631; 5,696,239; 5,652,361; 5,505,931; 5,489,425; 5,435,990; 5,428,139; 5,342,604;

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5,274,119; 4,994,560; and 5,808,003; the contents of each of which are hereby incorporated by reference in its entirety).

One embodiment of the invention is the detection and diagnosis of a disease or disorder associated with aberrant expression of a polypeptide of interest in an animal, preferably a mammal and most preferably a human. In one embodiment, diagnosis comprises: (a) administering (for example, parenterally, subcutaneously, or intraperitoneally) to a subject an effective amount of a labeled molecule which specifically binds to the polypeptide of interest; (b) waiting for a time interval following the administering for permitting the labeled molecule to preferentially concentrate at sites in the subject where the polypeptide is expressed (and for unbound labeled molecule to be cleared to background level); (c) determining background level; and (d) detecting the labeled molecule in the subject, such that detection of labeled molecule above the background level indicates that the subject has a particular disease or disorder associated with aberrant expression of the polypeptide of interest. Background level can be determined by various methods including, comparing the amount of labeled molecule detected to a standard value previously determined for a particular system. As described herein, specific embodiments of the invention are directed to the use of the antibodies of the invention to quantitate or qualify concentrations of cells of B cell lineage or cells of monocytic lineage.

Also as described herein, antibodies of the invention may be used to treat, diagnose, or prognose an individual having an immunodeficiency. In a specific embodiment, antibodies of the invention are used to treat, diagnose, and/or prognose an individual having common variable immunodeficiency disease (CVID) or a subset of this disease. In another embodiment, antibodies of the invention are used to diagnose, prognose, treat or prevent a disorder characterized by deficient serum immunoglobulin production, recurrent infections, and/or immune system dysfunction.

Also as described herein, antibodies of the invention may be used to treat, diagnose, or prognose an individual having an autoimmune disease or disorder. In a specific embodiment, antibodies of the invention are used to treat, diagnose, and/or prognose an individual having systemic lupus erythematosus, or a subset of the disease. In another specific embodiment, antibodies of the invention are used to treat, diagnose and/or prognose an individual having rheumatoid arthritis, or a subset of this disease.

It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of $^{99\text{m}}\text{Tc}$. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S. W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments," (Chapter 13 in *Tumor Imaging: The Radiochemical Detection of Cancer*, S. W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).

Depending on several variables, including the type of label used and the mode of administration, the time interval following the administration for permitting the labeled molecule to preferentially concentrate at sites in the subject and for unbound labeled molecule to be cleared to background level is 6 to 48 hours or 6 to 24 hours or 6 to 12 hours. In another embodiment the time interval following administration is 5 to 20 days or 5 to 10 days.

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In an embodiment, monitoring of the disease or disorder is carried out by repeating the method for diagnosing the disease or disease, for example, one month after initial diagnosis, six months after initial diagnosis, one year after initial diagnosis, etc.

Presence of the labeled molecule can be detected in the patient using methods known in the art for in vivo scanning. These methods depend upon the type of label used. Skilled artisans will be able to determine the appropriate method for detecting a particular label. Methods and devices that may be used in the diagnostic methods of the invention include, but are not limited to, computed tomography (CT), whole body scan such as position emission tomography (PET), magnetic resonance imaging (MRI), and sonography.

In a specific embodiment, the molecule is labeled with a radioisotope and is detected in the patient using a radiation responsive surgical instrument (Thurston et al., U.S. Pat. No. 5,441,050). In another embodiment, the molecule is labeled with a fluorescent compound and is detected in the patient using a fluorescence responsive scanning instrument. In another embodiment, the molecule is labeled with a positron emitting metal and is detected in the patient using positron emission tomography. In yet another embodiment, the molecule is labeled with a paramagnetic label and is detected in a patient using magnetic resonance imaging (MRI).

Kits

The present invention provides kits that can be used in the above methods. In one embodiment, a kit comprises an antibody of the invention, preferably a purified antibody, in one or more containers. In a specific embodiment, the kits of the present invention contain a substantially isolated polypeptide comprising an epitope which is specifically immunoreactive with an antibody included in the kit. Preferably, the kits of the present invention further comprise a control antibody which does not react with the polypeptide of interest. In another specific embodiment, the kits of the present invention comprise two or more antibodies (monoclonal and/or polyclonal) that recognize the same and/or different sequences or regions of the polypeptide of the invention. In another specific embodiment, the kits of the present invention contain a means for detecting the binding of an antibody to a polypeptide of interest (e.g., the antibody may be conjugated to a detectable substrate such as a fluorescent compound, an enzymatic substrate, a radioactive compound or a luminescent compound, or a second antibody which recognizes the first antibody may be conjugated to a detectable substrate).

In another specific embodiment of the present invention, the kit is a diagnostic kit for use in screening serum containing antibodies specific against proliferative and/or cancerous polynucleotides and polypeptides. Such a kit may include a control antibody that does not react with the polypeptide of interest. Such a kit may include a substantially isolated polypeptide antigen comprising an epitope which is specifically immunoreactive with at least one anti-polypeptide antigen antibody. Further, such a kit includes means for detecting the binding of said antibody to the antigen (e.g., the antibody may be conjugated to a fluorescent compound such as fluorescein or rhodamine which can be detected by flow cytometry). In specific embodiments, the kit may include a recombinantly produced or chemically synthesized polypeptide antigen. The polypeptide antigen of the kit may also be attached to a solid support.

In a more specific embodiment the detecting means of the above-described kit includes a solid support to which said polypeptide antigen is attached. Such a kit may also include a non-attached reporter-labeled anti-human antibody. In this

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embodiment, binding of the antibody to the polypeptide antigen can be detected by binding of the said reporter-labeled antibody.

In an additional embodiment, the invention includes a diagnostic kit for use in screening serum containing antigens of the polypeptide of the invention. The diagnostic kit includes a substantially isolated antibody specifically immunoreactive with polypeptide or polynucleotide antigens, and means for detecting the binding of the polynucleotide or polypeptide antigen to the antibody. In one embodiment, the antibody is attached to a solid support. In a specific embodiment, the antibody may be a monoclonal antibody. The detecting means of the kit may include a second, labeled monoclonal antibody. Alternatively, or in addition, the detecting means may include a labeled, competing antigen.

In one diagnostic configuration, test serum is reacted with a solid phase reagent having a surface-bound antigen obtained by the methods of the present invention. After binding with specific antigen antibody to the reagent and removing unbound serum components by washing, the reagent is reacted with reporter-labeled anti-human antibody to bind reporter to the reagent in proportion to the amount of bound anti-antigen antibody on the solid support. The reagent is again washed to remove unbound labeled antibody, and the amount of reporter associated with the reagent is determined. Typically, the reporter is an enzyme which is detected by incubating the solid phase in the presence of a suitable fluorometric, luminescent or colorimetric substrate (Sigma, St. Louis, Mo.).

The solid surface reagent in the above assay is prepared by known techniques for attaching protein material to solid support material, such as polymeric beads, dip sticks, 96-well plate or filter material. These attachment methods generally include non-specific adsorption of the protein to the support or covalent attachment of the protein, typically through a free amine group, to a chemically reactive group on the solid support, such as an activated carboxyl, hydroxyl, or aldehyde group. Alternatively, streptavidin coated plates can be used in conjunction with biotinylated antigen(s).

Thus, the invention provides an assay system or kit for carrying out this diagnostic method. The kit generally includes a support with surface-bound recombinant antigens, and a reporter-labeled anti-human antibody for detecting surface-bound anti-antigen antibody.

The invention further relates to antibodies which act as agonists or antagonists of the polypeptides of the present invention. For example, the present invention includes antibodies which disrupt the receptor/ligand interactions with the polypeptides of the invention either partially or fully. Included are both receptor-specific antibodies and ligand-specific antibodies. Included are receptor-specific antibodies which do not prevent ligand binding but prevent receptor activation. Receptor activation (i.e., signaling) may be determined by techniques described herein or otherwise known in the art. Also included are receptor-specific antibodies which both prevent ligand binding and receptor activation. Likewise, included are neutralizing antibodies which bind the ligand and prevent binding of the ligand to the receptor, as well as antibodies which bind the ligand, thereby preventing receptor activation, but do not prevent the ligand from binding the receptor. Further included are antibodies which activate the receptor. These antibodies may act as agonists for either all or less than all of the biological activities affected by ligand-mediated receptor activation. The antibodies may be specified as agonists or antagonists for biological activities comprising specific activities disclosed herein. Further included are antibodies that bind to Neutrokin-alpha and/or

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Neurokinine-alphaSV irrespective of whether Neurokinine-alpha or Neurokinine-alphaSV is bound to a Neurokinine-alpha Receptor. These antibodies act as Neurokinine-alpha and/or Neurokinine-alphaSV agonists as reflected in an increase in cellular proliferation in response to binding of Neurokinine-alpha and/or Neurokinine-alphaSV to a Neurokinine-alpha receptor in the presence of these antibodies. The above antibody agonists can be made using methods known in the art. See e.g., WO 96/40281; U.S. Pat. No. 5,811,097; Deng, B. et al., *Blood* 92(6):1981-1988 (1998); Chen, Z. et al., *Cancer Res.* 58(16):3668-3678 (1998); Harrop, J. A. et al., *J. Immunol.* 161(4):1786-1794 (1998); Zhu, Z. et al., *Cancer Res.* 58(15):3209-3214 (1998); Yoon, D. Y. et al., *J. Immunol.* 160(7):3170-3179 (1998); Prat, M. et al., *J. Cell. Sci.* 111 (Pt2):237-247 (1998); Pitard, V. et al., *J. Immunol. Methods* 205(2):177-190 (1997); Liautard, J. et al., *Cytokine* 9(4): 233-241 (1997); Carlson, M. G. et al., *J. Biol. Chem.* 272(17): 11295-11301 (1997); Taryman, R. I. et al., *Neuron* 14(4): 755-762 (1995); Muller, Y. A. et al., *Structure* 6(9):1153-1167 (1998); Bartunek, P. et al., *Cytokine* 8(1):14-20 (1996) (said references incorporated by reference in their entireties).

At least fourteen monoclonal antibodies have been generated against Neurokinine-alpha. These monoclonal antibodies are designated: 12D6, 2I5, 9B6, 1B8, 5F4, 9A5, 10G12, 11G12, 16B4, 3D4, 16C9, 13D5, 15C10, and 12C5. Preliminary analysis of these antibodies indicates that each binds Neurokinine-alpha protein in a Western blot analysis and when Neurokinine-alpha protein is bound to an ELISA plate. However, further analysis of antibodies 12D6, 2I5, 9B6, 1B8, 5F4, 9A5, 10G12, 11G12, and 16B4 indicates that only the antibodies designated 12D6, 9B6, 2I5, 10G12, 9A5, and 11G12 bind a membrane-bound form of Neurokinine-alpha. Thus, a subset of the monoclonal antibodies generated against Neurokinine-alpha have been determined to bind only the membrane-bound form of Neurokinine-alpha (i.e., this subset does not bind the soluble form of Neurokinine-alpha corresponding to amino acids 134 to 285 of SEQ ID NO:2), which as discussed herein, is primarily limited to expression on monocytes and dendritic cells.

Antibody 9B6 has been found to bind specifically to the membrane-bound form of Neurokinine-alpha, but not to the soluble form of Neurokinine-alpha.

Epitope mapping of antibody 9B6 has indicated that this antibody binds specifically to an amino acid sequence contained in amino acid residues from about Ser-171 to about Phe-194 of SEQ ID NO:2. More particularly, epitope mapping has indicated that antibody 9B6 binds specifically to a peptide comprising amino acid residues 1ys-173 to 1ys-188 of SEQ ID NO:2.

In contrast, antibodies 16C9 and 15C10 have been found to bind the soluble form of Neurokinine-alpha (amino acids 134 to 285 of SEQ ID NO:2) and to inhibit Neurokinine-alpha-mediated proliferation of B cells. See for example, Example 10. The 15C10 antibody has also been found to inhibit binding of Neurokinine-alpha to its receptor. Epitope mapping of antibody 15C10 has indicated that this antibody binds specifically to an amino acid sequence contained in amino acid residues from about Glu-223 to about Tyr-246 of SEQ ID NO:2. More particularly, epitope mapping has indicated that antibody 15C10 binds specifically to a peptide comprising amino acid residues Val-227 to Asn-242 of SEQ ID NO:2. Antibody 15C10 also binds specifically to a peptide comprising amino acid residues Phe-230 to Cys-245 of SEQ ID NO:2.

As described above, anti-Neurokinine-alpha monoclonal antibodies have been prepared. Hybridomas producing the antibodies referred to as 9B6 and 15C10 have been deposited with the ATCC and have been assigned deposit accession

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numbers PTA-1158 and PTA-1159, respectively. In one embodiment, the antibodies of the invention have one or more of the same biological characteristics as one or more of the antibodies secreted by the hybridoma cell lines deposited under accession numbers PTA-1158 or PTA-1159. By "biological characteristics" is meant, the in vitro or in vivo activities or properties of the antibodies, such as, for example, the ability to bind to Neurokinine-alpha (e.g., the polypeptide of SEQ ID NO:2, the mature form of Neurokinine-alpha, the membrane-bound form of Neurokinine-alpha, the soluble form of Neurokinine-alpha (amino acids 134 to 285 of SEQ ID NO:2), and an antigenic and/or epitope region of Neurokinine-alpha), the ability to substantially block Neurokinine-alpha/Neurokinine-alpha receptor binding, or the ability to block Neurokinine-alpha mediated biological activity (e.g., stimulation of B cell proliferation and immunoglobulin production). Optionally, the antibodies of the invention will bind to the same epitope as at least one of the antibodies specifically referred to herein. Such epitope binding can be routinely determined using assays known in the art.

Thus, in one embodiment, the invention provides antibodies that specifically bind the membrane-bound form of Neurokinine-alpha and do not bind the soluble form of Neurokinine-alpha. These antibodies have uses which include, but are not limited to, as diagnostic probes for identifying and/or isolating monocyte lineages expressing the membrane bound form of Neurokinine-alpha. For example, the expression of the membrane bound form of Neurokinine-alpha is elevated on activated monocytes, and accordingly, antibodies encompassed by the invention may be used to detect and/or quantify levels of activated monocytes. Additionally, antibodies that only bind the membrane bound form of Neurokinine-alpha may be used to target toxins to neoplastic, preneoplastic, and/or other cells that express the membrane bound form of Neurokinine-alpha (e.g., monocytes and dendritic cells).

In another embodiment, antibodies of the invention specifically bind only the soluble form of Neurokinine-alpha (amino acids 134 to 285 of SEQ ID NO:2). These antibodies have uses which include, but are not limited to, uses such as diagnostic probes for assaying soluble Neurokinine-alpha in biological samples, and as therapeutic agents that target toxins to cells expressing Neurokinine-alpha receptors (e.g., B cells), and/or to reduce or block in vitro or in vivo Neurokinine-alpha mediated biological activity (e.g., stimulation of B cell proliferation and/or immunoglobulin production).

The invention also provides for antibodies that specifically bind both the membrane-bound and soluble form of Neurokinine-alpha.

As described above, the invention encompasses antibodies that inhibit or reduce the ability of Neurokinine-alpha and/or Neurokinine-alphaSV to bind Neurokinine-alpha receptor and/or Neurokinine-alphaSV receptor in vitro and/or in vivo. In a specific embodiment, antibodies of the invention inhibit or reduce the ability of Neurokinine-alpha and/or Neurokinine-alphaSV to bind Neurokinine-alpha receptor and/or Neurokinine-alphaSV receptor in vitro. In another nonexclusive specific embodiment, antibodies of the invention inhibit or reduce the ability of Neurokinine-alpha and/or Neurokinine-alphaSV to bind Neurokinine-alpha receptor and/or Neurokinine-alphaSV receptor in vivo. Such inhibition can be assayed using techniques described herein or otherwise known in the art.

The invention also encompasses, antibodies that bind specifically to Neurokinine-alpha and/or Neurokinine-alphaSV, but do not inhibit the ability of Neurokinine-alpha and/or Neurokinine-alphaSV to bind Neurokinine-alpha receptor and/or Neurokinine-alphaSV receptor in vitro and/or in vivo. In a

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specific embodiment, antibodies of the invention do not inhibit or reduce the ability of Neurokinine-alpha and/or Neurokinine-alphaSV to bind Neurokinine-alpha receptor and/or Neurokinine-alphaSV receptor in vitro. In another nonexclusive specific embodiment, antibodies of the invention do not inhibit or reduce the ability of Neurokinine-alpha and/or Neurokinine-alphaSV to bind Neurokinine-alpha receptor and/or Neurokinine-alphaSV receptor in vivo.

As described above, the invention encompasses antibodies that inhibit or reduce a Neurokinine-alpha and/or Neurokinine-alphaSV-mediated biological activity in vitro and/or in vivo. In a specific embodiment, antibodies of the invention inhibit or reduce Neurokinine-alpha- and/or Neurokinine-alphaSV-mediated B cell proliferation in vitro. Such inhibition can be assayed by routinely modifying B cell proliferation assays described herein or otherwise known in the art. In another nonexclusive specific embodiment, antibodies of the invention inhibit or reduce Neurokinine-alpha- and/or Neurokinine-alphaSV-mediated B cell proliferation in vivo. In a specific embodiment, the antibody of the invention is 15C10, or a humanized form thereof. In another preferred specific embodiment, the antibody is 16C9, or a humanized form thereof. Thus, in specific embodiments of the invention, a 16C9 and/or 15C10 antibody, or humanized forms thereof, are used to bind soluble Neurokinine-alpha and/or Neurokinine-alphaSV and/or agonists and/or antagonists thereof and thereby inhibit (either partially or completely) B cell proliferation.

Alternatively, the invention also encompasses antibodies that bind specifically to a Neurokinine-alpha and/or Neurokinine-alphaSV, but do not inhibit or reduce a Neurokinine-alpha and/or Neurokinine-alphaSV-mediated biological activity in vitro and/or in vivo (e.g., stimulation of B cell proliferation). In a specific embodiment, antibodies of the invention do not inhibit or reduce a Neurokinine-alpha and/or Neurokinine-alphaSV-mediated biological activity in vitro. In another non-exclusive embodiment, antibodies of the invention do not inhibit or reduce a Neurokinine-alpha and/or Neurokinine-alphaSV mediated biological activity in vivo. In a specific embodiment, the antibody of the invention is 9B6, or a humanized form thereof.

As described above, the invention encompasses antibodies that specifically bind to the same epitope as at least one of the antibodies specifically referred to herein, in vitro and/or in vivo.

In a specific embodiment, the antibodies of the invention specifically bind to an amino acid sequence contained in amino acid residues from about Ser-171 to about Phe-194 of SEQ ID NO:2, in vitro. In another specific, non-exclusive embodiment, the antibodies of the invention specifically bind to an amino acid sequence contained in amino acid residues from about Ser-171 to about Phe-194 of SEQ ID NO:2, in vivo. In another specific, non-exclusive embodiment, the antibodies of the invention specifically bind to an amino acid sequence contained in amino acid residues from Lys-173 to Lys-188 of SEQ ID NO:2, in vitro. In another specific, non-exclusive embodiment, the antibodies of the invention specifically bind to an amino acid sequence contained in amino acid residues from Lys-173 to Lys-188 of SEQ ID NO:2, in vivo.

In an additional specific embodiment, the antibodies of the invention specifically bind to an amino acid sequence contained in amino acid residues from about Glu-223 to about Tyr-246 of SEQ ID NO:2, in vitro. In another specific, non-exclusive embodiment, the antibodies of the invention specifically bind to an amino acid sequence contained in amino acid residues from about Glu-223 to about Tyr-246 of SEQ ID

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NO:2, in vivo. In another specific, non-exclusive embodiment, the antibodies of the invention specifically bind to an amino acid sequence contained in amino acid residues from Val-227 to Asn-242 of SEQ ID NO:2, in vitro. In another specific, non-exclusive embodiment, the antibodies of the invention specifically bind to an amino acid sequence contained in amino acid residues from Val-227 to Asn-242 of SEQ ID NO:2, in vivo. In another specific, non-exclusive embodiment, the antibodies of the invention specifically bind to an amino acid sequence contained in amino acid residues from Phe-230 to Cys-245 of SEQ ID NO:2, in vitro. In another specific, non-exclusive embodiment, the antibodies of the invention specifically bind to an amino acid sequence contained in amino acid residues from Phe-230 to Cys-245 of SEQ ID NO:2, in vivo.

The invention also provides antibodies that competitively inhibit the binding of the 9B6 monoclonal antibody produced by the hybridoma deposited as PTA-1159 to a polypeptide of the invention, preferably the polypeptide of SEQ ID NO:2, more preferably to a polypeptide having the amino acid sequence of residues Ser-171 to Phe-194 of SEQ ID NO:2. Competitive inhibition can be determined by any method known in the art, for example, using the competitive binding assays described herein. In preferred embodiments, the antibody competitively inhibits the binding of 9B6 monoclonal antibody by at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, at least 50%, to the polypeptide of SEQ ID NO:2, or more preferably to a polypeptide having the amino acid sequence of residues Ser-171 to Phe-194 of SEQ ID NO:2.

The invention also provides antibodies that competitively inhibit the binding of the 15C10 monoclonal antibody produced by the hybridoma deposited as PTA-1158 to a polypeptide of the invention, preferably the polypeptide of SEQ ID NO:2, more preferably to a polypeptide having the amino acid sequence of residues Glu-223 to Tyr-246 of SEQ ID NO:2. In preferred embodiments, the antibody competitively inhibits the binding of 15C10 monoclonal antibody by at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, at least 50%, to the polypeptide of SEQ ID NO:2, or more preferably to a polypeptide having the amino acid sequence of residues Glu-223 to Tyr-246 of SEQ ID NO:2.

Additional embodiments of the invention are directed to the 9B6 antibody and to the hybridoma cell line expressing this antibody. A hybridoma cell line expressing Antibody 9B6 was deposited with the ATCC on Jan. 7, 2000 and has been assigned ATCC Deposit No. PTA-1159. In a preferred embodiment, antibody 9B6 is humanized.

Additional embodiments of the invention are directed to the 15C10 antibody and to the hybridoma cell line expressing this antibody. A hybridoma cell line expressing Antibody 15C10 was deposited with the ATCC on Jan. 7, 2000 and has been assigned ATCC Deposit No. PTA-1158. In a preferred embodiment, antibody 15C10 is humanized.

In a specific embodiment, the specific antibodies described above are humanized using techniques described herein or otherwise known in the art and then used as therapeutics as described herein.

In another specific embodiment, any of the antibodies listed above are used in a soluble form.

In another specific embodiment, any of the antibodies listed above are conjugated to a toxin or a label (as described infra). Such conjugated antibodies are used to kill a particular population of cells or to quantitate a particular population of cells. In a preferred embodiment, such conjugated antibodies are used to kill B cells expressing Neurokinine-alpha receptor

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on their surface. In another preferred embodiment, such conjugated antibodies are used to quantitate B cells expressing Neutrokin-alpha receptor on their surface.

In another specific embodiment, any of the antibodies listed above are conjugated to a toxin or a label (as described *infra*). Such conjugated antibodies are used to kill a particular population of cells or to quantitate a particular population of cells. In a preferred embodiment, such conjugated antibodies are used to kill monocyte cells expressing the membrane-bound form of Neutrokin-alpha. In another preferred embodiment, such conjugated antibodies are used to quantitate monocyte cells expressing the membrane-bound form of Neutrokin-alpha.

The antibodies of the invention also have uses as therapeutics and/or prophylactics which include, but are not limited to, in activating monocytes or blocking monocyte activation and/or killing monocyte lineages that express the membrane bound form of Neutrokin-alpha on their cell surfaces (e.g., to treat, prevent, and/or diagnose myeloid leukemias, monocyte based leukemias and lymphomas, monocytosis, monocytopenia, rheumatoid arthritis, and other diseases or conditions associated with activated monocytes). In a specific embodiment, the antibodies of the invention fix complement. In other specific embodiments, as further described herein, the antibodies of the invention (or fragments thereof) are associated with heterologous polypeptides or nucleic acids (e.g., toxins, such as, compounds that bind and activate endogenous cytotoxic effector systems, and radioisotopes; and cytotoxic products).

In another embodiment, one or more monoclonal antibodies are produced wherein they recognize or bind Neutrokin-alpha and/or a mutein thereof, but do not recognize or bind Neutrokin-alphaSV and/or a mutein thereof. In a related embodiment, one or more monoclonal antibodies are produced wherein they recognize or bind Neutrokin-alphaSV and/or a mutein thereof, but do not recognize or bind Neutrokin-alpha and/or a mutein thereof.

As discussed above, antibodies to the Neutrokin-alpha and/or Neutrokin-alpha SV polypeptides of the invention can, in turn, be utilized to generate anti-idiotypic antibodies that "mimic" the Neutrokin-alpha, using techniques well known to those skilled in the art. (See, e.g., Greenspan & Bona, *FASEB J.* 7(5):437-444 (1989), and Nissinoff, *J. Immunol.* 147(8):2429-2438 (1991)). For example, antibodies which bind to Neutrokin-alpha and/or Neutrokin-alpha SV and competitively inhibit the Neutrokin-alpha and/or Neutrokin-alpha SV multimerization and/or binding to ligand can be used to generate anti-idiotypes that "mimic" the Neutrokin-alpha TNF multimerization and/or binding domain and, as a consequence, bind to and neutralize Neutrokin-alpha or Neutrokin-alpha SV and/or its ligand. Such neutralizing anti-idiotypes or Fab fragments of such anti-idiotypes can be used in therapeutic regimens to neutralize Neutrokin-alpha ligand. For example, such anti-idiotypic antibodies can be used to bind Neutrokin-alpha and/or Neutrokin-alpha SV, or to bind Neutrokin-alpha and/or Neutrokin-alpha SV receptors on the surface of cells of B cell lineage, and thereby block Neutrokin-alpha and/or Neutrokin-alpha SV mediated B cell activation, proliferation, and/or differentiation.

Immune System-Related Disorder Diagnosis

Neutrokin-alpha is expressed in kidney, lung, peripheral leukocyte, bone marrow, T cell lymphoma, B cell lymphoma, activated T cells, stomach cancer, smooth muscle, macrophages, and cord blood tissue, and particularly cells of monocytic lineage. Moreover, Neutrokin-alphaSV is expressed in primary dendritic cells. Additionally, Neutrokin-alpha is

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expressed on the cell surface of the following non-hematopoietic tumor cell lines. Colon carcinomas HCT 116 (ATCC Accession No. CCL-247) and HT-29 (ATCC Accession No. HTB-38); Colon adenocarcinomas Caco-2 (ATCC Accession No. HTB-37), COLO 201 (ATCC Accession No. CCL-224), and WiDr (ATCC Accession No. CCL-218); Breast adenocarcinoma MDA-MB-231 (ATCC Accession No. HTB-26); Bladder squamous carcinoma SCaBER (ATCC Accession No. HTB-3); Bladder carcinoma HT-1197 (ATCC Accession No. CRL-1473); Kidney carcinomas A-498 (ATCC Accession No. HTB-44), Caki-1 (ATCC Accession No. HTB-46), and Caki-2 (ATCC Accession No. HTG-47); Kidney, Wilms tumor SK-NIP-1 (ATCC Accession No. HTB-48); and Pancreas carcinomas Hs 766T (ATCC Accession No. HTB-134), MIA PaCa-2 (ATCC Accession No. CRL-1420), and SU.86.86 (ATCC Accession No. CRL-1837). For a number of immune system-related disorders, substantially altered (increased or decreased) levels of Neutrokin-alpha and/or Neutrokin-alphaSV gene expression can be detected in immune system tissue or other cells or bodily fluids (e.g., sera, plasma, urine, synovial fluid or spinal fluid) taken from an individual having such a disorder, relative to a "standard" Neutrokin-alpha and/or Neutrokin-alphaSV gene expression level, that is, the Neutrokin-alpha and/or Neutrokin-alphaSV expression level in immune system tissues or bodily fluids from an individual not having the immune system disorder. Thus, the invention provides a diagnostic method useful during diagnosis of an immune system disorder, which involves measuring the expression level of the gene encoding the Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide in immune system tissue or other cells or body fluid from an individual and comparing the measured gene expression level with a standard Neutrokin-alpha and/or Neutrokin-alphaSV gene expression level, whereby an increase or decrease in the gene expression level compared to the standard is indicative of an immune system disorder or normal activation, proliferation, differentiation, and/or death.

In particular, it is believed that certain tissues in mammals with cancer of cells or tissue of the immune system express significantly enhanced or reduced levels of the Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide and mRNA encoding the Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide when compared to a corresponding "standard" level. Further, it is believed that enhanced or depressed levels of the Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide can be detected in certain body fluids (e.g., sera, plasma, urine, and spinal fluid) or cells or tissue from mammals with such a cancer when compared to sera from mammals of the same species not having the cancer.

For example, as disclosed herein, Neutrokin-alpha is highly expressed in cells of monocytic lineage. Accordingly, polynucleotides of the invention (e.g., polynucleotide sequences complementary to all or a portion of Neutrokin-alpha mRNA and/or Neutrokin-alphaSV mRNA) and antibodies (and antibody fragments) directed against the polypeptides of the invention may be used to quantitate or qualitative concentrations of cells of monocytic lineage (e.g., monocytic leukemia cells) expressing Neutrokin-alpha on their cell surfaces. These antibodies additionally have diagnostic applications in detecting abnormalities in the level of Neutrokin-alpha gene expression, or abnormalities in the structure and/or temporal, tissue, cellular, or subcellular location of Neutrokin-alpha and/or Neutrokin-alphaSV. These diagnostic assays may be performed *in vivo* or *in vitro*, such as, for example, on blood samples, biopsy tissue or autopsy tissue.

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Additionally, as disclosed herein, Neurokinine-alpha receptor is expressed primarily on cells of B cell lineage. Accordingly, Neurokinine-alpha polypeptides of the invention (including labeled Neurokinine-alpha polypeptides and Neurokinine-alpha fusion proteins), and anti-Neurokinine-alpha antibodies (including anti-Neurokinine-alpha antibody fragments) against the polypeptides of the invention may be used to quantitate or qualitate concentrations of cells of B cell lineage (e.g., B cell related leukemias or lymphomas) expressing Neurokinine-alpha receptor on their cell surfaces. These Neurokinine-alpha polypeptides and antibodies additionally have diagnostic applications in detecting abnormalities in the level of Neurokinine-alpha receptor gene expression, or abnormalities in the structure and/or temporal, tissue, cellular, or subcellular location of Neurokinine-alpha receptor and/or diagnosing activity/defects in signalling pathways associated with Neurokinine-alpha. These diagnostic assays may be performed in vivo or in vitro, such as, for example, on blood samples or biopsy tissue using techniques described herein or otherwise known in the art.

In one embodiment, Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides or polypeptides or Neurokinine-alpha and/or Neurokinine-alphaSV agonists or antagonists (e.g., anti-Neurokinine-alpha and/or anti-Neurokinine-alphaSV antibodies) of the invention are used to treat, prevent, diagnose, or prognose an individual having an immunodeficiency.

Immunodeficiencies that may be treated, prevented, diagnosed, and/or prognosed with the Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides or polypeptides or Neurokinine-alpha and/or Neurokinine-alphaSV agonists or antagonists (e.g., anti-Neurokinine-alpha and/or anti-Neurokinine-alphaSV antibodies) of the invention, include, but are not limited to one or more immunodeficiencies selected from: severe combined immunodeficiency (SCID)-X linked, SCID-autosomal, adenosine deaminase deficiency (ADA deficiency), X-linked agammaglobulinemia (XLA), Bruton's disease, congenital agammaglobulinemia, X-linked infantile agammaglobulinemia, acquired agammaglobulinemia, adult onset agammaglobulinemia, late-onset agammaglobulinemia, dysgammaglobulinemia, hypogammaglobulinemia, transient hypogammaglobulinemia of infancy, unspecified hypogammaglobulinemia, agammaglobulinemia, common variable immunodeficiency (CVID) (acquired), Wiskott-Aldrich Syndrome (WAS), X-linked immunodeficiency with hyper IgM, non X-linked immunodeficiency with hyper IgM, selective IgA deficiency, IgG subclass deficiency (with or without IgA deficiency), antibody deficiency with normal or elevated Igs, immunodeficiency with thymoma, Ig heavy chain deletions, kappa chain deficiency, B cell lymphoproliferative disorder (BLPD), selective IgM immunodeficiency, recessive agammaglobulinemia (Swiss type), reticular dysgenesis, neonatal neutropenia, severe congenital leukopenia, thymic aplasia/aplasia or dysplasia with immunodeficiency, ataxia-telangiectasia, short limbed dwarfism, X-linked lymphoproliferative syndrome (XLP), Nezelof syndrome-combined immunodeficiency with Igs, purine nucleoside phosphorylase deficiency (PNP), MHC Class II deficiency (Bare Lymphocyte Syndrome) and severe combined immunodeficiency.

According to this embodiment, an individual having an immunodeficiency expresses aberrantly low levels of Neurokinine-alpha and/or Neurokinine-alphaSV when compared to an individual not having an immunodeficiency. Any means described herein or otherwise known in the art may be applied to detect Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides or polypeptides of the invention (e.g., FACS analysis or ELISA detection of Neurokinine-alpha and/or Neu-

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trokinine-alphaSV polypeptides of the invention and hybridization or PCR detection of Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides of the invention) and to determine the expression profile of Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides and/or polypeptides of the invention in a biological sample.

A biological sample of a person afflicted with an immunodeficiency is characterized by low levels of expression of Neurokinine-alpha and/or Neurokinine-alphaSV when compared to that observed in individuals not having an immunodeficiency. Thus, Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides and/or polypeptides of the invention, and/or agonists or antagonists thereof, may be used according to the methods of the invention in the diagnosis and/or prognosis of an immunodeficiency. For example, a biological sample obtained from a person suspected of being afflicted with an immunodeficiency ("the subject") may be analyzed for the relative expression level(s) of Neurokinine-alpha, and/or Neurokinine-alphaSV polynucleotides and/or polypeptides of the invention. The expression level(s) of one or more of these molecules of the invention is (are) then compared to the expression level(s) of the same molecules of the invention as expressed in a person known not to be afflicted with an immunodeficiency. A significant difference in expression level(s) of Neurokinine-alpha, and/or Neurokinine-alphaSV polynucleotides and/or polypeptides of the invention, and/or agonists and/or antagonists thereof, between samples obtained from the subject and the control suggests that the subject is afflicted with an immunodeficiency.

In another embodiment, Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides or polypeptides or Neurokinine-alpha and/or Neurokinine-alphaSV agonists or antagonists (e.g., anti-Neurokinine-alpha and/or anti-Neurokinine-alphaSV antibodies) of the invention are used to treat, diagnose and/or prognose an individual having common variable immunodeficiency disease ("CVID"; also known as "acquired agammaglobulinemia" and "acquired hypogammaglobulinemia") or a subset of this disease. According to this embodiment, an individual having CVID or a subset of individuals having CVID expresses aberrant levels of Neurokinine-alpha and/or Neurokinine-alpha Receptor on their B cells and/or monocytes, when compared to individuals not having CVID. Any means described herein or otherwise known in the art may be applied to detect Neurokinine-alpha polynucleotides or polypeptides of the invention and/or Neurokinine-alpha Receptor polypeptides (e.g., FACS analysis or ELISA detection of Neurokinine-alpha and/or Neurokinine-alphaSV polypeptides of the invention and hybridization or PCR detection of Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides of the invention) and to determine differentially the expression profile of Neurokinine-alpha, and/or Neurokinine-alphaSV polynucleotides or polypeptides of the invention and/or Neurokinine-alpha receptor polypeptides in a sample containing at least monocyte cells or some component thereof (e.g., RNA) as compared to a sample containing at least B cells or a component thereof (e.g., RNA). In the instance where a sample containing at least monocyte cells or some component thereof (e.g., RNA) is determined to reflect Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotide or polypeptide expression and a sample containing at least B cells or a component thereof (e.g., RNA) is determined to reflect less than normal levels of Neurokinine-alpha receptor polynucleotide or polypeptide expression, the samples may be correlated with the occurrence of CVID (i.e., "acquired agammaglobulinemia" or "acquired hypogammaglobulinemia").

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A subset of persons afflicted with CVID are characterized by high levels of expression of both Neutrokin- α and the Neutrokin- α receptor ("NAR") in peripheral or circulating B cells when compared to that observed in individuals not having CVID. In contrast, persons who are not afflicted with CVID are typically characterized by low levels of Neutrokin- α expression and high levels of NAR expression in peripheral or circulating B cells. Thus, Neutrokin- α , Neutrokin- α SV polypeptides, and/or NAR polypeptides, polynucleotides and/or polypeptides of the invention, and/or agonists or antagonists thereof, may be used according to the methods of the invention in the differential diagnosis of this subset of CVID. For example, a sample of peripheral B cells obtained from a person suspected of being afflicted with CVID ("the subject") may be analyzed for the relative expression level(s) of Neutrokin- α , Neutrokin- α SV, and/or NAR polynucleotides and/or polypeptides of the invention. The expression level(s) of one or more of these molecules of the invention is (are) then compared to the expression level(s) of the same molecules of the invention as expressed in a person known not to be afflicted with CVID ("the control"). A significant difference in expression level(s) of Neutrokin- α and/or Neutrokin- α SV polynucleotides or polypeptides of the invention, and/or NAR polypeptides, and/or agonists and/or antagonists thereof, between samples obtained from the subject and the control suggests that the subject is afflicted with this subset of CVID.

In a specific embodiment, Neutrokin- α and/or Neutrokin- α SV polynucleotides or polypeptides, or agonists or antagonists thereof (e.g., anti-Neutrokin- α , and/or anti-Neutrokin- α SV, antibodies) are used to diagnose, prognose, treat, or prevent a disorder characterized by deficient serum immunoglobulin production, recurrent infections, and/or immune system dysfunction. Moreover, Neutrokin- α , and/or Neutrokin- α SV polynucleotides or polypeptides, or agonists or antagonists thereof (e.g., anti-Neutrokin- α and/or anti-Neutrokin- α SV antibodies) may be used to diagnose, prognose, treat, or prevent infections of the joints, bones, skin, and/or parotid glands, blood-borne infections (e.g., sepsis, meningitis, septic arthritis, and/or osteomyelitis), autoimmune diseases (e.g., those disclosed herein), inflammatory disorders, and malignancies, and/or any disease or disorder or condition associated with these infections, diseases, disorders and/or malignancies) including, but not limited to, CVID, other primary immune deficiencies, HIV disease, CLL, recurrent bronchitis, sinusitis, otitis media, conjunctivitis, pneumonia, hepatitis, meningitis, herpes zoster (e.g., severe herpes zoster), and/or *Pneumocystis carinii*.

In another embodiment, Neutrokin- α and/or Neutrokin- α SV polynucleotides or polypeptides or Neutrokin- α and/or Neutrokin- α SV agonists or antagonists (e.g., anti-Neutrokin- α and/or anti-Neutrokin- α SV antibodies) of the invention are used to treat, diagnose, or prognose an individual having an autoimmune disease or disorder.

Autoimmune diseases or disorders that may be treated, diagnosed, or prognosed using Neutrokin- α and/or Neutrokin- α SV polynucleotides or polypeptides or Neutrokin- α and/or Neutrokin- α SV agonists or antagonists (e.g., anti-Neutrokin- α and/or anti-Neutrokin- α SV antibodies) of the invention include, but are not limited to, one or more of the following: autoimmune hemolytic anemia, autoimmune neonatal thrombocytopenia, idiopathic thrombocytopenia purpura, autoimmune hemolytic anemia, antiphospholipid syndrome, dermatitis, allergic encephalomyelitis, myocarditis, relapsing poly-

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chondritis, rheumatic heart disease, glomerulonephritis (e.g., IgA nephropathy), Multiple Sclerosis, Neuritis, Uveitis Ophthalmia, Polyendocrinopathies, Purpura (e.g., Henoch-Schoenlein purpura), Reiter's Disease, Still-Man Syndrome, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune inflammatory eye, autoimmune thyroiditis, hypothyroidism (i.e., Hashimoto's thyroiditis, systemic lupus erythematosus, Goodpasture's syndrome, Pemphigus, Receptor autoimmunities such as, for example, (a) Graves' Disease, (b) Myasthenia Gravis, and (c) insulin resistance, autoimmune hemolytic anemia, autoimmune thrombocytopenic purpura, rheumatoid arthritis, scleroderma with anti-collagen antibodies, mixed connective tissue disease, polymyositis/dermatomyositis, pernicious anemia, idiopathic Addison's disease, infertility, glomerulonephritis such as primary glomerulonephritis and IgA nephropathy, bullous pemphigoid, Sjogren's syndrome, diabetes mellitus, and adrenergic drug resistance (including adrenergic drug resistance with asthma or cystic fibrosis), chronic active hepatitis, primary biliary cirrhosis, other endocrine gland failure, vitiligo, vasculitis, post-MI, cardiomy syndrome, urticaria, atopic dermatitis, asthma, inflammatory myopathies, and other inflammatory, granulomatous, degenerative, and atrophic disorders.

According to this embodiment, an individual having an autoimmune disease or disorder expresses aberrantly high levels of Neutrokin- α , Neutrokin- α SV, and/or NAR when compared to an individual not having an autoimmune disease or disorder. Any means described herein or otherwise known in the art may be applied to detect Neutrokin- α , and/or Neutrokin- α SV polynucleotides or polypeptides of the invention and/or NAR polypeptides (e.g., FACS analysis or ELISA detection of Neutrokin- α and/or Neutrokin- α SV polypeptides of the invention and hybridization or PCR detection of Neutrokin- α and/or Neutrokin- α SV polynucleotides of the invention) and to determine the expression profile of Neutrokin- α and/or Neutrokin- α SV, polynucleotides and/or polypeptides of the invention and/or NAR polypeptides in a biological sample.

A biological sample of persons afflicted with an autoimmune disease or disorder is characterized by high levels of expression of Neutrokin- α , Neutrokin- α SV, and/or NAR when compared to that observed in individuals not having an autoimmune disease or disorder. Thus, Neutrokin- α and/or Neutrokin- α SV polynucleotides and/or polypeptides of the invention, and/or agonists or antagonists thereof, may be used according to the methods of the invention in the diagnosis and/or prognosis of an autoimmune disease or disorder. For example, a biological sample obtained from a person suspected of being afflicted with an autoimmune disease or disorder ("the subject") may be analyzed for the relative expression level(s) of Neutrokin- α , and/or Neutrokin- α SV polynucleotides and/or polypeptides of the invention and/or NAR polypeptides. The expression level(s) of one or more of these molecules of the invention is (are) then compared to the expression level(s) of the same molecules of the invention as expressed in a person known not to be afflicted with an autoimmune disease or disorder. A significant difference in expression level(s) of Neutrokin- α , and/or Neutrokin- α SV, polynucleotides and/or polypeptides of the invention, and/or agonists and/or antagonists thereof, and/or NAR polypeptides between samples obtained from the subject and the control suggests that the subject is afflicted with an autoimmune disease or disorder.

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In another embodiment, Neutrokin- α and/or Neutrokin- α SV polynucleotides or polypeptides or Neutrokin- α and/or Neutrokin- α SV agonists or antagonists (e.g., anti-Neutrokin- α and/or anti-Neutrokin- α SV antibodies) of the invention are used to treat, diagnose, or prognose an individual having systemic lupus erythematosus or a subset of this disease. According to this embodiment, an individual having systemic lupus erythematosus or a subset of individuals having systemic lupus erythematosus expresses aberrantly high levels of Neutrokin- α and/or Neutrokin- α SV when compared to an individual not having systemic lupus erythematosus or this subset of systemic lupus erythematosus. Any means described herein or otherwise known in the art may be applied to detect Neutrokin- α and/or Neutrokin- α SV polynucleotides or polypeptides of the invention (e.g., FACS analysis or ELISA detection of Neutrokin- α and/or Neutrokin- α SV polypeptides of the invention and hybridization or PCR detection of Neutrokin- α and/or Neutrokin- α SV polynucleotides of the invention) and to determine the expression profile of Neutrokin- α and/or Neutrokin- α SV, polynucleotides and/or polypeptides of the invention in a biological sample.

A biological sample of persons afflicted with systemic lupus erythematosus is characterized by high levels of expression of Neutrokin- α and/or Neutrokin- α SV when compared to that observed in individuals not having systemic lupus erythematosus. Thus, Neutrokin- α and/or Neutrokin- α SV polynucleotides and/or polypeptides of the invention, and/or agonists or antagonists thereof, may be used according to the methods of the invention in the diagnosis and/or prognosis of systemic lupus erythematosus or a subset of systemic lupus erythematosus. For example, a biological sample obtained from a person suspected of being afflicted with systemic lupus erythematosus ("the subject") may be analyzed for the relative expression level(s) of Neutrokin- α , and/or Neutrokin- α SV polynucleotides and/or polypeptides of the invention. The expression level(s) of one or more of these molecules of the invention is (are) then compared to the expression level(s) of the same molecules of the invention as expressed in a person known not to be afflicted with systemic lupus erythematosus. A significant difference in expression level(s) of Neutrokin- α , and/or Neutrokin- α SV, polynucleotides and/or polypeptides of the invention, and/or agonists and/or antagonists thereof, between samples obtained from the subject and the control suggests that the subject is afflicted with systemic lupus erythematosus or a subset thereof.

Furthermore, there is a direct correlation between the severity of systemic lupus erythematosus, or a subset of this disease, and the concentration of Neutrokin- α and/or Neutrokin- α SV polynucleotides (RNA) and/or polypeptides of the invention. Thus, Neutrokin- α and/or Neutrokin- α SV polynucleotides, (RNA), polypeptides and/or agonists or antagonists of the invention, may be used according to the methods of the invention in prognosis of the severity of systemic lupus erythematosus or a subset of systemic lupus erythematosus. For example, a biological sample obtained from a person suspected of being afflicted with systemic lupus erythematosus ("the subject") may be analyzed for the relative expression level(s) of Neutrokin- α , and/or Neutrokin- α SV polynucleotides and/or polypeptides of the invention. The expression level(s) of one or more of these molecules of the invention is (are) then compared to the expression level(s) of the same molecules of the invention as expressed in a panel of persons known to represent a range in severities of this disease. According to this method, the

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match of expression level with a characterized member of the panel indicates the severity of the disease.

In another embodiment, Neutrokin- α and/or Neutrokin- α SV polynucleotides or polypeptides or Neutrokin- α and/or Neutrokin- α SV agonists or antagonists (e.g., anti-Neutrokin- α and/or anti-Neutrokin- α SV antibodies) of the invention are used to treat, diagnose, or prognose an individual having rheumatoid arthritis or a subset of this disease. According to this embodiment, an individual having rheumatoid arthritis or a subset of individuals having rheumatoid arthritis expresses aberrantly high levels of Neutrokin- α and/or Neutrokin- α SV when compared to an individual not having rheumatoid arthritis or this subset of rheumatoid arthritis. Any means described herein or otherwise known in the art may be applied to detect Neutrokin- α and/or Neutrokin- α SV polynucleotides or polypeptides of the invention (e.g., FACS analysis or ELISA detection of Neutrokin- α and/or Neutrokin- α SV polypeptides of the invention and hybridization or PCR detection of Neutrokin- α and/or Neutrokin- α SV polynucleotides of the invention) and to determine the expression profile of Neutrokin- α and/or Neutrokin- α SV, polynucleotides and/or polypeptides of the invention in a biological sample.

A biological sample of persons afflicted with rheumatoid arthritis is characterized by high levels of expression of Neutrokin- α and/or Neutrokin- α SV when compared to that observed in individuals not having rheumatoid arthritis. Thus, Neutrokin- α and/or Neutrokin- α SV polynucleotides and/or polypeptides of the invention, and/or agonists or antagonists thereof, may be used according to the methods of the invention in the diagnosis and/or prognosis of rheumatoid arthritis or a subset of rheumatoid arthritis. For example, a biological sample obtained from a person suspected of being afflicted with rheumatoid arthritis ("the subject") may be analyzed for the relative expression level(s) of Neutrokin- α , and/or Neutrokin- α SV polynucleotides and/or polypeptides of the invention. The expression level(s) of one or more of these molecules of the invention is (are) then compared to the expression level(s) of the same molecules of the invention as expressed in a person known not to be afflicted with rheumatoid arthritis. A significant difference in expression level(s) of Neutrokin- α , and/or Neutrokin- α SV, polynucleotides and/or polypeptides of the invention, and/or agonists and/or antagonists thereof, between samples obtained from the subject and the control suggests that the subject is afflicted with rheumatoid arthritis or a subset thereof.

Thus, the invention provides a diagnostic method useful during diagnosis of a immune system disorder, including cancers of this system, and immunodeficiencies and/or autoimmune diseases which involves measuring the expression level of the gene encoding the Neutrokin- α and/or Neutrokin- α SV polypeptide in immune system tissue or other cells or body fluid from an individual and comparing the measured gene expression level with a standard Neutrokin- α and/or Neutrokin- α SV gene expression level, whereby an increase or decrease in the gene expression level compared to the standard is indicative of an immune system disorder.

Where a diagnosis of a disorder in the immune system, including, but not limited to, diagnosis of a tumor, diagnosis of an immunodeficiency, and/or diagnosis of an autoimmune disease, has already been made according to conventional methods, the present invention is useful as a prognostic indicator, whereby patients exhibiting enhanced or depressed Neutrokin- α and/or Neutrokin- α SV gene expres-

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sion will experience a worse clinical outcome relative to patients expressing the gene at a level nearer the standard level.

By analyzing or determining the expression level of the gene encoding the Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide is intended qualitatively or quantitatively measuring or estimating the level of the Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide or the level of the mRNA encoding the Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide in a first biological sample either directly (e.g., by determining or estimating absolute protein level or mRNA level) or relatively (e.g., by comparing to the Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide level or mRNA level in a second biological sample). Preferably, the Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide level or mRNA level in the first biological sample is measured or estimated and compared to a standard Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide level or mRNA level, the standard being taken from a second biological sample obtained from an individual not having the disorder or being determined by averaging levels from a population of individuals not having a disorder of the immune system. As will be appreciated in the art, once a standard Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide level or mRNA level is known, it can be used repeatedly as a standard for comparison.

By "biological sample" is intended any biological sample obtained from an individual, body fluid, cell line, tissue culture, or other source which contains Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide or mRNA. As indicated, biological samples include body fluids (such as sera, plasma, urine, synovial fluid and spinal fluid) which contain free extracellular domains of the Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide, immune system tissue, and other tissue sources found to express complete or free extracellular domain of the Neurokinine-alpha and/or Neurokinine-alphaSV or a Neurokinine-alpha and/or Neurokinine-alphaSV receptor. Methods for obtaining tissue biopsies and body fluids from mammals are well known in the art. Where the biological sample is to include mRNA, a tissue biopsy is the preferred source.

The compounds of the present invention are useful for diagnosis, prognosis, or treatment of various immune system-related disorders in mammals, preferably humans. Such disorders include, but are not limited to tumors (e.g., B cell and monocytic cell leukemias and lymphomas) and tumor metastasis, infections by bacteria, viruses and other parasites, immunodeficiencies, inflammatory diseases, lymphadenopathy, autoimmune diseases (e.g., rheumatoid arthritis, systemic lupus erythematosus, Sjogren syndrome, mixed connective tissue disease, and inflammatory myopathies), and graft versus host disease.

Total cellular RNA can be isolated from a biological sample using any suitable technique such as the single-step guanidinium-thiocyanate-phenol-chloroform method described in Chomczynski and Sacchi, *Anal. Biochem.* 162: 156-159 (1987). Levels of mRNA encoding the Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide are then assayed using any appropriate method. These include Northern blot analysis, S1 nuclease mapping, the polymerase chain reaction (PCR), reverse transcription in combination with the polymerase chain reaction (RT-PCR), and reverse transcription in combination with the ligase chain reaction (RT-LCR).

Assaying Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide levels in a biological sample can occur using antibody-based techniques. For example, Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide expression in tis-

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ues can be studied with classical immunohistological methods (Jalkanen, M., et al., *J. Cell. Biol.* 101:976-985 (1985); Jalkanen, M., et al., *J. Cell. Biol.* 105:3087-3096 (1987)). Other antibody-based methods useful for detecting Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (^{131}I , ^{125}I , ^{127}I), carbon (^{14}C), sulfur (^{35}S), tritium (^3H), indium (^{115m}In , ^{113m}In , ^{112}In , ^{111}In), and technetium (^{99m}Tc , ^{99}Tc), thallium (^{201}Tl), gallium (^{68}Ga , ^{67}Ga), palladium (^{103}Pd), molybdenum (^{99}Mo), xenon (^{133}Xe), fluorine (^{18}F), ^{153}Sm , ^{177}Lu , ^{159}Gd , ^{149}Pm , ^{140}La , ^{175}Yb , ^{166}Ho , ^{90}Y , ^{47}Sc , ^{186}Re , ^{188}Re , ^{142}Pr , ^{105}Rh , ^{97}Ru ; luminescent labels, such as luminol; and fluorescent labels, such as fluorescein and rhodamine, and biotin.

Techniques known in the art may be applied to label antibodies of the invention. Such techniques include, but are not limited to, the use of bifunctional conjugating agents (see e.g., U.S. Pat. Nos. 5,756,065; 5,714,631; 5,696,239; 5,652,361; 5,505,931; 5,489,425; 5,435,990; 5,428,139; 5,342,604; 5,274,119; 4,994,560; and 5,808,003; the contents of each of which are hereby incorporated by reference in its entirety).

The tissue or cell type to be analyzed will generally include those which are known, or suspected, to express the Neurokinine-alpha gene (such as, for example, cells of monocytic lineage) or cells or tissue which are known, or suspected, to express the Neurokinine-alpha receptor gene (such as, for example, cells of B cell lineage and the spleen). The protein isolation methods employed herein may, for example, be such as those described in Harlow and Lane (Harlow, E. and Lane, D., 1988, "Antibodies: A Laboratory Manual", Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.), which is incorporated herein by reference in its entirety. The isolated cells can be derived from cell culture or from a patient. The analysis of cells taken from culture may be a necessary step in the assessment of cells that could be used as part of a cell-based gene therapy technique or, alternatively, to test the effect of compounds on the expression of the Neurokinine-alpha gene or Neurokinine-alpha receptor gene.

For example, antibodies, or fragments of antibodies, such as those described herein, may be used to quantitatively or qualitatively detect the presence of Neurokinine-alpha gene products or conserved variants or peptide fragments thereof. This can be accomplished, for example, by immunofluorescence techniques employing a fluorescently labeled antibody coupled with light microscopic, flow cytometric, or fluorimetric detection.

The antibodies (or fragments thereof) or Neurokinine-alpha polypeptides or polypeptides of the present invention may, additionally, be employed histologically, as in immunofluorescence, immunoelectron microscopy or non-immunological assays, for in situ detection of Neurokinine-alpha gene products or conserved variants or peptide fragments thereof, or for Neurokinine-alpha binding to Neurokinine-alpha receptor. In situ detection may be accomplished by removing a histological specimen from a patient, and applying thereto a labeled antibody or Neurokinine-alpha polypeptide of the present invention. The antibody (or fragment) or Neurokinine-alpha polypeptide is preferably applied by overlaying the labeled antibody (or fragment) onto a biological sample. Through the use of such a procedure, it is possible to determine not only the presence of the Neurokinine-alpha gene product, or conserved variants or peptide fragments, or Neurokinine-alpha polypeptide binding, but also its distribution in the examined tissue. Using the present invention, those of

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ordinary skill will readily perceive that any of a wide variety of histological methods (such as staining procedures) can be modified in order to achieve such *in situ* detection.

Immunoassays and non-immunoassays for Neutrokin- α gene products or conserved variants or peptide fragments thereof will typically comprise incubating a sample, such as a biological fluid, a tissue extract, freshly harvested cells, or lysates of cells which have been incubated in cell culture, in the presence of a detectably labeled antibody capable of identifying Neutrokin- α gene products or conserved variants or peptide fragments thereof, and detecting the bound antibody by any of a number of techniques well-known in the art.

Immunoassays and non-immunoassays for Neutrokin- α receptor gene products or conserved variants or peptide fragments thereof will typically comprise incubating a sample, such as a biological fluid, a tissue extract, freshly harvested cells, or lysates of cells which have been incubated in cell culture, in the presence of a detectable or labeled Neutrokin- α polypeptide capable of identifying Neutrokin- α receptor gene products or conserved variants or peptide fragments thereof, and detecting the bound Neutrokin- α polypeptide by any of a number of techniques well-known in the art.

The biological sample may be brought in contact with and immobilized onto a solid phase support or carrier such as nitrocellulose, or other solid support which is capable of immobilizing cells, cell particles or soluble proteins. The support may then be washed with suitable buffers followed by treatment with the detectably labeled anti-Neutrokin- α antibody or detectable Neutrokin- α polypeptide. The solid phase support may then be washed with the buffer a second time to remove unbound antibody or polypeptide. Optionally the antibody is subsequently labeled. The amount of bound label on solid support may then be detected by conventional means.

By "solid phase support or carrier" is intended any support capable of binding an antigen or an antibody. Well-known supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention. The support material may have virtually any possible structural configuration so long as the coupled molecule is capable of binding to an antigen or antibody. Thus, the support configuration may be spherical, as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface may be flat such as a sheet, test strip, etc. Preferred supports include polystyrene beads. Those skilled in the art will know many other suitable carriers for binding antibody or antigen, or will be able to ascertain the same by use of routine experimentation.

The binding activity of a given lot of anti-Neutrokin- α antibody or Neutrokin- α polypeptide may be determined according to well-known methods. Those skilled in the art will be able to determine operative and optimal assay conditions for each determination by employing routine experimentation.

In addition to assaying Neutrokin- α and/or Neutrokin- α SV polypeptide levels or polynucleotide levels in a biological sample obtained from an individual, Neutrokin- α and/or Neutrokin- α SV polypeptides or polynucleotides can also be detected *in vivo* by imaging. For example, in one embodiment of the invention, Neutrokin- α and/or Neutrokin- α SV polypeptide and/or anti-Neutrokin- α antibody is used to image B cell lymphomas. In another embodiment, Neutrokin- α and/or

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Neutrokin- α SV polypeptides and/or anti-Neutrokin- α antibodies and/or Neutrokin- α polynucleotides of the invention (e.g., polynucleotides complementary to all or a portion of Neutrokin- α and/or Neutrokin- α SV mRNA) is used to image lymphomas (e.g., monocyte and B cell lymphomas).

Antibody labels or markers for *in vivo* imaging of Neutrokin- α and/or Neutrokin- α SV polypeptide include those detectable by X-radiography, NMR, MRI, CAT-scans or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma. Where *in vivo* imaging is used to detect enhanced levels of Neutrokin- α and/or Neutrokin- α SV polypeptide for diagnosis in humans, it may be preferable to use human antibodies or "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using techniques described herein or otherwise known in the art. For example methods for producing chimeric antibodies are known in the art. See, for review, Morrison, *Science* 229:1202 (1985); Oi et al., *BioTechniques* 4:214 (1986); Cabilly et al., U.S. Pat. No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., *Nature* 312:643 (1984); Neuberger et al., *Nature* 314:268 (1985).

Additionally, any Neutrokin- α polypeptide whose presence can be detected, can be administered. For example, Neutrokin- α polypeptides labeled with a radio-opaque or other appropriate compound can be administered and visualized *in vivo*, as discussed, above for labeled antibodies. Further such Neutrokin- α polypeptides can be utilized for *in vitro* diagnostic procedures.

A Neutrokin- α and/or Neutrokin- α SV polypeptide-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, ^{125}I , ^{125}In , ^{111}In , ^{131}I , ^{125}I , ^{125}I , ^{125}I), carbon (^{14}C), sulfur (^{35}S), tritium (^3H), indium ($^{115\text{m}}\text{In}$, $^{113\text{m}}\text{In}$, ^{112}In , ^{111}In), and technetium ($^{99\text{m}}\text{Tc}$, $^{99\text{m}}\text{Tc}$), thallium (^{201}Tl), gallium (^{67}Ga , ^{67}Ga), palladium (^{103}Pd), molybdenum (^{99}Mo), xenon (^{133}Xe), fluorine (^{18}F), ^{177}Lu , ^{159}Gd , ^{149}Pm , ^{140}La , ^{175}Yb , ^{166}Ho , ^{90}Y , ^{47}Sc , ^{154}Sm , ^{188}Re , ^{142}Pr , ^{105}Rh , ^{97}Ru), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously or intraperitoneally) into the mammal to be examined for immune system disorder. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of $^{99\text{m}}\text{Tc}$. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain Neutrokin- α protein. *In vivo* tumor imaging is described in S. W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments" (Chapter 13 in *Tumor Imaging: The Radiochemical Detection of Cancer*, S. W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982)).

With respect to antibodies, one of the ways in which the anti-Neutrokin- α antibody can be detectably labeled is by linking the same to an enzyme and using the linked product in an enzyme immunoassay (EIA) (Voller, A., "The Enzyme

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Linked Immunosorbent Assay (ELISA)". 1978. Diagnostic Horizons 2:1-7. Microbiological Associates Quarterly Publication, Walkersville, Md.; Voller et al., *J. Clin. Pathol.* 31:507-520 (1978); Butler, J. E., *Meth. Enzymol.* 73:482-523 (1981); Maggio, E. (ed.), 1980. Enzyme Immunoassay, CRC Press, Boca Raton, Fla.; Ishikawa, E. et al., (eds.), 1981, Enzyme Immunoassay, Kyaku Shoin, Tokyo). The enzyme which is bound to the antibody will react with an appropriate substrate, preferably a chromogenic substrate, in such a manner as to produce a chemical moiety which can be detected, for example, by spectrophotometric, fluorimetric or by visual means. Enzymes which can be used to detectably label the antibody include, but are not limited to, malate dehydrogenase, staphylococcal nuclease, delta-5-steroid isomerase, yeast alcohol dehydrogenase, alpha-glycerophosphate dehydrogenase, triose phosphate isomerase, horseradish peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase and acetylcholinesterase. Additionally, the detection can be accomplished by colorimetric methods which employ a chromogenic substrate for the enzyme. Detection may also be accomplished by visual comparison of the extent of enzymatic reaction of a substrate in comparison with similarly prepared standards.

Detection may also be accomplished using any of a variety of other immunoassays. For example, by radioactively labeling the antibodies or antibody fragments, it is possible to detect Neutrokin-alpha through the use of a radioimmunoassay (RIA) (see, for example, Weintraub, B., Principles of Radioimmunoassays, Seventh Training Course on Radioligand Assay Techniques, The Endocrine Society, March, 1986, which is incorporated by reference herein). The radioactive isotope can be detected by means including, but not limited to, a gamma counter, a scintillation counter, or autoradiography.

It is also possible to label the antibody with a fluorescent compound. When the fluorescently labeled antibody is exposed to light of the proper wave-length, its presence can then be detected due to fluorescence. Among the most commonly used fluorescent labeling compounds are fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, ophthaldehyde and fluorescamine.

The antibody can also be detectably labeled using fluorescence emitting metals such as ^{152}Eu , or others of the lanthanide series. These metals can be attached to the antibody using such metal chelating groups as diethylenetriaminepentaacetic acid (DTPA) or ethylenediaminetetraacetic acid (EDTA).

The antibody also can be detectably labeled by coupling it to a chemiluminescent compound. The presence of the chemiluminescent-tagged antibody is then determined by detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of particularly useful chemiluminescent labeling compounds are luminol, isoluminol, thionin, acridinium ester, imidazole, acridinium salt and oxalate ester.

Likewise, a bioluminescent compound may be used to label the antibody of the present invention. Bioluminescence is a type of chemiluminescence found in biological systems in which a catalytic protein increases the efficiency of the chemiluminescent reaction. The presence of a bioluminescent protein is determined by detecting the presence of luminescence. Important bioluminescent compounds for purposes of labeling include, but are not limited to, luciferin, luciferase and aequorin.

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Treatment of Immune System-Related Disorders

As noted above, Neutrokin-alpha and/or Neutrokin-alphaSV polynucleotides and polypeptides, and anti-Neutrokin-alpha antibodies, are useful for diagnosis of conditions involving abnormally high or low expression of Neutrokin-alpha and/or Neutrokin-alphaSV activities. Given the cells and tissues where Neutrokin-alpha and/or Neutrokin-alphaSV is expressed as well as the activities modulated by Neutrokin-alpha and/or Neutrokin-alphaSV, it is readily apparent that a substantially altered (increased or decreased) level of expression of Neutrokin-alpha and/or Neutrokin-alphaSV in an individual compared to the standard or "normal" level produces pathological conditions related to the bodily system(s) in which Neutrokin-alpha and/or Neutrokin-alphaSV is expressed and/or is active.

It will also be appreciated by one of ordinary skill that, since the Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides of the invention are members of the TNF family, the extracellular domains of the respective proteins may be released in soluble form from the cells which express Neutrokin-alpha and/or Neutrokin-alphaSV by proteolytic cleavage and therefore, when Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide (particularly a soluble form of the respective extracellular domains) is added from an exogenous source to cells, tissues or the body of an individual, the polypeptide will exert its modulating activities on any of its target cells of that individual. Also, cells expressing this type II transmembrane protein may be added to cells, tissues or the body of an individual whereby the added cells will bind to cells expressing receptor for Neutrokin-alpha and/or Neutrokin-alphaSV whereby the cells expressing Neutrokin-alpha and/or Neutrokin-alphaSV can cause actions (e.g., proliferation or cytotoxicity) on the receptor-bearing target cells.

In one embodiment, the invention provides a method of delivering compositions containing the polypeptides of the invention (e.g., compositions containing Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides or anti-Neutrokin-alpha and/or anti-Neutrokin-alphaSV antibodies associated with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs) to targeted cells, such as, for example, B cells expressing Neutrokin-alpha and/or Neutrokin-alphaSV receptor, or monocytes expressing the cell surface bound form of Neutrokin-alpha and/or Neutrokin-alphaSV. Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides or anti-Neutrokin-alpha and/or anti-Neutrokin-alphaSV antibodies of the invention may be associated with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs via hydrophobic, hydrophilic, ionic and/or covalent interactions.

In one embodiment, the invention provides a method for the specific delivery of compositions of the invention to cells by administering polypeptides of the invention (e.g., Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides or anti-Neutrokin-alpha and/or anti-Neutrokin-alphaSV antibodies) that are associated with heterologous polypeptides or nucleic acids. In one example, the invention provides a method for delivering a therapeutic protein into the targeted cell. In another example, the invention provides a method for delivering a single stranded nucleic acid (e.g., antisense or ribozymes) or double stranded nucleic acid (e.g., DNA that can integrate into the cell's genome or replicate episomally and that can be transcribed) into the targeted cell.

In another embodiment, the invention provides a method for the specific destruction of cells (e.g., the destruction of tumor cells) by administering polypeptides of the invention (e.g., Neutrokin-alpha and/or Neutrokin-alphaSV

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polypeptides or anti-Neutrokin- α and/or anti-Neutrokin- α SV antibodies) in association with toxins or cytotoxic prodrugs.

In a specific embodiment, the invention provides a method for the specific destruction of cells of B cell lineage (e.g., B cell related leukemias or lymphomas) by administering Neutrokin- α and/or Neutrokin- α SV polypeptides in association with toxins or cytotoxic prodrugs.

In another specific embodiment, the invention provides a method for the specific destruction of cells of monocytic lineage (e.g., monocytic leukemias or lymphomas) by administering anti-Neutrokin- α and/or anti-Neutrokin- α SV antibodies in association with toxins or cytotoxic prodrugs.

By "toxin" is meant compounds that bind and activate endogenous cytotoxic effector systems, radioisotopes, holotoxins, modified toxins, catalytic subunits of toxins, cytotoxins (cytotoxic agents), or any molecules or enzymes not normally present in or on the surface of a cell that under defined conditions cause the cell's death. Toxins that may be used according to the methods of the invention include, but are not limited to, radioisotopes known in the art, compounds such as, for example, antibodies (or complement fixing containing portions thereof) that bind an inherent or induced endogenous cytotoxic effector system, thymidine kinase, endonuclease, RNase, alpha toxin, ricin, abrin, *Pseudomonas* exotoxin A, diphtheria toxin, saporin, momordin, gelonin, pokeweed antiviral protein, alpha-sarcin and cholera toxin. "Toxin" also includes a cytostatic or cytotoxic agent, a therapeutic agent or a radioactive metal ion, e.g., alpha-emitters such as, for example, ^{213}Bi , or other radioisotopes such as, for example, ^{103}Pd , ^{125}I , ^{131}I , ^{67}Ge , ^{57}Co , ^{65}Zn , ^{85}Sr , ^{32}P , ^{33}S , ^{90}Y , ^{153}Sm , ^{152}Gd , ^{169}Yb , ^{51}Cr , ^{54}Mn , ^{75}Se , ^{113}Sn , $^{90}\text{Yttrium}$, ^{117}Tm , $^{186}\text{Rhenium}$, $^{166}\text{Holmium}$, and $^{188}\text{Rhenium}$; luminescent labels, such as luminol; and fluorescent labels, such as fluorescein and rhodamine, and biotin.

Techniques known in the art may be applied to label antibodies of the invention. Such techniques include, but are not limited to, the use of bifunctional conjugating agents (see e.g., U.S. Pat. Nos. 5,756,065; 5,714,631; 5,696,239; 5,652,361; 5,505,931; 5,489,425; 5,435,990; 5,428,139; 5,342,604; 5,274,119; 4,994,560; and 5,808,003; the contents of each of which are hereby incorporated by reference in its entirety). A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include paclitaxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, teniposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (e.g., methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU)), cyclophosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly actinomycin), bleomycin, mitramycin, and anthramycin (AMC)), and anti-mitotic agents (e.g., vincristine and vinblastine).

By "cytotoxic prodrug" is meant a non-toxic compound that is converted by an enzyme, normally present in the cell, into a cytotoxic compound. Cytotoxic prodrugs that may be used according to the methods of the invention include, but

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are not limited to, glutamyl derivatives of benzoic acid mustard alkylating agent, phosphate derivatives of etoposide or mitomycin C, cytosine arabinoside, daunorubicin, and phenoxacetamide derivatives of doxorubicin.

It will be appreciated that conditions caused by a decrease in the standard or normal level of Neutrokin- α and/or Neutrokin- α SV activity in an individual, particularly disorders of the immune system, can be treated by administration of Neutrokin- α and/or Neutrokin- α SV polypeptide (in the form of soluble extracellular domain or cells expressing the complete protein) or agonist. Thus, the invention also provides a method of treatment of an individual in need of an increased level of Neutrokin- α and/or Neutrokin- α SV activity comprising administering to such an individual a pharmaceutical composition comprising an amount of an isolated Neutrokin- α and/or Neutrokin- α SV polypeptide of the invention, or agonist thereof, effective to increase the Neutrokin- α and/or Neutrokin- α SV activity level in such an individual.

It will also be appreciated that conditions caused by a decrease in the standard or normal level of Neutrokin- α and/or Neutrokin- α SV activity in an individual, particularly disorders of the immune system, can be treated by administration of Neutrokin- α and/or Neutrokin- α SV polypeptides (in the form of soluble extracellular domain or cells expressing the complete protein) or antagonist (e.g., an anti-Neutrokin- α antibody). Thus, the invention also provides a method of treatment of an individual in need of an increased level of Neutrokin- α and/or Neutrokin- α SV activity comprising administering to such an individual a pharmaceutical composition comprising an amount of an isolated Neutrokin- α and/or Neutrokin- α SV polypeptide of the invention, or antagonist thereof, effective to decrease the Neutrokin- α and/or Neutrokin- α SV activity level in such an individual.

Neutrokin- α and/or Neutrokin- α SV polynucleotides or polypeptides of the invention, or agonists of Neutrokin- α and/or Neutrokin- α SV, can be used in the treatment of infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, Neutrokin- α , and/or Neutrokin- α SV polynucleotides or polypeptides, or agonists of Neutrokin- α and/or Neutrokin- α SV, may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated by Neutrokin- α and/or Neutrokin- α SV polynucleotides or polypeptides, or agonists of Neutrokin- α and/or Neutrokin- α SV. Examples of viruses, include, but are not limited to the following DNA and RNA viruses and viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Bunyaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Dengue, EBV, HIV, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza A, Influenza B, and parainfluenza), Papilloma virus, Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiolitis, respiratory

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syncytial virus, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), Japanese B encephalitis, Junin, Chikungunya, Rift Valley fever, yellow fever, meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's warts), and viremia. Neutrokin-alpha and/or Neutrokin-alphaSV polynucleotides or polypeptides, or agonists or antagonists of Neutrokin-alpha and/or Neutrokin-alphaSV, can be used to treat, prevent, diagnose, and/or detect any of these symptoms or diseases. In specific embodiments, Neutrokin alpha polynucleotides, polypeptides, or agonists are used to treat, prevent, and/or diagnose: meningitis, Dengue, EBV, and/or hepatitis (e.g., hepatitis B). In an additional specific embodiment Neutrokin alpha polynucleotides, polypeptides, or agonists are used to treat patients nonresponsive to one or more other commercially available hepatitis vaccines. In a further specific embodiment, Neutrokin alpha polynucleotides, polypeptides, or agonists are used to treat, prevent, and/or diagnose AIDS. In an additional specific embodiment Neutrokin-alpha and/or Neutrokin-alphaSV and/or Neutrokin-alpha Receptor polynucleotides, polypeptides, agonists, and/or antagonists are used to treat, prevent, and/or diagnose patients with cryptosporidiosis.

Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated by Neutrokin-alpha, and/or Neutrokin-alphaSV polynucleotides or polypeptides, or agonists or antagonists of Neutrokin-alpha, and/or Neutrokin-alphaSV, include, but are not limited to, the following Gram-Negative and Gram-positive bacteria and bacterial families and fungi: Actinomycetales (e.g., *Corynebacterium*, *Mycobacterium*, *Nocardia*), *Cryptococcus neoformans*, Aspergilliosis, Bacillaceae (e.g., Anthrax, *Clostridium*), Bacteroidaceae, Blastomycosis, *Bordetella*, *Borrelia* (e.g., *Borrelia burgdorferi*), Brucellosis, Candidiasis, *Campylobacter*, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, *E. coli* (e.g., Enterotoxigenic *E. coli* and Enterohemorrhagic *E. coli*), Enterobacteriaceae (*Klebsiella*, *Salmonella* (e.g., *Salmonella typhi*, and *Salmonella paratyphi*), *Serratia*, *Yersinia*), *Erysipelothrix*, *Helicobacter*, Legionellosis, Leptospirosis, *Listeria* (e.g., *Listeria monocytogenes*), Mycoplasmales, *Mycobacterium leprae*, *Vibrio cholerae*, Neisseriaceae (e.g., *Acinetobacter*, Gonorrhea, Meningococcal), *Neisseria meningitidis*, Pasteurellaceae Infections (e.g., *Actinobacillus*, *Haemophilus* (e.g., *Haemophilus influenza* type B), *Pasteurella*), *Pseudomonas*, Rickettsiaceae, Chlamydiaceae, Syphilis, *Shigella* spp., Staphylococcal, Meningococcal, Pneumococcal and Streptococcal (e.g., *Streptococcus pneumoniae* and Group B *Streptococcus*). These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea, meningitis (e.g., meningitis types A and B), Chlamydia, Syphilis, Diphtheria, Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections. Neutrokin-alpha, and/or Neutrokin-alphaSV polynucleotides or

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polypeptides, or agonists or antagonists of Neutrokin-alpha, and/or Neutrokin-alphaSV, can be used to treat, prevent, diagnose, and/or detect any of these symptoms or diseases. In specific embodiments, Neutrokin alpha polynucleotides, polypeptides, or agonists thereof are used to treat, prevent, and/or diagnose: tetanus, Diphtheria, botulism, and/or meningitis type B.

Moreover, parasitic agents causing disease or symptoms that can be treated by Neutrokin-alpha and/or Neutrokin-alphaSV polynucleotides or polypeptides, or agonists of Neutrokin-alpha and/or Neutrokin-alphaSV, include, but not limited to, the following families or class: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and *Trichomonas* and Sporozoans (e.g., *Plasmodium virax*, *Plasmodium falciparum*, *Plasmodium malariae* and *Plasmodium ovale*). These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), malaria, pregnancy complications, and toxoplasmosis. Neutrokin-alpha and/or Neutrokin-alphaSV polynucleotides or polypeptides, or agonists or antagonists of Neutrokin-alpha and/or Neutrokin-alphaSV, can be used to treat, prevent, diagnose, and/or detect any of these symptoms or diseases. In specific embodiments, Neutrokin alpha polynucleotides, polypeptides, or agonists thereof are used to treat, prevent, and/or diagnose malaria.

In another embodiment, Neutrokin-alpha and/or Neutrokin-alphaSV polynucleotides or polypeptides of the invention and/or agonists and/or antagonists thereof, are used to treat, prevent, and/or diagnose inner ear infection (such as, for example, otitis media), as well as other infections characterized by infection with *Streptococcus pneumoniae* and other pathogenic organisms.

In a specific embodiment, Neutrokin-alpha and/or Neutrokin-alphaSV polynucleotides or polypeptides, or agonists or antagonists thereof (e.g., anti-Neutrokin-alpha, and/or anti-Neutrokin-alphaSV antibodies) are used to treat or prevent a disorder characterized by deficient serum immunoglobulin production, recurrent infections, and/or immune system dysfunction. Moreover, Neutrokin-alpha, and/or Neutrokin-alphaSV polynucleotides or polypeptides, or agonists or antagonists thereof (e.g., anti-Neutrokin-alpha, and/or anti-Neutrokin-alphaSV antibodies) may be used to treat or prevent infections of the joints, bones, skin, and/or parotid glands, blood-borne infections (e.g., sepsis, meningitis, septic arthritis, and/or osteomyelitis), autoimmune diseases (e.g., those disclosed herein), inflammatory disorders, and malignancies, and/or any disease or disorder or condition associated with these infections, diseases, disorders and/or malignancies) including, but not limited to, COVID, other primary immune deficiencies, HIV disease, CLL, recurrent bronchitis, sinusitis, otitis media, conjunctivitis, pneumonia, hepatitis, meningitis, herpes zoster (e.g., severe herpes zoster), and/or *pneumocystis carinii*.

Neutrokin-alpha and/or Neutrokin-alphaSV polynucleotides or polypeptides of the invention, or agonists or antagonists thereof, may be used to diagnose, prognose, treat or prevent one or more of the following diseases or disorders, or conditions associated therewith: primary immunodeficiencies, immune-mediated thrombocytopenia, Kawasaki syndrome, bone marrow transplant (e.g., recent bone marrow transplant in adults or children), chronic B-cell lymphocytic

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leukemia, HIV infection (e.g., adult or pediatric HIV infection), chronic inflammatory demyelinating polyneuropathy, and post-transfusion purpura.

Additionally, Neutrokin- α and/or Neutrokin- α SV polynucleotides or polypeptides of the invention, or agonists or antagonists thereof, may be used to diagnose, prognose, treat or prevent one or more of the following diseases, disorders, or conditions associated therewith, Guillain-Barre syndrome, anemia (e.g., anemia associated with parvovirus B19, patients with stable multiple myeloma who are at high risk for infection (e.g., recurrent infection), autoimmune hemolytic anemia (e.g., warm-type autoimmune hemolytic anemia), thrombocytopenia (e.g., neonatal thrombocytopenia), and immune-mediated neutropenia), transplantation (e.g., cytomegalovirus (CMV)-negative recipients of CMV-positive organs), hypogammaglobulinemia (e.g., hypogammaglobulinemic neonates with risk factor for infection or morbidity), epilepsy (e.g., intractable epilepsy), systemic vasculitic syndromes, myasthenia gravis (e.g., decompensation in myasthenia gravis), dermatomyositis, and polymyositis.

Additional preferred embodiments of the invention include, but are not limited to, the use of Neutrokin- α and/or Neutrokin- α SV polypeptides, Neutrokin- α and/or Neutrokin- α SV polynucleotides, and functional agonists thereof, in the following applications:

Administration to an animal (e.g., mouse, rat, rabbit, hamster, guinea pig, pigs, micro-pig, chicken, camel, goat, horse, cow, sheep, dog, cat, non-human primate, and human, most preferably human) to boost the immune system to produce increased quantities of one or more antibodies (e.g., IgG, IgA, IgM, and IgE), to induce higher affinity antibody production (e.g., IgG, IgA, IgM, and IgE), and/or to increase an immune response. In a specific nonexclusive embodiment, Neutrokin- α polypeptides of the invention, and/or agonists thereof, are administered to boost the immune system to produce increased quantities of IgG. In another specific non-exclusive embodiment, Neutrokin- α polypeptides of the invention and/or agonists thereof, are administered to boost the immune system to produce increased quantities of IgA. In another specific nonexclusive embodiment, Neutrokin- α polypeptides of the invention and/or agonists thereof, are administered to boost the immune system to produce increased quantities of IgM.

Administration to an animal (including, but not limited to, those listed above, and also including transgenic animals) incapable of producing functional endogenous antibody molecules or having an otherwise compromised endogenous immune system, but which is capable of producing human immunoglobulin molecules by means of a reconstituted or partially reconstituted immune system from another animal (see, e.g., published PCT Application Nos. WO98/24893, WO/9634096, WO/9633735, and WO/9110741).

A vaccine adjuvant that enhances immune responsiveness to specific antigen. In a specific embodiment, the vaccine adjuvant is a Neutrokin- α and/or Neutrokin- α SV polypeptide described herein. In another specific embodiment, the vaccine adjuvant is a Neutrokin- α and/or Neutrokin- α SV polynucleotide described herein (i.e., the Neutrokin- α and/or Neutrokin- α SV polynucleotide is a genetic vaccine adjuvant). As discussed herein, Neutrokin- α and/or Neutrokin- α SV polynucleotides may be administered using techniques known in the art, including but not limited to, liposomal delivery, recombinant vector delivery, injection of naked DNA, and gene gun delivery.

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An adjuvant to enhance tumor-specific immune responses.

An adjuvant to enhance anti-viral immune responses. Anti-viral immune responses that may be enhanced using the compositions of the invention as an adjuvant, include, but are not limited to, virus and virus associated diseases or symptoms described herein or otherwise known in the art. In specific embodiments, the compositions of the invention are used as an adjuvant to enhance an immune response to a virus, disease, or symptom selected from the group consisting of: AIDS, meningitis, Dengue, EBV, and hepatitis (e.g., hepatitis B). In another specific embodiment, the compositions of the invention are used as an adjuvant to enhance an immune response to a virus, disease, or symptom selected from the group consisting of: HIV/AIDS, Respiratory syncytial virus, Dengue, Rotavirus, Japanese B encephalitis, Influenza A and B, Parainfluenza, Measles, Cytomegalovirus, Rabies, Junin, Chikungunya, Rift Valley fever, Herpes simplex, and yellow fever. In another specific embodiment, the compositions of the invention are used as an adjuvant to enhance an immune response to the HIV gp120 antigen.

An adjuvant to enhance anti-bacterial or anti-fungal immune responses. Anti-bacterial or anti-fungal immune responses that may be enhanced using the compositions of the invention as an adjuvant, include bacteria or fungus and bacteria or fungus associated diseases or symptoms described herein or otherwise known in the art. In specific embodiments, the compositions of the invention are used as an adjuvant to enhance an immune response to a bacteria or fungus, disease, or symptom selected from the group consisting of: tetanus, Diphtheria, botulism, and meningitis type B. In another specific embodiment, the compositions of the invention are used as an adjuvant to enhance an immune response to a bacteria or fungus, disease, or symptom selected from the group consisting of: *Vibrio cholerae*, *Mycobacterium leprae*, *Salmonella typhi*, *Salmonella paratyphi*, *Neisseria meningitidis*, *Streptococcus pneumoniae*, Group B streptococcus, *Shigella* spp., Enterotoxigenic *Escherichia coli*, Enterohemorrhagic *E. coli*, *Borrelia burgdorferi*, and *Plasmodium* (malaria).

An adjuvant to enhance anti-parasitic immune responses. Anti-parasitic immune responses that may be enhanced using the compositions of the invention as an adjuvant, include parasite and parasite associated diseases or symptoms described herein or otherwise known in the art. In specific embodiments, the compositions of the invention are used as an adjuvant to enhance an immune response to a parasite. In another specific embodiment, the compositions of the invention are used as an adjuvant to enhance an immune response to *Plasmodium* (malaria).

As a stimulator of B cell responsiveness to pathogens.

As an agent that elevates the immune status of an individual prior to their receipt of immunosuppressive therapies.

As an agent to induce higher affinity antibodies.

As an agent to increase serum immunoglobulin concentrations.

As an agent to accelerate recovery of immunocompromised individuals.

As an agent to boost immunoresponsiveness among aged populations.

As an immune system enhancer prior to, during, or after bone marrow transplant and/or other transplants (e.g., allogeneic or xenogeneic organ transplantation). With respect to transplantation, compositions of the invention may be administered prior to, concomitant with, and/or after transplantation. In a specific embodiment, compositions of the invention are administered after transplantation, prior to the beginning of recovery of T-cell populations. In another specific embodi-

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ment, compositions of the invention are first administered after transplantation after the beginning of recovery of T cell populations, but prior to full recovery of B cell populations.

As an agent to boost immunoresponsiveness among B cell immunodeficient individuals, such as, for example, an individual who has undergone a partial or complete splenectomy, B cell immunodeficiencies that may be ameliorated or treated by administering the Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides or polynucleotides of the invention, or agonists thereof, include, but are not limited to, severe combined immunodeficiency (SCID)-X linked, SCID-autosomal, adenosine deaminase deficiency (ADA deficiency), X-linked agammaglobulinemia (XLA), Bruton's disease, congenital agammaglobulinemia, X-linked infantile agammaglobulinemia, acquired agammaglobulinemia, adult onset agammaglobulinemia, late-onset agammaglobulinemia, dysgammaglobulinemia, hypogammaglobulinemia, transient hypogammaglobulinemia of infancy, unspecified hypogammaglobulinemia, agammaglobulinemia, common variable immunodeficiency (CVID)(acquired), Wiskott-Aldrich Syndrome (WAS), X-linked immunodeficiency with hyper IgM, non X-linked immunodeficiency with hyper IgM, selective IgA deficiency, IgG subclass deficiency (with or without IgA deficiency), antibody deficiency with normal or elevated Igs, immunodeficiency with thymoma, Ig heavy chain deletions, kappa chain deficiency, B cell lymphoproliferative disorder (BLPD), selective IgM immunodeficiency, recessive agammaglobulinemia (Swiss type), reticular dysgenesis, neonatal neutropenia, severe congenital leukopenia, thymic aplasia/aplasia or dysplasia with immunodeficiency, ataxia-telangiectasia, short limbed dwarfism, X-linked lymphoproliferative syndrome (XLP), Nezelof syndrome-combined immunodeficiency with Igs, purine nucleoside phosphorylase deficiency (PNP), MHC Class II deficiency (Bare Lymphocyte Syndrome) and severe combined immunodeficiency.

As an agent to boost immunoresponsiveness among individuals having an acquired loss of B cell function, Conditions resulting in an acquired loss of B cell function that may be ameliorated or treated by administering the Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides or polynucleotides of the invention, or agonists thereof, include, but are not limited to, HIV Infection, AIDS, bone marrow transplant, and B cell chronic lymphocytic leukemia (CLL).

As an agent to boost immunoresponsiveness among individuals having a temporary immune deficiency, Conditions resulting in a temporary immune deficiency that may be ameliorated or treated by administering the Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides or polynucleotides of the invention, or agonists thereof, include, but are not limited to, recovery from viral infections (e.g., influenza), conditions associated with malnutrition, recovery from infectious mononucleosis, or conditions associated with stress, recovery from measles, recovery from blood transfusion, recovery from surgery.

As a regulator of antigen presentation by monocytes, dendritic cells, and/or B-cells. In one embodiment, Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides (in soluble, membrane-bound or transmembrane forms) or polynucleotides enhance antigen presentation or antagonize antigen presentation in vitro or in vivo. Moreover, in related embodiments, this enhancement or antagonization of antigen presentation may be useful in anti-tumor treatment or to modulate the immune system.

As a mediator of mucosal immune responses. The expression of Neutrokin-alpha by monocytes and the responsiveness of B cells to this factor suggests that it may be involved in exchange of signals between B cells and monocytes or their

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differentiated progeny. This activity is in many ways analogous to the CD40-CD154 signaling between B cells and T cells. Neutrokin-alpha may therefore be an important regulator of T cell independent immune responses to environmental pathogens. In particular, the unconventional B cell populations (CD5+) that are associated with mucosal sites and responsible for much of the innate immunity in humans may respond to Neutrokin-alpha thereby enhancing an individual's protective immune status.

As an agent to direct an individual's immune system towards development of a humoral response (i.e. TH2) as opposed to a TH1 cellular response.

As a means to induce tumor proliferation and thus make it more susceptible to anti-neoplastic agents. For example, multiple myeloma is a slowly dividing disease and is thus refractory to virtually all anti-neoplastic regimens. If these cells were forced to proliferate more rapidly their susceptibility profile would likely change.

As a B cell specific binding protein to which specific activators or inhibitors of cell growth may be attached. The result would be to focus the activity of such activators or inhibitors onto normal, diseased, or neoplastic B cell populations.

As a means of detecting B-lineage cells by virtue of its specificity. This application may require labeling the protein with biotin or other agents (e.g., as described herein) to afford a means of detection.

As a stimulator of B cell production in pathologies such as AIDS, chronic lymphocyte disorder and/or Common Variable Immunodeficiency.

As part of a B cell selection device the function of which is to isolate B cells from a heterogeneous mixture of cell types. Neutrokin-alpha could be coupled to a solid support to which B cells would then specifically bind. Unbound cells would be washed out and the bound cells subsequently eluted. A nonlimiting use of this selection would be to allow purging of tumor cells from, for example, bone marrow or peripheral blood prior to transplant.

As a therapy for generation and/or regeneration of lymphoid tissues following surgery, trauma or genetic defect.

As a gene-based therapy for genetically inherited disorders resulting in immuno-incompetence such as observed among SCID patients.

As an antigen for the generation of antibodies to inhibit or enhance Neutrokin-alpha mediated responses.

As a means of activating monocytes/macrophages to defend against parasitic diseases that effect monocytes such as *Leishmania*.

As pretreatment of bone marrow samples prior to transplant. Such treatment would increase B cell representation and thus accelerate recovery.

As a means of regulating secreted cytokines that are elicited by Neutrokin-alpha.

Neutrokin-alpha or Neutrokin-alphaSV polypeptides or polynucleotides of the invention, or agonists may be used to modulate IgG concentrations in vitro or in vivo.

Additionally, Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides or polynucleotides of the invention, or agonists thereof, may be used to treat, prevent, and/or diagnose IgE-mediated allergic reactions. Such allergic reactions include, but are not limited to, asthma, rhinitis, and eczema.

In a specific embodiment, Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides or polynucleotides of the invention, or agonists thereof, are administered to treat, prevent, diagnose, and/or ameliorate selective IgA deficiency.

In another specific embodiment, Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides or polynucleotides of the

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invention, or agonists thereof, are administered to treat, prevent, diagnose, and/or ameliorate ataxia-telangiectasia.

branes of the body. Such diseases or disorders include, but are not limited to, for example, mucositis, mucoclasia, mucocolitis, mucocutaneous leishmaniasis (such as, for example, American leishmaniasis, leishmaniasis americana, nasopharyngeal leishmaniasis, and New World leishmaniasis), mucocutaneous lymph node syndrome (for example, Kawasaki disease), mucocenteritis, mucocutaneous carcinoma, mucocutaneous tumor, mucocutaneous dysplasia, mucocutaneous adenocarcinoma, mucocutaneous degeneration, myxomatous degeneration, myxomatous degeneration (for example, cystic medial necrosis), mucopolipidosis (including, for example, mucopolipidosis I, mucopolipidosis II, mucopolipidosis III, and mucopolipidosis IV), mucopolysaccharidosis, mucocutaneous enteritis, mucocenteritis, mucopolysaccharidosis (such as, for example, type I mucopolysaccharidosis (i.e., Hurler's syndrome), type II mucopolysaccharidosis (i.e., Scheie's syndrome or type V mucopolysaccharidosis), type III mucopolysaccharidosis (i.e., Hunter's syndrome), type IV mucopolysaccharidosis (i.e., Sanfilippo's syndrome), type V mucopolysaccharidosis (i.e., Morquio's syndrome), type VI mucopolysaccharidosis (i.e., Maroteaux-Lamy syndrome), type VII mucopolysaccharidosis (i.e., mucopolysaccharidosis due to beta-glucuronidase deficiency), and mucosulfatidosis), mucopolysacchariduria, mucopurulent conjunctivitis, mucopus, mucormycosis (i.e., zygomycosis), mucosal disease (i.e., bovine virus diarrhea), mucous colitis (such as, for example, mucocolitis and myxomembranous colitis), and mucoviscidosis (such as, for example, cystic fibrosis, cystic fibrosis of the pancreas, Clarke-Hadfield syndrome, fibrocystic disease of the pancreas, mucoviscidosis, and viscidosis). In a highly preferred embodiment, Neutrokin- α , and/or Neutrokin- α SV polynucleotides, polypeptides, and/or agonists and/or antagonists thereof are used to treat, prevent, and/or diagnose mucositis, especially as associated with chemotherapy.

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Thus, Neutrokin- α may, like CD40 and its ligand, be regulated by the status of the immune system and the microenvironment in which the cell is located.

A therapy for preventing the B cell proliferation and Ig secretion associated with autoimmune diseases such as idiopathic thrombocytopenic purpura, systemic lupus erythematosus and MS.

An inhibitor of graft versus host disease or transplant rejection.

A therapy for B cell malignancies such as ALL, Hodgkins disease, non-Hodgkins lymphoma, Chronic lymphocyte leukemia, plasmacytomas, multiple myeloma, Burkitt's lymphoma, and EBV-transformed diseases.

A therapy for chronic hypergammaglobulinemia evident in such diseases as monoclonal gammopathy of undetermined significance (MGUS), Waldenstrom's disease, related idiopathic monoclonal gammopathies, and plasmacytomas.

A therapy for decreasing cellular proliferation of large B-cell lymphomas.

A means of decreasing the involvement of B cells and Ig associated with Chronic Myelogenous Leukemia.

An immunosuppressive agent(s).

Neutrokin- α or Neutrokin- α SV polypeptides or polynucleotides of the invention, or antagonists may be used to modulate IgE concentrations in vitro or in vivo.

In another embodiment, administration of Neutrokin- α or Neutrokin- α SV polypeptides or polynucleotides of the invention, or antagonists thereof, may be used to treat, prevent, and/or diagnose IgE-mediated allergic reactions including, but not limited to, asthma, rhinitis, and eczema.

An inhibitor of signaling pathways involving ERK1, COX2 and Cyclin D2 which have been associated with Neutrokin- α induced B cell activation.

The above-recited applications have uses in a wide variety of hosts. Such hosts include, but are not limited to, human, murine, rabbit, goat, guinea pig, camel, horse, mouse, rat, hamster, pig, micro-pig, chicken, goat, cow, sheep, dog, cat, non-human primate, and human. In specific embodiments, the host is a mouse, rabbit, goat, guinea pig, chicken, rat, hamster, pig, sheep, dog or cat. In preferred embodiments, the host is a mammal. In most preferred embodiments, the host is a human.

The agonists and antagonists may be employed in a composition with a pharmaceutically acceptable carrier, e.g., as described herein.

The antagonists may be employed for instance to inhibit Neutrokin- α -mediated and/or Neutrokin- α SV-mediated chemotaxis and activation of macrophages and their precursors, and of neutrophils, basophils, B lymphocytes and some T-cell subsets, e.g., activated and CD8 cytotoxic T cells and natural killer cells, in certain auto-immune and chronic inflammatory and infective diseases. Examples of autoimmune diseases include multiple sclerosis, and insulin-dependent diabetes. The antagonists may also be employed to treat, prevent, and/or diagnose infectious diseases including silicosis, sarcoidosis, idiopathic pulmonary fibrosis by preventing the recruitment and activation of mononuclear phagocytes. They may also be employed to treat, prevent, and/or diagnose idiopathic hyper-eosinophilic syndrome by preventing eosinophil production and migration. Endotoxic shock may also be treated by the antagonists by preventing the migration of macrophages and their production of the Neutrokin- α and/or Neutrokin- α SV polypeptides of the present invention. The antagonists may also be employed for treating atherosclerosis, by preventing monocyte infiltration in the artery wall. The antagonists may also be employed to treat, prevent, and/or diagnose histamine-mediated allergic reac-

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tions and immunological disorders including late phase allergic reactions, chronic urticaria, and atopic dermatitis by inhibiting chemokine-induced mast cell and basophil degranulation and release of histamine. IgE-mediated allergic reactions such as allergic asthma, rhinitis, and eczema may also be treated. The antagonists may also be employed to treat, prevent, and/or diagnose chronic and acute inflammation by preventing the attraction of monocytes to a wound area. They may also be employed to regulate normal pulmonary macrophage populations, since chronic and acute inflammatory pulmonary diseases are associated with sequestration of mononuclear phagocytes in the lung. Antagonists may also be employed to treat, prevent, and/or diagnose rheumatoid arthritis by preventing the attraction of monocytes into synovial fluid in the joints of patients. Monocyte influx and activation plays a significant role in the pathogenesis of both degenerative and inflammatory arthropathies. The antagonists may be employed to interfere with the deleterious cascades attributed primarily to IL-1 and TNF, which prevents the biosynthesis of other inflammatory cytokines. In this way, the antagonists may be employed to prevent inflammation. The antagonists may also be employed to inhibit prostaglandin-independent fever induced by Neutrokin- α and/or Neutrokin- α SV. The antagonists may also be employed to treat, prevent, and/or diagnose cases of bone marrow failure, for example, aplastic anemia and myelodysplastic syndrome. The antagonists may also be employed to treat, prevent, and/or diagnose asthma and allergy by preventing eosinophil accumulation in the lung. The antagonists may also be employed to treat, prevent, and/or diagnose subepithelial basement membrane fibrosis which is a prominent feature of the asthmatic lung. The antagonists may also be employed to treat, prevent, and/or diagnose lymphomas (e.g., one or more of the extensive, but not limiting, list of lymphomas provided herein).

All of the above described applications as they may apply to veterinary medicine. Moreover, all applications described herein may also apply to veterinary medicine.

Neutrokin- α and/or Neutrokin- α SV polynucleotides or polypeptides of the invention and/or agonists and/or antagonists thereof, may be used to treat, prevent, and/or diagnose various immune system-related disorders and/or conditions associated with these disorders, in mammals, preferably humans. Many autoimmune disorders result from inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of Neutrokin- α and/or Neutrokin- α SV polynucleotides or polypeptides of the invention and/or agonists and/or antagonists thereof that can inhibit an immune response, particularly the proliferation of B cells and/or the production of immunoglobulins, may be an effective therapy in treating and/or preventing autoimmune disorders. Thus, in preferred embodiments, Neutrokin- α and/or Neutrokin- α SV antagonists of the invention (e.g., polypeptide fragments of Neutrokin- α and/or Neutrokin- α SV and anti-Neutrokin- α antibodies) are used to treat, prevent, and/or diagnose an autoimmune disorder.

Autoimmune disorders and conditions associated with these disorders that may be treated, prevented, and/or diagnosed with the Neutrokin- α polynucleotides, polypeptides, and/or antagonists of the invention (e.g., anti-Neutrokin- α antibodies), include, but are not limited to, autoimmune hemolytic anemia, autoimmune neonatal thrombocytopenia, idiopathic thrombocytopenia purpura, autoimmune cytopenia, hemolytic anemia, antiphospholipid syn-

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drome, dermatitis, allergic encephalomyelitis, myocarditis, relapsing polychondritis, rheumatic heart disease, glomerulonephritis (e.g., IgA nephropathy), Multiple Sclerosis, Neuritis, Uveitis, Ophthalmia, Polyendocrinopathies, Purpura (e.g., Henoch-Schoenlein purpura), Reiter's Disease, Still-Man Syndrome, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune inflammatory eye disease.

Additional autoimmune disorders (that are highly probable) that may be treated, prevented, and/or diagnosed with the compositions of the invention include, but are not limited to, autoimmune thyroiditis, hypothyroidism (i.e., Hashimoto's thyroiditis) (often characterized, e.g., by cell-mediated and humoral thyroid cytotoxicity), systemic lupus erythematosus (often characterized, e.g., by circulating and locally generated immune complexes), Goodpasture's syndrome (often characterized, e.g., by anti-basement membrane antibodies), Pemphigus (often characterized, e.g., by epidermal acantholytic antibodies), Receptor autoimmunities such as, for example, (a) Graves' Disease (often characterized, e.g., by TSH receptor antibodies), (b) Myasthenia Gravis (often characterized, e.g., by acetylcholine receptor antibodies), and (c) insulin resistance (often characterized, e.g., by insulin receptor antibodies), autoimmune hemolytic anemia (often characterized, e.g., by phagocytosis of antibody-sensitized RBCs), autoimmune thrombocytopenic purpura (often characterized, e.g., by phagocytosis of antibody-sensitized platelets).

Additional autoimmune disorders (that are probable) that may be treated, prevented, and/or diagnosed with the compositions of the invention include, but are not limited to, rheumatoid arthritis (often characterized, e.g., by immune complexes in joints), scleroderma with anti-collagen antibodies (often characterized, e.g., by nucleolar and other nuclear antibodies), mixed connective tissue disease (often characterized, e.g., by antibodies to extractable nuclear antigens (e.g., ribonucleoprotein)), polymyositis/dermatomyositis (often characterized, e.g., by nonhistone ANA), pernicious anemia (often characterized, e.g., by antiparietal cell, microsomes, and intrinsic factor antibodies), idiopathic Addison's disease (often characterized, e.g., by humoral and cell-mediated adrenal cytotoxicity, infertility (often characterized, e.g., by antispermatozoal antibodies), glomerulonephritis (often characterized, e.g., by glomerular basement membrane antibodies or immune complexes) such as primary glomerulonephritis and IgA nephropathy, bullous pemphigoid (often characterized, e.g., by IgG and complement in basement membrane), Sjogren's syndrome (often characterized, e.g., by multiple tissue antibodies, and/or a specific nonhistone ANA (SS-B)), diabetes mellitus (often characterized, e.g., by cell-mediated and humoral islet cell antibodies), and adrenergic drug resistance (including adrenergic drug resistance with asthma or cystic fibrosis) (often characterized, e.g., by beta-adrenergic receptor antibodies).

Additional autoimmune disorders (that are possible) that may be treated, prevented, and/or diagnosed with the compositions of the invention include, but are not limited to, chronic active hepatitis (often characterized, e.g., by smooth muscle antibodies), primary biliary cirrhosis (often characterized, e.g., by mitochondrial antibodies), other endocrine gland failure (often characterized, e.g., by specific tissue antibodies in some cases), vitiligo (often characterized, e.g., by melanocyte antibodies), vasculitis (often characterized, e.g., by Ig and complement in vessel walls and/or low serum complement), post-MI (often characterized, e.g., by myocardial antibodies), cardiomyopathy syndrome (often characterized, e.g., by myocardial antibodies), urticaria (often characterized, e.g., by IgG

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and IgM antibodies to IgE), atopic dermatitis (often characterized, e.g., by IgG and IgM antibodies to IgE), asthma (often characterized, e.g., by IgG and IgM antibodies to IgE), inflammatory myopathies, and many other inflammatory, granulomatous, degenerative, and atrophic disorders.

In a preferred embodiment, the autoimmune diseases and disorders and/or conditions associated with the diseases and disorders recited above are treated, prevented, and/or diagnosed using anti-Neurokinine-alpha antibodies and/or anti-Neurokinine-alphaSV.

In a specific preferred embodiment, rheumatoid arthritis is treated, prevented, and/or diagnosed using anti-Neurokinine-alpha antibodies and/or anti-Neurokinine-alphaSV antibodies and/or other antagonist of the invention.

In a specific preferred embodiment, lupus is treated, prevented, and/or diagnosed using anti-Neurokinine-alpha antibodies and/or anti-Neurokinine-alphaSV antibodies and/or other antagonist of the invention.

In a specific preferred embodiment, nephritis associated with lupus is treated, prevented, and/or diagnosed using anti-Neurokinine-alpha antibodies and/or anti-Neurokinine-alphaSV antibodies and/or other antagonist of the invention.

In a specific embodiment, Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides or polypeptides, or antagonists thereof (e.g., anti-Neurokinine-alpha and/or anti-Neurokinine-alphaSV antibodies) are used to treat or prevent systemic lupus erythematosus and/or diseases, disorders or conditions associated therewith. Lupus-associated diseases, disorders, or conditions that may be treated or prevented with Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides or polypeptides, or antagonists of the invention, include, but are not limited to, hematologic disorders (e.g., hemolytic anemia, leukopenia, lymphopenia, and thrombocytopenia), immunologic disorders (e.g., anti-DNA antibodies, and anti-Sm antibodies), rashes, photosensitivity, oral ulcers, arthritis, fever, fatigue, weight loss, serositis (e.g., pleuritis (pleurisy)), renal disorders (e.g., nephritis), neurological disorders (e.g., seizures, peripheral neuropathy, CNS related disorders), gastrointestinal disorders, Raynaud phenomenon, and pericarditis. In a preferred embodiment, the Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides or polypeptides, or antagonists thereof (e.g., anti-Neurokinine-alpha and/or anti-Neurokinine-alphaSV antibodies) are used to treat or prevent renal disorders associated with systemic lupus erythematosus. In a most preferred embodiment, Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides or polypeptides, or antagonists thereof (e.g., anti-Neurokinine-alpha and/or anti-Neurokinine-alphaSV antibodies) are used to treat or prevent nephritis associated with systemic lupus erythematosus.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides or polypeptides of the invention and/or agonists and/or antagonists thereof. Moreover, these molecules can be used to treat, prevent, and/or diagnose anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides or polypeptides of the invention and/or agonists and/or antagonists thereof, may also be used to treat, prevent, and/or diagnose organ rejection or graft-versus-host disease (GVHD) and/or conditions associated therewith. Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tis-

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sues. The administration of Neutrokin-alpha and/or Neutrokin-alphaSV polynucleotides or polypeptides of the invention and/or agonists and/or antagonists thereof, that inhibit an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, Neutrokin-alpha and/or Neutrokin-alphaSV polynucleotides or polypeptides of the invention and/or agonists and/or antagonists thereof, may also be used to modulate inflammation. For example, Neutrokin-alpha and/or Neutrokin-alphaSV polynucleotides or polypeptides of the invention and/or agonists and/or antagonists thereof, may inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat, prevent, and/or diagnose inflammatory conditions, both chronic and acute conditions, including chronic prostatitis, granulomatous prostatitis and malacoplakia, inflammation associated with infection (e.g., septic shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1).

In a specific embodiment, anti-Neutrokin-alpha antibodies and/or anti-Neutrokin-alphaSV antibodies of the invention are used to treat, prevent, modulate, detect, and/or diagnose inflammation.

In a specific embodiment, anti-Neutrokin-alpha antibodies and/or anti-Neutrokin-alphaSV antibodies of the invention are used to treat, prevent, modulate, detect, and/or diagnose inflammatory disorders.

In another specific embodiment, anti-Neutrokin-alpha antibodies and/or anti-Neutrokin-alphaSV antibodies of the invention are used to treat, prevent, modulate, detect, and/or diagnose allergy and/or hypersensitivity.

Antibodies against Neutrokin-alpha and/or Neutrokin-alphaSV may be employed to bind to and inhibit Neutrokin-alpha and/or Neutrokin-alphaSV activity to treat, prevent, and/or diagnose ARDS, by preventing infiltration of neutrophils into the lung after injury. The agonists and antagonists of the instant may be employed in a composition with a pharmaceutically acceptable carrier, e.g., as described hereinafter.

Neutrokin-alpha and/or Neutrokin-alphaSV and/or Neutrokin-alpha receptor polynucleotides or polypeptides of the invention and/or agonists and/or antagonists thereof, are used to treat, prevent, and/or diagnose diseases and disorders of the pulmonary system (e.g., bronchi such as, for example, sinopulmonary and bronchial infections and conditions associated with such diseases and disorders and other respiratory diseases and disorders. In specific embodiments, such diseases and disorders include, but are not limited to, bronchial adenoma, bronchial asthma, pneumonia (such as, e.g., bronchial pneumonia, bronchopneumonia, and tuberculous bronchopneumonia), chronic obstructive pulmonary disease (COPD), bronchial polyps, bronchiectasia (such as, e.g., bronchiectasia sicca, cylindrical bronchiectasis, and sacular bronchiectasis), bronchiolar adenocarcinoma, bronchiolar carcinoma, bronchiolitis (such as, e.g., exudative bronchiolitis, bronchiolitis fibrosa obliterans, and proliferative bronchiolitis), bronchiolo-alveolar carcinoma, bronchitic asthma, bronchitis (such as, e.g., asthmatic bronchitis, Castellani's bronchitis, chronic bronchitis, croupous bronchitis, fibrinous bronchitis, hemorrhagic bronchitis, infectious avian bronchitis, obliterative bronchitis, plastic bronchitis, pseudomembranous bronchitis, putrid bronchitis, and verminous bronchitis), bronchocentric granulomatosis, bronchoedema,

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bronchoesophageal fistula, bronchogenic carcinoma, bronchogenic cyst, broncholithiasis, bronchomalacia, bronchomycosis (such as, e.g., bronchopulmonary aspergillosis), bronchopulmonary spirochetosis, hemorrhagic bronchitis, bronchorrhea, bronchospasm, bronchostasis, bronchostenosis, Biot's respiration, bronchial respiration, Kussmaul respiration, Kussmaul-Kien respiration, respiratory acidosis, respiratory alkalosis, respiratory distress syndrome of the newborn, respiratory insufficiency, respiratory scleroma, respiratory syncytial virus, and the like.

In a specific embodiment, Neutrokin-alpha and/or Neutrokin-alphaSV polynucleotides or polypeptides of the invention and/or agonists and/or antagonists thereof, are used to treat, prevent, and/or diagnose chronic obstructive pulmonary disease (COPD).

In another embodiment, Neutrokin-alpha and/or Neutrokin-alphaSV polynucleotides or polypeptides of the invention and/or agonists and/or antagonists thereof, are used to treat, prevent, and/or diagnose fibroses and conditions associated with fibroses, such as, for example, but not limited to, cystic fibrosis (including such fibroses as cystic fibrosis of the pancreas, Clarke-Hadfield syndrome, fibrocystic disease of the pancreas, mucoviscidosis, and viscidosis), endomyocardial fibrosis, idiopathic retroperitoneal fibrosis, leptomenigeal fibrosis, mediastinal fibrosis, nodular subepidermal fibrosis, pericentral fibrosis, perimuscular fibrosis, pipestem fibrosis, replacement fibrosis, subadventitial fibrosis, and Symmers' clay pipestem fibrosis.

The TNF family ligands are known to be among the most pleiotropic cytokines, inducing a large number of cellular responses, including cytotoxicity, anti-viral activity, immunoregulatory activities, and the transcriptional regulation of several genes (D. V. Goeddel et al., "Tumor Necrosis Factors: Gene Structure and Biological Activities," *Symp. Quant. Biol.* 51:597-609 (1986); Cold Spring Harbor; B. Beutler and A. Cerami, *Annu. Rev. Biochem.* 57:505-518 (1988); L. J. Old, *Sci. Am.* 258:59-75 (1988); W. Fiers, *FEBS Lett.* 285:199-224 (1991)). The TNF-family ligands, including Neutrokin-alpha and/or Neutrokin-alphaSV of the present invention, induce such various cellular responses by binding to TNF-family receptors. Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides are believed to elicit a potent cellular response including any genotypic, phenotypic, and/or morphologic change to the cell, cell line, tissue, tissue culture or patient. As indicated, such cellular responses include not only normal physiological responses to TNF-family ligands, but also diseases associated with increased apoptosis or the inhibition of apoptosis. Apoptosis-programmed cell death is a physiological mechanism involved in the deletion of peripheral B and/or T lymphocytes of the immune system, and its dysregulation can lead to a number of different pathogenic processes (J. C. Ameisen, *AIDS* 8:1197-1213 (1994); P. H. Krammer et al., *Curr. Opin. Immunol.* 6:279-289 (1994)).

Diseases associated with increased cell survival, or the inhibition of apoptosis that may be diagnosed, treated, or prevented with the Neutrokin-alpha and/or Neutrokin-alphaSV polynucleotides or polypeptides of the invention, and agonists and antagonists thereof, include cancers (such as follicular lymphomas, carcinomas with p53 mutations, and hormone-dependent tumors, including, but not limited to, colon cancer, cardiac tumors, pancreatic cancer, melanoma, retinoblastoma, glioblastoma, lung cancer, intestinal cancer, testicular cancer, stomach cancer, neuroblastoma, myxoma, myoma, lymphoma, endothelioma, osteoblastoma, osteoclastoma, osteosarcoma, chondrosarcoma, adenoma, breast cancer, prostate cancer, Kaposi's sarcoma and ovarian cancer); autoimmune disorders (such as systemic lupus erythe-

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matosus and immune-related glomerulonephritis rheumatoid arthritis); viral infections (such as herpes viruses, pox viruses and adenoviruses); inflammation: graft vs. host disease; acute graft rejection and chronic graft rejection. Thus, in preferred embodiments Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides or polypeptides of the invention and/or agonists or antagonists thereof, are used to treat, prevent, and/or diagnose autoimmune diseases and/or inhibit the growth, progression, and/or metastasis of cancers, including, but not limited to, those cancers disclosed herein, such as, for example, lymphocytic leukemias (including, for example, MLL and chronic lymphocytic leukemia (CLL)) and follicular lymphomas. In another embodiment Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides or polypeptides of the invention are used to activate, differentiate or proliferate cancerous cells or tissue (e.g., B cell lineage related cancers (e.g., CLL and MLL), lymphocytic leukemia, or lymphoma) and thereby render the cells more vulnerable to cancer therapy (e.g., chemotherapy or radiation therapy).

Moreover, in other embodiments, Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides or polypeptides of the invention or agonists or antagonists thereof, are used to inhibit the growth, progression, and/or metastases of malignancies and related disorders such as leukemia (including acute leukemias (e.g., acute lymphocytic leukemia, acute myelocytic leukemia (including myeloblastic, promyelocytic, myelomonocytic, monocytic, and erythroleukemia)) and chronic leukemias (e.g., chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia)), polycythemia vera, lymphomas (e.g., Hodgkin's disease and non-Hodgkin's disease), multiple myeloma, Waldenstrom's macroglobulinemia, heavy chain disease, and solid tumors including, but not limited to, sarcomas and carcinomas such as fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovium, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, seminoma, embryonal carcinoma, Wilms' tumor, cervical cancer, testicular tumor, lung carcinoma, small cell lung carcinoma, bladder carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, melanoma, neuroblastoma, and retinoblastoma.

Diseases associated with increased apoptosis that may be diagnosed, treated, or prevented with the Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides or polypeptides of the invention, and agonists and antagonists thereof, include AIDS; neurodegenerative disorders (such as Alzheimer's disease, Parkinson's disease, Amyotrophic lateral sclerosis, Refinitis pigmentosa, Cerebellar degeneration); myelodysplastic syndromes (such as aplastic anemia), ischemic injury (such as that caused by myocardial infarction, stroke and reperfusion injury), toxin-induced liver disease (such as that caused by alcohol), septic shock, cachexia and anorexia. Thus, in preferred embodiments Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides or polypeptides

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of the invention and/or agonists or antagonists thereof, are used to treat, prevent, and/or diagnose the diseases and disorders listed above.

In preferred embodiments, Neurokinine-alpha and/or Neurokinine-alphaSV polypeptides of the invention and/or agonists or antagonists thereof (e.g., anti-Neurokinine-alpha antibodies) inhibit the growth of human histiocytic lymphoma U-937 cells in a dose-dependent manner. In additional preferred embodiments, Neurokinine-alpha and/or Neurokinine-alphaSV polypeptides of the invention and/or agonists or antagonists thereof (e.g., anti-Neurokinine-alpha antibodies) inhibit the growth of PC-3 cells, HT-29 cells, Hela cells, MCF-7 cells, and A293 cells. In highly preferred embodiments, Neurokinine-alpha and/or Neurokinine-alphaSV polynucleotides or polypeptides of the invention and/or agonists or antagonists thereof (e.g., anti-Neurokinine-alpha antibodies) are used to inhibit growth, progression, and/or metastasis of prostate cancer, colon cancer, cervical carcinoma, and breast carcinoma.

Thus, in additional preferred embodiments, the present invention is directed to a method for enhancing apoptosis induced by a TNF-family ligand, which involves administering to a cell which expresses a Neurokinine-alpha and/or Neurokinine-alphaSV receptor an effective amount of Neurokinine-alpha and/or Neurokinine-alphaSV, or an agonist or antagonist thereof, capable of increasing or decreasing Neurokinine-alpha and/or Neurokinine-alphaSV mediated signaling. Preferably, Neurokinine-alpha and/or Neurokinine-alphaSV mediated signaling is increased or decreased to treat, prevent, and/or diagnose a disease wherein decreased apoptosis or decreased cytokine and adhesion molecule expression is exhibited. An agonist or antagonist can include soluble forms of Neurokinine-alpha and/or Neurokinine-alphaSV and monoclonal antibodies directed against the Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide.

In a further aspect, the present invention is directed to a method for inhibiting apoptosis induced by a TNF-family ligand, which involves administering to a cell which expresses the Neurokinine-alpha and/or Neurokinine-alphaSV receptor an effective amount of an agonist or antagonist capable of increasing or decreasing Neurokinine-alpha and/or Neurokinine-alphaSV mediated signaling. Preferably, Neurokinine-alpha and/or Neurokinine-alphaSV mediated signaling is increased or decreased to treat, prevent, and/or diagnose a disease wherein increased apoptosis or NF-kappaB expression is exhibited. An agonist or antagonist can include soluble forms of Neurokinine-alpha and/or Neurokinine-alphaSV and monoclonal antibodies directed against the Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide.

Because Neurokinine-alpha and/or Neurokinine-alphaSV belong to the TNF superfamily, the polypeptides should also modulate angiogenesis. In addition, since Neurokinine-alpha and/or Neurokinine-alphaSV inhibit immune cell functions, the polypeptides will have a wide range of anti-inflammatory activities. Neurokinine-alpha and/or Neurokinine-alphaSV may be employed as an anti-neovascularizing agent to treat, prevent, and/or diagnose solid tumors by stimulating the invasion and activation of host defense cells, e.g., cytotoxic T cells and macrophages and by inhibiting the angiogenesis of tumors. Those of skill in the art will recognize other non-cancer indications where blood vessel proliferation is not wanted. They may also be employed to enhance host defenses against resistant chronic and acute infections, for example, mycobacterial infections via the attraction and activation of microbicidal leukocytes. Neurokinine-alpha and/or Neurokinine-alphaSV may also be employed to inhibit T-cell proliferation by the inhibition of IL-2 biosynthesis for the treat-

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ment of T-cell mediated auto-immune diseases and lymphocytic leukemias (including, for example, chronic lymphocytic leukemia (CLL)). Neutrokin-alpha and/or Neutrokin-alphaSV may also be employed to stimulate wound healing, both via the recruitment of debris clearing and connective tissue promoting inflammatory cells. In this same manner, Neutrokin-alpha and/or Neutrokin-alphaSV may also be employed to treat, prevent, and/or diagnose other fibrotic disorders, including liver cirrhosis, osteoarthritis and pulmonary fibrosis. Neutrokin-alpha and/or Neutrokin-alphaSV also increases the presence of eosinophils that have the distinctive function of killing the larvae of parasites that invade tissues, as in schistosomiasis, trichinosis and ascariasis. It may also be employed to regulate hematopoiesis, by regulating the activation and differentiation of various hematopoietic progenitor cells, for example, to release mature leukocytes from the bone marrow following chemotherapy, i.e., in stem cell mobilization. Neutrokin-alpha and/or Neutrokin-alphaSV may also be employed to treat, prevent, and/or diagnose sepsis.

Polynucleotides and/or polypeptides of the invention and/or agonists and/or antagonists thereof are useful in the diagnosis and treatment or prevention of a wide range of diseases and/or conditions. Such diseases and conditions include, but are not limited to, cancer (e.g., immune cell related cancers, breast cancer, prostate cancer, ovarian cancer, follicular lymphoma, cancer associated with mutation or alteration of p53, brain tumor, bladder cancer, uterocervical cancer, colon cancer, colorectal cancer, non-small cell carcinoma of the lung, small cell carcinoma of the lung, stomach cancer, etc.), lymphoproliferative disorders (e.g., lymphadenopathy), microbial (e.g., viral, bacterial, etc.) infection (e.g., HIV-1 infection, HIV-2 infection, herpesvirus infection (including, but not limited to, HSV-1, HSV-2, CMV, VZV, HHV-6, HHV-7, EBV), adenovirus infection, poxvirus infection, human papilloma virus infection, hepatitis infection (e.g., HAV, HBV, HCV, etc.), *Helicobacter pylori* infection, invasive Staphylococcus, etc.), parasitic infection, nephritis, bone disease (e.g., osteoporosis), atherosclerosis, pain, cardiovascular disorders (e.g., neovascularization, hypovascularization or reduced circulation (e.g., ischemic disease (e.g., myocardial infarction, stroke, etc.)), AIDS, allergy, inflammation, neurodegenerative disease (e.g., Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, pigmentary retinitis, cerebellar degeneration, etc.), graft rejection (acute and chronic), graft vs. host disease, diseases due to osteomyelodysplasia (e.g., aplastic anemia, etc.), joint tissue destruction in rheumatism, liver disease (e.g., acute and chronic hepatitis, liver injury, and cirrhosis), autoimmune disease (e.g., multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, immune complex glomerulonephritis, autoimmune diabetes, autoimmune thrombocytopenic purpura, Grave's disease, Hashimoto's thyroiditis, etc.), cardiomyopathy (e.g., dilated cardiomyopathy), diabetes, diabetic complications (e.g., diabetic nephropathy, diabetic neuropathy, diabetic retinopathy), influenza, asthma, psoriasis, glomerulonephritis, septic shock, and ulcerative colitis.

Polynucleotides and/or polypeptides of the invention and/or agonists and/or antagonists thereof are useful in promoting angiogenesis, wound healing (e.g., wounds, burns, and bone fractures). Polynucleotides and/or polypeptides of the invention and/or agonists and/or antagonists thereof are also useful as an adjuvant to enhance immune responsiveness to specific antigen, anti-viral immune responses.

More generally, polynucleotides and/or polypeptides of the invention and/or agonists and/or antagonists thereof are useful in regulating (i.e., elevating or reducing) immune

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response. For example, polynucleotides and/or polypeptides of the invention may be useful in preparation or recovery from surgery, trauma, radiation therapy, chemotherapy, and transplantation, or may be used to boost immune response and/or recovery in the elderly and immunocompromised individuals. Alternatively, polynucleotides and/or polypeptides of the invention and/or agonists and/or antagonists thereof are useful as immunosuppressive agents, for example in the treatment or prevention of autoimmune disorders. In specific embodiments, polynucleotides and/or polypeptides of the invention are used to treat or prevent chronic inflammatory, allergic or autoimmune conditions, such as those described herein or are otherwise known in the art.

Preferably, treatment using Neutrokin-alpha and/or Neutrokin-alphaSV polynucleotides or polypeptides, and/or agonists or antagonists of Neutrokin-alpha and/or Neutrokin-alphaSV (e.g., anti-Neutrokin-alpha antibody), could either be by administering an effective amount of Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide of the invention, or agonist or antagonist thereof, to the patient, or by removing cells from the patient, supplying the cells with Neutrokin-alpha and/or Neutrokin-alphaSV polynucleotide, and returning the engineered cells to the patient (ex vivo therapy). Moreover, as further discussed herein, the Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide or polynucleotide can be used as an adjuvant in a vaccine to raise an immune response against infectious disease.

Formulations and Administration

The Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide composition (preferably containing a polypeptide which is a soluble form of the Neutrokin-alpha and/or Neutrokin-alphaSV extracellular domains) will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide alone), the site of delivery of the Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide composition, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" of Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide for purposes herein is thus determined by such considerations.

As a general proposition, the total pharmaceutically effective amount of Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide administered parenterally per dose will be in the range of about 1 microgram/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and most preferably for humans between about 0.01 and 1 mg/kg/day.

In another embodiment, the Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide of the invention is administered to a human at a dose between 0.0001 and 0.045 mg/kg/day, preferably, at a dose between 0.0045 and 0.045 mg/kg/day, and more preferably, at a dose of about 45 microgram/kg/day in humans; and at a dose of about 3 mg/kg/day in mice.

If given continuously, the Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide is typically administered at a dose rate of about 1 microgram/kg/hour to about 50 micrograms/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed.

The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending on the desired effect.

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In a specific embodiment, the total pharmaceutically effective amount of Neutrokin- α and/or Neutrokin- α SV polypeptide administered parenterally per dose will be in the range of about 0.1 microgram/kg/day to 45 micrograms/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.1 microgram/kg/day, and most preferably for humans between about 0.01 and 50 micrograms/kg/day for the protein. Neutrokin- α and/or Neutrokin- α SV may be administered as a continuous infusion, multiple discrete injections per day (e.g., three or more times daily, or twice daily), single injection per day, or as discrete injections given intermittently (e.g., twice daily, once daily, every other day, twice weekly, weekly, biweekly, monthly, bimonthly, and quarterly). If given continuously, the Neutrokin- α and/or Neutrokin- α SV polypeptide is typically administered at a dose rate of about 0.001 to 10 microgram/kg/hour to about 50 micrograms/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump.

Effective dosages of the compositions of the present invention to be administered may be determined through procedures well known to those in the art which address such parameters as biological half-life, bioavailability, and toxicity. Such determination is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

Bioexposure of an organism to Neutrokin- α and/or Neutrokin- α SV polypeptide during therapy may also play an important role in determining a therapeutically and/or pharmacologically effective dosing regime. Variations of dosing such as repeated administrations of a relatively low dose of Neutrokin- α and/or Neutrokin- α SV polypeptide for a relatively long period of time may have an effect which is therapeutically and/or pharmacologically distinguishable from that achieved with repeated administrations of a relatively high dose of Neutrokin- α and/or Neutrokin- α SV for a relatively short period of time. See, for instance, the serum immunoglobulin level experiments presented in Example 6.

Using the equivalent surface area dosage conversion factors supplied by Freireich, E. J., et al. (*Cancer Chemotherapy Reports* 50(4):219-44 (1966)), one of ordinary skill in the art is able to conveniently convert data obtained from the use of Neutrokin- α and/or Neutrokin- α SV in a given experimental system into an accurate estimation of a pharmaceutically effective amount of Neutrokin- α and/or Neutrokin- α SV polypeptide to be administered per dose in another experimental system. Experimental data obtained through the administration of Neutrokin- α in mice (see, for instance, Example 6) may be converted through the conversion factors supplied by Freireich, et al., to accurate estimates of pharmaceutically effective doses of Neutrokin- α in rat, monkey, dog, and human. The following conversion table (Table III) is a summary of the data provided by Freireich, et al. Table III gives approximate factors for converting doses expressed in terms of mg/kg from one species to an equivalent surface area dose expressed as mg/kg in another species tabulated.

TABLE III

Equivalent Surface Area Dosage Conversion Factors.					
FROM	TO				
	Mouse (20 g)	Rat (150 g)	Monkey (3.5 kg)	Dog (8 kg)	Human (60 kg)
Mouse	1	1/2	1/4	1/6	1/12
Rat	2	1	1/2	1/4	1/7
Monkey	4	2	1	3/5	1/3

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TABLE III-continued

Equivalent Surface Area Dosage Conversion Factors.					
FROM	TO				
	Mouse (20 g)	Rat (150 g)	Monkey (3.5 kg)	Dog (8 kg)	Human (60 kg)
Dog	6	4	5/3	1	1/2
Human	12	7	3	2	1

Thus, for example, using the conversion factors provided in Table III, a dose of 50 mg/kg in the mouse converts to an appropriate dose of 12.5 mg/kg in the monkey because $(50 \text{ mg/kg}) \times (1/4) = 12.5 \text{ mg/kg}$. As an additional example, doses of 0.02, 0.08, 0.8, 2, and 8 mg/kg in the mouse equate to effect doses of 1.667 micrograms/kg, 6.67 micrograms/kg, 66.7 micrograms/kg, 166.7 micrograms/kg, and 0.667 mg/kg, respectively, in the human.

Pharmaceutical compositions containing Neutrokin- α and/or Neutrokin- α SV polypeptides of the invention may be administered orally, rectally, parenterally, subcutaneously, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, drops or transdermal patch), buccally, or as an oral or nasal spray (e.g., via inhalation of a vapor or powder). In one embodiment, "pharmaceutically acceptable carrier" means a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. In a specific embodiment, "pharmaceutically acceptable" means approved by a regulatory agency of the federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly humans. Nonlimiting examples of suitable pharmaceutical carriers according to this embodiment are provided in "Remington's Pharmaceutical Sciences" by E. W. Martin, and include sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can be employed as liquid carriers, particularly for injectable solutions. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained-release formulations and the like.

The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

In a preferred embodiment, Neutrokin- α and/or Neutrokin- α SV compositions of the invention (including polypeptides, polynucleotides, and antibodies, and agonists and/or antagonists thereof) are administered subcutaneously.

In another preferred embodiment, Neutrokin- α and/or Neutrokin- α SV compositions of the invention (including polypeptides, polynucleotides, and antibodies, and agonists and/or antagonists thereof) are administered intravenously.

Neutrokin- α and/or Neutrokin- α SV compositions of the invention are also suitably administered by sustained-release systems. Suitable examples of sustained-release compositions include suitable polymeric materials (such as, for example, semi-permeable polymer matrices) in the form of shaped articles, e.g., films, or microcapsules).

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suitable hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, and sparingly soluble derivatives (such as, for example, a sparingly soluble salt).

Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919; EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman, U. et al., *Biopolymers* 22:547-556 (1983)), poly (2-hydroxyethyl methacrylate) (R. Langer et al., *J. Biomed. Mater. Res.* 15:167-277 (1981), and R. Langer, *Chem. Tech.* 12:98-105 (1982)), ethylene vinyl acetate (R. Langer et al., *Id.*) or poly-D-(-)-3-hydroxybutyric acid (EP 133,988).

Sustained-release compositions also include liposomally entrapped compositions of the invention (see generally, Langer, *Science* 249:1527-1533 (1990); Treat et al., in *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 317-327 and 353-365 (1989)). Liposomes containing Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide may be prepared by methods known per se: DE 3,218,121; Epstein et al., *Proc. Natl. Acad. Sci. (USA)* 82:3688-3692 (1985); Hwang et al., *Proc. Natl. Acad. Sci. (USA)* 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide therapy.

In another embodiment sustained release compositions of the invention include crystal formulations known in the art.

In yet an additional embodiment, the compositions of the invention are delivered by way of a pump (see Langer, *supra*; Sefion, *CRC Crit. Rev. Biomed. Eng.* 14:201 (1987); Buchwald et al., *Surgery* 88:507 (1980); Saudek et al., *N. Engl. J. Med.* 321:574 (1989)).

Other controlled release systems are discussed in the review by Langer (*Science* 249:1527-1533 (1990)).

For parenteral administration, in one embodiment, the Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not include oxidizing agents and other compounds that are known to be deleterious to polypeptides.

Generally, the formulations are prepared by contacting the Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum

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albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, mannose, sucrose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; preservatives, such as cresol, phenol, chlorobutanol, benzyl alcohol and parabens, and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide is typically formulated in such vehicles at a concentration of about 0.001 mg/ml to 100 mg/ml, or 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml or 1-10 mg/ml, at a pH of about 3 to 10, or 3 to 8, more preferably 5-8, most preferably 6-7. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide salts.

Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide to be used for therapeutic administration must be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutic Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide using bacteriostatic Water-for-Injection.

Alternatively, Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide is stored in single dose containers in lyophilized form. The infusion solution is reconstituted using a sterile carrier for injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally, associated with such container(s) is a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the present invention may be employed in conjunction with other therapeutic compounds.

The compositions of the invention may be administered alone or in combination with other adjuvants. Adjuvants that may be administered with the compositions of the invention include, but are not limited to, alum, alum plus deoxycholate (ImmunoAg), MTP-PE (Biocine Corp.), QS21 (Genentech, Inc.), BCG, and MPL. In a specific embodiment, compositions of the invention are administered in combination with alum. In another specific embodiment, compositions of the invention are administered in combination with QS-21. Further adjuvants that may be administered with the compositions of the invention include, but are not limited to, Monophosphoryl lipid immunomodulator, AdjuVax 100a, QS-21, QS-18, CRL1005, Aluminum salts, MF-59, and Viroosomal adjuvant technology. Vaccines that may be administered with

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the compositions of the invention include, but are not limited to, vaccines directed toward protection against MMR (measles, mumps, rubella), polio, varicella, tetanus/diphtheria, hepatitis A, hepatitis B, *Haemophilus influenzae* B, whooping cough, pneumonia, influenza, Lyme's Disease, rotavirus, cholera, yellow fever, Japanese encephalitis, poliomyelitis, rabies, typhoid fever, and pertussis, and/or PNEUMOVAX-23™. Combinations may be administered either concomitantly, e.g., as an admixture, separately but simultaneously or concurrently; or sequentially. This includes presentations in which the combined agents are administered together as a therapeutic mixture, and also procedures in which the combined agents are administered separately but simultaneously, e.g., as through separate intravenous lines into the same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given first, followed by the second.

In another specific embodiment, compositions of the invention are used in combination with PNEUMOVAX-23™ to treat, prevent, and/or diagnose infection and/or any disease, disorder, and/or condition associated therewith. In one embodiment, compositions of the invention are used in combination with PNEUMOVAX-23™ to treat, prevent, and/or diagnose any Gram positive bacterial infection and/or any disease, disorder, and/or condition associated therewith. In another embodiment, compositions of the invention are used in combination with PNEUMOVAX-23™ to treat, prevent, and/or diagnose infection and/or any disease, disorder, and/or condition associated with one or more members of the genus *Enterococcus* and/or the genus *Streptococcus*. In another embodiment, compositions of the invention are used in any combination with PNEUMOVAX-23™ to treat, prevent, and/or diagnose infection and/or any disease, disorder, and/or condition associated with one or more members of the Group B streptococci. In another embodiment, compositions of the invention are used in combination with PNEUMOVAX-23™ to treat, prevent, and/or diagnose infection and/or any disease, disorder, and/or condition associated with *Streptococcus pneumoniae*.

The compositions of the invention may be administered alone or in combination with other therapeutic agents, including but not limited to, chemotherapeutic agents, antibiotics, antivirals, steroidal and non-steroidal anti-inflammatories, conventional immunotherapeutic agents and cytokines. Combinations may be administered either concomitantly, e.g., as an admixture, separately but simultaneously or concurrently; or sequentially. This includes presentations in which the combined agents are administered together as a therapeutic mixture, and also procedures in which the combined agents are administered separately but simultaneously, e.g., as through separate intravenous lines into the same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given first, followed by the second.

In one embodiment, the compositions of the invention are administered in combination with other members of the TNF family, TNF, TNF-related or TNF-like molecules that may be administered with the compositions of the invention include, but are not limited to, soluble forms of TNF- α , lymphotoxin- α (LT- α , also known as TNF- β), LT- β (found in complex heterotrimer LT- α 2- β), OPG, FasL, CD27L, CD30L, CD40L, 4-1BBL, DcR3, OX40L, TNF-gamma (International Publication No. WO 96/14328), AIM-I (International Publication No. WO 97/33899), AIM-II (International Publication No. WO 97/34911), APRIL (J. Exp. Med. 188(6):1185-1190), endokine- α (International Publication No. WO 98/07880), TR6 (International

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Publication No. WO 98/30694), OPG, and neurokinine- α (International Publication No. WO 98/18921, OX40, and nerve growth factor (NGF), and soluble forms of Fas, CD30, CD27, CD40 and 4-1BBL, TR2 (International Publication No. WO 96/34095), DR3 (International Publication No. WO 97/33904), DR4 (International Publication No. WO 98/32856), TR5 (International Publication No. WO 98/30693), TR6 (International Publication No. WO 98/30694), TR7 (International Publication No. WO 98/41629), TRANK, TR9 (International Publication No. WO 98/56892), TR10 (International Publication No. WO 98/54202), 312C2 (International Publication No. WO 98/06842), and TR12.

In a preferred embodiment, the compositions of the invention are administered in combination with CD40 ligand (CD40L), a soluble form of CD40L (e.g., AVREND™), biologically active fragments, variants, or derivatives of CD40L, anti-CD40L antibodies (e.g., agonistic or antagonistic antibodies), and/or anti-CD40 antibodies (e.g., agonistic or antagonistic antibodies).

In certain embodiments, compositions of the invention are administered in combination with antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, and/or protease inhibitors. Nucleoside reverse transcriptase inhibitors that may be administered in combination with the compositions of the invention, include, but are not limited to, RETROVIR™ (zidovudine/AZT), VIREX™ (didanosine/ddI), HIVID™ (zalcitabine/ddC), ZERT™ (stavudine/d4T), EPIVIR™ (lamivudine/3TC), and COMBIVIR™ (zidovudine/lamivudine). Non-nucleoside reverse transcriptase inhibitors that may be administered in combination with the compositions of the invention, include, but are not limited to, VIRAMUNE™ (nevirapine), RESCRIPTOR™ (delavirdine), and SUSTIVA™ (efavirenz). Protease inhibitors that may be administered in combination with the compositions of the invention, include, but are not limited to, CRIVAN™ (indinavir), NORVIR™ (ritonavir), INVIRASE™ (saquinavir), and VIRACEPT™ (nelfinavir). In a specific embodiment, antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, and/or protease inhibitors may be used in any combination with compositions of the invention to treat, prevent, and/or diagnose AIDS and/or to treat, prevent, and/or diagnose HIV infection.

In other embodiments, compositions of the invention may be administered in combination with anti-opportunistic infection agents. Anti-opportunistic agents that may be administered in combination with the compositions of the invention, include, but are not limited to, TRIMETHOPRIM-SULFAMETHOXAZOLE™, DAPSONE™, PENTAMIDINE™, ATOVAQUONE™, ISONIAZID™, RIFAMPIN™, PYRAZINAMIDE™, ETHAMBUTOL™, RIFABUTIN™, CLARITHROMYCIN™, AZITHROMYCIN™, GANCICLOVIR™, FOSCARNET™, CIDOFOVIR™, FLUCONAZOLE™, ITRACONAZOLE™, KETOCONAZOLE™, ACYCLOVIR™, FAMCICLOVIR™, PYRIMETHAMINE™, LEUCOVORIN™, NEUPOGEN™ (filgrastim/G-CSF), and LEUKINE™ (sargramostim/GM-CSF). In a specific embodiment, compositions of the invention are used in any combination with TRIMETHOPRIM-SULFAMETHOXAZOLE™, DAPSONE™, PENTAMIDINE™, and/or ATOVAQUONE™ to prophylactically treat, prevent, and/or diagnose an opportunistic *Pneumocystis carinii* pneumonia infection. In another specific embodiment, compositions of the invention are used in any combination with ISONIAZID™, RIFAMPIN™, PYRAZINAMIDE™, and/or ETHAMBU-

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TOI™ to prophylactically treat, prevent, and/or diagnose an opportunistic *Mycobacterium avium* complex infection. In another specific embodiment, compositions of the invention are used in any combination with RIFABUTIN™, CLARITHROMYCIN™, and/or AZITHROMYCIN™ to prophylactically treat, prevent, and/or diagnose an opportunistic *Mycobacterium tuberculosis* infection. In another specific embodiment, compositions of the invention are used in any combination with GANCICLOVIR™, FOSCARNET™, and/or CIDOFOVIR™ to prophylactically treat, prevent, and/or diagnose an opportunistic cytomegalovirus infection. In another specific embodiment, compositions of the invention are used in any combination with FLUCONAZOLE™, ITRACONAZOLE™, and/or KETOCONAZOLE™ to prophylactically treat, prevent, and/or diagnose an opportunistic fungal infection. In another specific embodiment, compositions of the invention are used in any combination with ACYCLOVIR™ and/or FAMCICLOVIR™ to prophylactically treat, prevent, and/or diagnose an opportunistic herpes simplex virus type I and/or type II infection. In another specific embodiment, compositions of the invention are used in any combination with PYRIMETHAMINE™ and/or LEUCOVORIN™ to prophylactically treat, prevent, and/or diagnose an opportunistic *Toxoplasma gondii* infection. In another specific embodiment, compositions of the invention are used in any combination with LEUCOVORIN™ and/or NEUPOGEN™ to prophylactically treat, prevent, and/or diagnose an opportunistic bacterial infection.

In a further embodiment, the compositions of the invention are administered in combination with an antiviral agent. Antiviral agents that may be administered with the compositions of the invention include, but are not limited to, acyclovir, ribavirin, amantadine, and remantidine.

In a further embodiment, the compositions of the invention are administered in combination with an antibiotic agent. Antibiotic agents that may be administered with the compositions of the invention include, but are not limited to, amoxicillin, aminoglycosides, beta-lactam (glycopeptide), beta-lactamases, Clindamycin, chloramphenicol, cephalosporins, ciprofloxacin, ciprofloxacin, erythromycin, fluoroquinolones, macrolides, metronidazole, penicillins, quinolones, rifampin, streptomycin, sulfonamide, tetracyclines, trimethoprim, trimethoprim-sulfamethoxazole, and vancomycin.

Conventional nonspecific immunosuppressive agents, that may be administered in combination with the compositions of the invention include, but are not limited to, steroids, cyclosporine, cyclosporine analogs cyclophosphamide, cyclophosphamide IV, methylprednisolone, prednisolone, azathioprine, FK-506, 15-deoxyspergualin, and other immunosuppressive agents that act by suppressing the function of responding T cells.

In specific embodiments, compositions of the invention are administered in combination with immunosuppressants. Immunosuppressants preparations that may be administered with the compositions of the invention include, but are not limited to, ORTHOCLON™ (OKT3), SANDIMMUNE™/NEORAL™/SANGDYA™ (cyclosporin), PROGRAF™ (tacrolimus), CELLCEPT™ (mycophenolate), Azathioprine, glucocorticosteroids, and RAPAMUNE™ (sirolimus). In a specific embodiment, immunosuppressants may be used to prevent rejection of organ or bone marrow transplantation.

In a preferred embodiment, the compositions of the invention are administered in combination with steroid therapy. Steroids that may be administered in combination with the compositions of the invention, include, but are not limited to, oral corticosteroids, prednisone, and methylprednisolone (e.g., IV methylprednisolone). In a specific embodiment,

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compositions of the invention are administered in combination with prednisone. In a further specific embodiment, the compositions of the invention are administered in combination with prednisone and an immunosuppressive agent. Immunosuppressive agents that may be administered with the compositions of the invention and prednisone are those described herein, and include, but are not limited to, azathioprine, cyclophosphamide, and cyclophosphamide IV. In another specific embodiment, compositions of the invention are administered in combination with methylprednisolone. In a further specific embodiment, the compositions of the invention are administered in combination with methylprednisolone and an immunosuppressive agent. Immunosuppressive agents that may be administered with the compositions of the invention and methylprednisolone are those described herein, and include, but are not limited to, azathioprine, cyclophosphamide, and cyclophosphamide IV.

In a preferred embodiment, the compositions of the invention are administered in combination with an antimalarial. Antimalarials that may be administered with the compositions of the invention include, but are not limited to, hydroxychloroquine, chloroquine, and/or quinine.

In a preferred embodiment, the compositions of the invention are administered in combination with an NSAID.

In a nonexclusive embodiment, the compositions of the invention are administered in combination with one, two, three, four, five, ten, or more of the following drugs: NR-101 (Hoechst Marion Roussel), diclofenac (Dimethaid), oxaprozin potassium (Monsanto), meclizemine (Chiron), 1-614 (Toyama), pemetrexed disodium (Eli Lilly), areleuton (Abbott), valdecoxib (Monsanto), eltenac (Byk Gulden), campath, AGM-1470 (Takeda), CDP-571 (Celtech Chiroscience), CM-101 (CarboMed), ML-3000 (Merkle), CB-2431 (KS Biomedix), CBF-BS2 (KS Biomedix), IL-1Ra gene therapy (Valentis), JTE-522 (Japan Tobacco), paclitaxel (Angiotech), DW-1661C (Dong Wha), darbafelone mesylate (Warner-Lambert), soluble TNF receptor 1 (synergen; Amgen), IPR-6001 (Institute for Pharmaceutical Research), trocade (Hoffman-La Roche), EF-5 (Scotia Pharmaceuticals), BIL-284 (Boehringer Ingelheim), BIL-1149 (Boehringer Ingelheim), LeukoVax (Inflammatics), MK-663 (Merck), ST-1482 (Sigma-Tau), and butixocort propionate (Warner-Lambert).

In a preferred embodiment, the compositions of the invention are administered in combination with one, two, three, four, five or more of the following drugs: methotrexate, sulfasalazine, sodium aurothiomalate, auranofin, cyclosporine, penicillamine, azathioprine, an antimalarial drug (e.g., as described herein), cyclophosphamide, chlorambucil, gold, ENBREI™ (Etanercept), anti-TNF antibody, and prednisolone.

In a more preferred embodiment, the compositions of the invention are administered in combination with an antimalarial, methotrexate, anti-TNF antibody, ENBREI™ and/or sulfasalazine. In one embodiment, the compositions of the invention are administered in combination with methotrexate. In another embodiment, the compositions of the invention are administered in combination with anti-TNF antibody. In another embodiment, the compositions of the invention are administered in combination with methotrexate and anti-TNF antibody. In another embodiment, the compositions of the invention are administered in combination with sulfasalazine. In another specific embodiment, the compositions of the invention are administered in combination with methotrexate, anti-TNF antibody, and sulfasalazine. In another embodiment, the compositions of the invention are administered in combination with ENBREI™. In another embodiment, the com-

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positions of the invention are administered in combination with ENBREJTM and methotrexate. In another embodiment, the compositions of the invention are administered in combination with ENBREJTM, methotrexate and sulfasalazine. In another embodiment, the compositions of the invention are administered in combination with ENBREJTM, methotrexate and sulfasalazine. In other embodiments, one or more anti-malarials is combined with one of the above-recited combinations. In a specific embodiment, the compositions of the invention are administered in combination with an anti-malarial (e.g., hydroxychloroquine), ENBREJTM, methotrexate and sulfasalazine. In another specific embodiment, the compositions of the invention are administered in combination with an anti-malarial (e.g., hydroxychloroquine), sulfasalazine, anti-TNF antibody, and methotrexate.

In an additional embodiment, compositions of the invention are administered alone or in combination with one or more intravenous immune globulin preparations. Intravenous immune globulin preparations that may be administered with the compositions of the invention include, but not limited to, GAMMARTTM, IVEEGAMTM, SANDOGLOBULINTM, GAMMAGARD SDTM, and GAMIMUNETM. In a specific embodiment, compositions of the invention are administered in combination with intravenous immune globulin preparations in transplantation therapy (e.g., bone marrow trans-

plant). CD40 ligand (CD40L), a soluble form of CD40L (e.g., AVRENITM), biologically active fragments, variants, or derivatives of CD40L, anti-CD40L antibodies (e.g., agonistic or antagonistic antibodies), and/or anti-CD40 antibodies (e.g., agonistic or antagonistic antibodies).

In an additional embodiment, the compositions of the invention are administered alone or in combination with an anti-inflammatory agent. Anti-inflammatory agents that may be administered with the compositions of the invention include, but are not limited to, glucocorticoids and the non-steroidal anti-inflammatories, aminoarylcarboxylic acid derivatives, arylacetic acid derivatives, arylbutyric acid derivatives, arylcarboxylic acids, arylpropionic acid derivatives, pyrazoles, pyrazolones, salicylic acid derivatives, thiazinecarboxamides, α -acetamidocaproic acid, S-adenosyl-methionine, 3-amino-4-hydroxybutyric acid, amixetrine, bendazac, benzydamine, bucalone, difenpiramide, diltazol, emorlazon, guaiazulene, nabumetone, nimesulide, orgotein, oxaceprol, paranyline, perisoxal, pifoxime, proquazone, proxazole, and tenidap.

In another embodiment, compositions of the invention are administered in combination with a chemotherapeutic agent. Chemotherapeutic agents that may be administered with the compositions of the invention include, but are not limited to, antibiotic derivatives (e.g., doxorubicin, bleomycin, daunorubicin, and dactinomycin); antiestrogens (e.g., tamoxifen); antimetabolites (e.g., fluorouracil, 5-FU, methotrexate, floxuridine, interferon alpha-2b, glutamic acid, plicamycin, mercaptopurine, and 6-thioguanine); cytotoxic agents (e.g., carmustine, BCNU, lomustine, CCNU, cytosine arabinoside, cyclophosphamide, estramustine, hydroxyurea, procarbazine, mitomycin, busulfan, cis-platin, and vincristine sulfate); hormones (e.g., medroxyprogesterone, estramustine phosphate sodium, ethinyl estradiol, estradiol, megestrol acetate, methyltestosterone, diethylstilbestrol diphosphate, chlorotrianisene, and testolactone); nitrogen mustard derivatives (e.g., meplazen, chorambucil, mechlorethamine (nitrogen mustard) and thiotepe); steroids and combinations (e.g., bethamethasone sodium phosphate); and others (e.g., dicarbazine, asparaginase, mitotane, vincristine sulfate, vinblastine sulfate, and etoposide).

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In a specific embodiment, compositions of the invention are administered in combination with CHOP (cyclophosphamide, doxorubicin, vincristine, and prednisone) or any combination of the components of CHOP. In another embodiment, compositions of the invention are administered in combination with Rituximab. In a further embodiment, compositions of the invention are administered with Rituximab and CHOP, or Rituximab and any combination of the components of CHOP.

In an additional embodiment, the compositions of the invention are administered in combination with cytokines. Cytokines that may be administered with the compositions of the invention include, but are not limited to, GM-CSF, G-CSF, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-10, IL-12, IL-13, IL-15, anti-CD40, CD40L, IFN-alpha, IFN-beta, IFN-gamma, TNF-alpha, and TNF-beta. In another embodiment, compositions of the invention may be administered with any interleukin, including, but not limited to, IL-1alpha, IL-1beta, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IL-16, IL-17, IL-18, IL-19, IL-20, IL-21, and IL-22. In preferred embodiments, the compositions of the invention are administered in combination with IL-4 and IL-10. Both IL-4 and IL-10 have been observed by the inventors to enhance Neutrokin-alpha mediated B cell proliferation.

In an additional embodiment, the compositions of the invention are administered with a chemokine. In another embodiment, the compositions of the invention are administered with chemokine beta-8, chemokine beta-1, and/or macrophage inflammatory protein-4. In a preferred embodiment, the compositions of the invention are administered with chemokine beta-8.

In an additional embodiment, the compositions of the invention are administered in combination with an IL-4 antagonist. IL-4 antagonists that may be administered with the compositions of the invention include, but are not limited to: soluble IL-4 receptor polypeptides, multimeric forms of soluble IL-4 receptor polypeptides; anti-IL-4 receptor antibodies that bind the IL-4 receptor without transducing the biological signal elicited by IL-4, anti-IL-4 antibodies that block binding of IL-4 to one or more IL-4 receptors, and mutants of IL-4 that bind IL-4 receptors but do not transduce the biological signal elicited by IL-4. Preferably, the antibodies employed according to this method are monoclonal antibodies (including antibody fragments, such as, for example, those described herein).

In an additional embodiment, the compositions of the invention are administered in combination with hematopoietic growth factors. Hematopoietic growth factors that may be administered with the compositions of the invention include, but are not limited to, ILUKINITM (SARGRAMOSTIMTM) and NEUPROGENTM (FILGRASTIMTM).

In an additional embodiment, the compositions of the invention are administered in combination with fibroblast growth factors. Fibroblast growth factors that may be administered with the compositions of the invention include, but are not limited to, FGF-1, FGF-2, FGF-3, FGF-4, FGF-5, FGF-6, FGF-7, FGF-8, FGF-9, FGF-10, FGF-11, FGF-12, FGF-13, FGF-14, and FGF-15.

Additionally, the compositions of the invention may be administered alone or in combination with other therapeutic regimens, including but not limited to, radiation therapy. Such combinatorial therapy may be administered sequentially and/or concomitantly.

Agonists and Antagonists Assays and Molecules

The invention also provides a method of screening compounds to identify those which enhance or block the action of Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide

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on cells, such as its interaction with Neutrokin- α and/or Neutrokin- α SV binding molecules such as receptor molecules. An agonist is a compound which increases the natural biological functions of Neutrokin- α and/or Neutrokin- α SV or which functions in a manner similar to Neutrokin- α and/or Neutrokin- α SV while antagonists decrease or eliminate such functions.

In another embodiment, the invention provides a method for identifying a receptor protein or other ligand-binding protein which binds specifically to a Neutrokin- α and/or Neutrokin- α SV polypeptide. For example, a cellular compartment, such as a membrane or a preparation thereof, may be prepared from a cell that expresses a molecule that binds Neutrokin- α and/or Neutrokin- α SV. The preparation is incubated with labeled Neutrokin- α and/or Neutrokin- α SV and complexes of Neutrokin- α and/or Neutrokin- α SV bound to the receptor or other binding protein are isolated and characterized according to routine methods known in the art. Alternatively, the Neutrokin- α and/or Neutrokin- α SV polypeptide may be bound to a solid support so that binding molecules solubilized from cells are bound to the column and then eluted and characterized according to routine methods.

In the assay of the invention for agonists or antagonists, a cellular compartment, such as a membrane or a preparation thereof, may be prepared from a cell that expresses a molecule that binds Neutrokin- α and/or Neutrokin- α SV such as a molecule of a signaling or regulatory pathway modulated by Neutrokin- α and/or Neutrokin- α SV. The preparation is incubated with labeled Neutrokin- α and/or Neutrokin- α SV in the absence or the presence of a candidate molecule which may be a Neutrokin- α and/or Neutrokin- α SV agonist or antagonist. The ability of the candidate molecule to bind the binding molecule is reflected in decreased binding of the labeled ligand. Molecules which bind gratuitously, i.e., without inducing the effects of Neutrokin- α on binding the Neutrokin- α and/or Neutrokin- α SV binding molecule, are most likely to be good antagonists. Molecules that bind well and elicit effects that are the same as or closely related to Neutrokin- α and/or Neutrokin- α SV are agonists.

Neutrokin- α and/or Neutrokin- α SV-like effects of potential agonists and antagonists may be measured, for instance, by determining activity of a second messenger system following interaction of the candidate molecule with a cell or appropriate cell preparation, and comparing the effect with that of Neutrokin- α and/or Neutrokin- α SV or molecules that elicit the same effects as Neutrokin- α and/or Neutrokin- α SV. Second messenger systems that may be useful in this regard include but are not limited to AMP guanylate cyclase, ion channel or phosphoinositide hydrolysis second messenger systems.

Another example of an assay for Neutrokin- α and/or Neutrokin- α SV antagonists is a competitive assay that combines Neutrokin- α and/or Neutrokin- α SV and a potential antagonist with membrane-bound receptor molecules or recombinant Neutrokin- α and/or Neutrokin- α SV receptor molecules under appropriate conditions for a competitive inhibition assay. Neutrokin- α and/or Neutrokin- α SV can be labeled, such as by radioactivity, such that the number of Neutrokin- α and/or Neutrokin- α SV molecules bound to a receptor molecule can be determined accurately to assess the effectiveness of the potential antagonist.

Potential antagonists include small organic molecules, peptides, polypeptides (e.g., II-13), and antibodies that bind to a polypeptide of the invention and thereby inhibit or extin-

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guish its activity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds the same sites on a binding molecule, such as a receptor molecule, without inducing Neutrokin- α and/or Neutrokin- α SV induced activities, thereby preventing the action of Neutrokin- α and/or Neutrokin- α SV by excluding Neutrokin- α and/or Neutrokin- α SV from binding.

Other potential antagonists include antisense molecules. Antisense technology can be used to control gene expression through antisense DNA or RNA or through triple-helix formation. Antisense techniques are discussed, for example, in Okano, J. *Neurochem.* 56: 560 (1991); "Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression," CRC Press, Boca Raton, Fla. (1988). Antisense technology can be used to control gene expression through antisense DNA or RNA, or through triple-helix formation. Antisense techniques are discussed for example, in Okano, J. *Neurochem.* 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, Fla. (1988). Triple helix formation is discussed in, for instance Lee et al., *Nucleic Acids Research* 6: 3073 (1979); Cooney et al., *Science* 241: 456 (1988); and Dervan et al., *Science* 251: 1360 (1991). The methods are based on binding of a polynucleotide to a complementary DNA or RNA. For example, the 5' coding portion of a polynucleotide that encodes the extracellular domain of the polypeptide of the present invention may be used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription thereby preventing transcription and the production of Neutrokin- α and/or Neutrokin- α SV. The antisense RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of the mRNA molecule into Neutrokin- α and/or Neutrokin- α SV polypeptide. The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed in vivo to inhibit production of Neutrokin- α and/or Neutrokin- α SV.

In one embodiment, the Neutrokin- α and/or Neutrokin- α SV antisense nucleic acid of the invention is produced intracellularly by transcription from an exogenous sequence. For example, a vector or a portion thereof, is transcribed, producing an antisense nucleic acid (RNA) of the invention. Such a vector would contain a sequence encoding the Neutrokin- α and/or Neutrokin- α SV antisense nucleic acid. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art, used for replication and expression in vertebrate cells. Expression of the sequence encoding Neutrokin- α and/or Neutrokin- α SV, or fragments thereof, can be by any promoter known in the art to act in vertebrate, preferably human cells. Such promoters can be inducible or constitutive. Such promoters include, but are not limited to, the SV40 early promoter region (Bernoist and Chambon, *Nature* 293:304-310 (1981), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., *Cell* 22:787-797 (1980), the herpes thymidine promoter (Wagner et al., *Proc. Natl. Acad. Sci. U.S.A.* 78:1441-1445 (1981), the regulatory sequences of the metallothionein gene (Brinster, et al., *Nature* 296:39-42 (1982)), etc.

The antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of an RNA transcript of a Neutrokin- α and/or Neutrokin- α SV

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gene. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double stranded Neutrokin- α and/or Neutrokin- α SV antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the larger the hybridizing nucleic acid, the more base mismatches with a Neutrokin- α and/or Neutrokin- α SV RNA it may contain and still form a stable duplex (or triplex as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

Oligonucleotides that are complementary to the 5' end of the message, e.g., the 5' untranslated sequence up to and including the AUG initiation codon, should work most efficiently at inhibiting translation. However, sequences complementary to the 3' untranslated sequences of mRNAs have been shown to be effective at inhibiting translation of mRNAs as well. See generally, Wagner, R., 1994, *Nature* 372:333-335. Thus, oligonucleotides complementary to either the 5'- or 3'-non-translated, non-coding regions of Neutrokin- α and Neutrokin- α SV shown in FIGS. 1A-B and 5A-B, respectively, could be used in an antisense approach to inhibit translation of endogenous Neutrokin- α and/or Neutrokin- α SV mRNA. Oligonucleotides complementary to the 5' untranslated region of the mRNA should include the complement of the AUG start codon. Antisense oligonucleotides complementary to mRNA coding regions are less efficient inhibitors of translation but could be used in accordance with the invention. Whether designed to hybridize to the 5', 3'- or coding region of Neutrokin- α and/or Neutrokin- α SV mRNA, antisense nucleic acids should be at least six nucleotides in length, and are preferably oligonucleotides ranging from 6 to about 50 nucleotides in length. In specific aspects the oligonucleotide is at least 10 nucleotides, at least 17 nucleotides, at least 25 nucleotides or at least 50 nucleotides.

The polynucleotides of the invention can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre et al., *Proc. Natl. Acad. Sci.* 84:648-652 (1987); PCT Publication No. WO88/09810, published Dec. 15, 1988) or the blood-brain barrier (see, e.g., PCT Publication No. WO89/10134, published Apr. 25, 1988), hybridization-triggered cleavage agents. (See, e.g., Krol et al., *BioTechniques* 6:958-976 (1988)) or intercalating agents. (See, e.g., Zon, *Pharm. Res.* 5:539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including, but not limited to, 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl)uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylquosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methyleytosine, 5-methyleytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylquosine, 5-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N-6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutosine, pseudouracil, quosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

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The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including, but not limited to, arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the antisense oligonucleotide comprises at least one modified phosphate backbone selected from the group including, but not limited to, a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In yet another embodiment, the antisense oligonucleotide is an alpha-anomeric oligonucleotide. An alpha-anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual beta-units, the strands run parallel to each other (Gautier et al., *Nucl. Acids Res.* 15:6625-6641 (1987)). The oligonucleotide is a 2-O-methylribonucleotide (Inoue et al., *Nucl. Acids Res.* 15:6131-6148 (1987)), or a chimeric RNA-DNA analogue (Inoue et al., *FEBS Lett.* 215:327-330 (1997)).

Polynucleotides of the invention may be synthesized by standard methods known in the art, e.g. by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al. (*Nucl. Acids Res.* 16:3209 (1988)), methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., *Proc. Natl. Acad. Sci. U.S.A.* 85:7448-7451 (1988)), etc.

While antisense nucleotides complementary to the Neutrokin- α and/or Neutrokin- α SV coding region sequence could be used, those complementary to the transcribed untranslated region are most preferred.

Potential antagonists according to the invention also include catalytic RNA, or a ribozyme (See, e.g., PCT International Publication WO 90/1364, published Oct. 4, 1990; Sarver et al., *Science* 247:1222-1225 (1990)). While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy Neutrokin- α and/or Neutrokin- α SV mRNAs, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, *Nature* 334:585-591 (1988). There are numerous potential hammerhead ribozyme cleavage sites within the nucleotide sequence of Neutrokin- α and Neutrokin- α SV (FIGS. 1A-B and 5A-B, respectively). Preferably, the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the Neutrokin- α and/or Neutrokin- α SV mRNA; i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

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As in the antisense approach, the ribozymes of the invention can be composed of modified oligonucleotides (e.g. for improved stability, targeting, etc.) and should be delivered to cells which express Neutrokinine-alpha and/or Neutrokinine-alphaSV in vivo. DNA constructs encoding the ribozyme may be introduced into the cell in the same manner as described above for the introduction of antisense encoding DNA. A preferred method of delivery involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive promoter, such as, for example, pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy endogenous Neutrokinine-alpha and/or Neutrokinine-alphaSV messages and inhibit translation. Since ribozymes unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

Endogenous gene expression can also be reduced by inactivating or "knocking out" the Neutrokinine-alpha and/or Neutrokinine-alphaSV gene and/or its promoter using targeted homologous recombination. (E.g., see Smithies et al., *Nature* 317:230-234 (1985); Thomas & Capecchi, *Cell* 51:503-512 (1987); Thompson et al., *Cell* 5:313-321 (1989); each of which is incorporated by reference herein in its entirety). For example, a mutant, non-functional polynucleotide of the invention (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous polynucleotide sequence (either the coding regions or regulatory regions of the gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express polypeptides of the invention in vivo. In another embodiment, techniques known in the art are used to generate knockouts in cells that contain, but do not express the gene of interest. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the targeted gene. Such approaches are particularly suited in research and agricultural fields where modifications to embryonic stem cells can be used to generate animal offspring with an inactive targeted gene (e.g., see Thomas & Capecchi 1987 and Thompson 1989, supra). However this approach can be routinely adapted for use in humans provided the recombinant DNA constructs are directly administered or targeted to the required site in vivo using appropriate viral vectors that will be apparent to those of skill in the art. The contents of each of the documents recited in this paragraph is herein incorporated by reference in its entirety.

In other embodiments, antagonists according to the present invention include soluble forms of Neutrokinine-alpha and/or Neutrokinine-alphaSV (e.g., fragments of Neutrokinine-alpha shown in FIGS. 1A-B that include the ligand binding domain, TNF conserved domain, and/or extracellular domain of Neutrokinine-alpha and/or Neutrokinine-alphaSV and fragments of Neutrokinine-alphaSV shown in FIGS. 5A-B that include the ligand binding domain, TNF conserved domain, and/or extracellular domain of Neutrokinine-alpha and/or Neutrokinine-alphaSV). Such soluble forms of the Neutrokinine-alpha and/or Neutrokinine-alphaSV, which may be naturally occurring or synthetic, antagonize Neutrokinine-alpha and/or Neutrokinine-alphaSV mediated signaling by competing with native Neutrokinine-alpha and/or Neutrokinine-alphaSV for binding to Neutrokinine-alpha and/or Neutrokinine-alphaSV receptors (e.g., DR5 (See, International Publication No. WO 98/41629), TR10 (See, International Publication No. WO 98/54202), 312C2 (See, International Publication No. WO 98/06842), and TR11, TR11SV1, and TR11SV2 (See, U.S. application Ser. No. 09/176,200, now U.S. Pat. No. 6,509,173)), and/or by forming a multimer that may or may not be capable of binding the receptor, but which is incapable of

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inducing signal transduction. Preferably, these antagonists inhibit Neutrokinine-alpha and/or Neutrokinine-alphaSV mediated stimulation of lymphocyte (e.g., B-cell) proliferation, differentiation, and/or activation. Antagonists of the present invention also include antibodies specific for TNF-family ligands (e.g., CD30) and Neutrokinine-alpha-Fc and/or Neutrokinine-alphaSV-Fc fusion proteins.

By a "TNF-family ligand" is intended naturally occurring, recombinant, and synthetic ligands that are capable of binding to a member of the TNF receptor family and inducing and/or blocking the ligand/receptor signaling pathway. Members of the TNF ligand family include, but are not limited to, TNF-alpha, lymphotoxin-alpha (LT-alpha, also known as TNF-beta), LT-beta (found in complex heterotrimer LT-alpha2-beta), FasL, CD40L, (TNF-gamma (International Publication No. WO 96/14328), AIM-I (International Publication No. WO 97/33899), AIM-II (International Publication No. WO 97/34911), APRIL (J. Exp. Med. 188(6):1185-1190), endokine-alpha (International Publication No. WO 98/07880), neutrokinine-alpha (International Publication No. WO 98/18921), CD27L, CD30L, 4-1BBL, OX40L, CD27, CD30, 4-1BB, OX40, and nerve growth factor (NGF). In preferred embodiments, the Neutrokinine-alpha and/or Neutrokinine-alphaSV TNF-family ligands of the invention are DR5 (See, International Publication No. WO 98/41629), TR10 (See, International Publication No. WO 98/54202), 312C2 (See, International Publication No. WO 98/06842), and TR11, TR11SV1, and TR11SV2 (See, U.S. application Ser. No. 09/176,200, now U.S. Pat. No. 6,509,173).

Antagonists of the present invention also include antibodies specific for TNF-family receptors or the Neutrokinine-alpha and/or Neutrokinine-alphaSV polypeptides of the invention. Antibodies according to the present invention may be prepared by any of a variety of standard methods using Neutrokinine-alpha and/or Neutrokinine-alphaSV immunogens of the present invention. As indicated, such Neutrokinine-alpha and/or Neutrokinine-alphaSV immunogens include the complete Neutrokinine-alpha and Neutrokinine-alphaSV polypeptides depicted in FIGS. 1A-B (SEQ ID NO:2) and FIGS. 5A-B (SEQ ID NO:19), respectively, (which may or may not include the leader sequence) and Neutrokinine-alpha and/or Neutrokinine-alphaSV polypeptide fragments comprising, for example, the ligand binding domain, TNF conserved domain, extracellular domain, transmembrane domain, and/or intracellular domain, or any combination thereof.

Polyclonal and monoclonal antibody agonists or antagonists according to the present invention can be raised according to the methods disclosed in Tartaglia and Goeddel, *J. Biol. Chem.* 267(7):4304-4307 (1992); Tartaglia et al., *Cell* 73:213-216 (1993), and PCT Application WO 94/09137 and are preferably specific to (i.e., bind uniquely to) polypeptides of the invention having the amino acid sequence of SEQ ID NO:2. The term "antibody" (Ab) or "monoclonal antibody" (mAb) as used herein is meant to include intact molecules as well as fragments thereof (such as, for example, Fab and F(ab') fragments) which are capable of binding an antigen. Fab, Fab' and F(ab') fragments lack the Fc fragment intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding of an intact antibody (Wahl et al., *J. Nucl. Med.*, 24:316-325 (1983)).

In a preferred method, antibodies according to the present invention are mAbs. Such mAbs can be prepared using hybridoma technology (Kohler and Millstein, *Nature* 256:495-497 (1975) and U.S. Pat. No. 4,376,110; Harlow et al., *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1988; *Monoclonal Antibodies and Hybridomas: A New Dimension in Biological Analyses*, Ple-

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num Press, New York, N.Y., 1980; Campbell, "Monoclonal Antibody Technology," In: *Laboratory Techniques in Biochemistry and Molecular Biology*, Volume 13 (Burdon et al., eds.), Elsevier, Amsterdam (1984)).

Proteins and other compounds which bind the Neutrokin-alpha and/or Neutrokin-alphaSV domains are also candidate agonists and antagonists according to the present invention. Such binding compounds can be "captured" using the yeast two-hybrid system (Fields and Song, *Nature* 340:245-246 (1989)). A modified version of the yeast two-hybrid system has been described by Roger Brent and his colleagues (Gyuris, *Cell* 75:791-803 (1993); Zervos et al., *Cell* 72:223-232 (1993)). Preferably, the yeast two-hybrid system is used according to the present invention to capture compounds which bind to the ligand binding domain, extracellular, intracellular, transmembrane, and death domain of the Neutrokin-alpha and/or Neutrokin-alphaSV. Such compounds are good candidate agonists and antagonists of the present invention.

For example, using the two-hybrid assay described above, the extracellular or intracellular domain of the Neutrokin-alpha and/or Neutrokin-alphaSV receptor, or a portion thereof, may be used to identify cellular proteins which interact with Neutrokin-alpha and/or Neutrokin-alphaSV the receptor in vivo. Such an assay may also be used to identify ligands with potential agonistic or antagonistic activity of Neutrokin-alpha and/or Neutrokin-alphaSV receptor function. This screening assay has previously been used to identify protein which interact with the cytoplasmic domain of the murine TNF-RII and led to the identification of two receptor associated proteins. Rothe et al., *Cell* 78:681 (1994). Such proteins and amino acid sequences which bind to the cytoplasmic domain of the Neutrokin-alpha and/or Neutrokin-alphaSV receptors are good candidate agonist and antagonist of the present invention.

Other screening techniques include the use of cells which express the polypeptide of the present invention (for example, transfected CHO cells) in a system which measures extracellular pH changes caused by receptor activation, for example, as described in Science, 246:181-296 (1989). In another example, potential agonists or antagonists may be contacted with a cell which expresses the polypeptide of the present invention and a second messenger response, e.g., signal transduction may be measured to determine whether the potential antagonist or agonist is effective.

Agonists according to the present invention include naturally occurring and synthetic compounds such as, for example, TNF family ligand peptide fragments, transforming growth factor, neurotransmitters (such as glutamate, dopamine, N-methyl-D-aspartate), tumor suppressors (p53), cytolytic T cells and antimetabolites. Preferred agonists include chemotherapeutic drugs such as, for example, cisplatin, doxorubicin, bleomycin, cytosine arabinoside, nitrogen mustard, methotrexate and vincristine. Others include ethanol and -amyloid peptide. (*Science* 267:1457-1458 (1995)).

Preferred agonists are fragments of Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides of the invention which stimulate lymphocyte (e.g., B cell) proliferation, differentiation and/or activation. Further preferred agonists include polyclonal and monoclonal antibodies raised against the Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides of the invention, or a fragment thereof. Such agonist antibodies raised against a TNF-family receptor are disclosed in Tartaglia et al., *Proc. Natl. Acad. Sci. USA* 88:9292-9296 (1991); and Tartaglia et al., *J. Biol. Chem.* 267:4304-4307 (1992). See, also, PCT Application WO 94/09137.

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In an additional embodiment, immunoregulatory molecules such as, for example, IL2, IL3, IL4, IL5, IL6, IL7, IL10, IL12, IL13, IL15, anti-CD40, CD40L, IFN-gamma and TNF-alpha, may be used as agonists of Neutrokin-alpha and/or Neutrokin-alphaSV polypeptides of the invention which stimulate lymphocyte (e.g., B cell) proliferation, differentiation and/or activation. In a specific embodiment, IL4 and/or IL10 are used to enhance the Neutrokin-alpha- and/or Neutrokin-alphaSV-mediated proliferation of B cells.

In further embodiments of the invention, cells that are genetically engineered to express the polypeptides of the invention, or alternatively, that are genetically engineered not to express the polypeptides of the invention (e.g., knockouts) are administered to a patient in vivo. Such cells may be obtained from the patient (i.e., animal, including human) or an MHC compatible donor and can include, but are not limited to fibroblasts, bone marrow cells, blood cells (e.g., lymphocytes), adipocytes, muscle cells, endothelial cells etc. The cells are genetically engineered in vitro using recombinant DNA techniques to introduce the coding sequence of polypeptides of the invention into the cells, or alternatively, to disrupt the coding sequence and/or endogenous regulatory sequence associated with the polypeptides of the invention, e.g., by transduction (using viral vectors, and preferably vectors that integrate the transgene into the cell genome) or transfection procedures, including, but not limited to, the use of plasmids, cosmids, YAC's, naked DNA, electroporation, liposomes, etc. The coding sequence of the polypeptides of the invention can be placed under the control of a strong constitutive or inducible promoter or promoter/enhancer to achieve expression, and preferably secretion, of the polypeptides of the invention. The engineered cells which express and preferably secrete the polypeptides of the invention can be introduced into the patient systemically, e.g., in the circulation, or intraperitoneally.

Alternatively, the cells can be incorporated into a matrix and implanted in the body, e.g., genetically engineered fibroblasts can be implanted as part of a skin graft; genetically engineered endothelial cells can be implanted as part of a lymphatic or vascular graft. (See, for example, Anderson et al. U.S. Pat. No. 5,399,349; and Mulligan & Wilson, U.S. Pat. No. 5,460,959 each of which is incorporated by reference herein in its entirety).

When the cells to be administered are non-autologous or non-MHC compatible cells, they can be administered using well known techniques which prevent the development of a host immune response against the introduced cells. For example, the cells may be introduced in an encapsulated form which, while allowing for an exchange of components with the immediate extracellular environment, does not allow the introduced cells to be recognized by the host immune system.

In yet another embodiment of the invention, the activity of Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide can be reduced using a "dominant negative." To this end, constructs which encode defective Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide, such as, for example, mutants lacking all or a portion of the TNF-conserved domain, can be used in gene therapy approaches to diminish the activity of Neutrokin-alpha and/or Neutrokin-alphaSV on appropriate target cells. For example, nucleotide sequences that direct host cell expression of Neutrokin-alpha and/or Neutrokin-alphaSV polypeptide in which all or a portion of the TNF-conserved domain is altered or missing can be introduced into monocytic cells or other cells or tissues (either by in vivo or ex vivo gene therapy methods described herein or otherwise known in the art). Alternatively, targeted homologous recombination can be utilized to introduce such

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deletions or mutations into the subject's endogenous Neutrokin- α and/or Neutrokin- α SV gene in monocytes. The engineered cells will express non-functional Neutrokin- α and/or Neutrokin- α SV polypeptides (i.e., a ligand (e.g., multimer) that may be capable of binding, but which is incapable of inducing signal transduction).

Chromosome Assays

The nucleic acid molecules of the present invention are also valuable for chromosome identification. The sequence is specifically targeted to and can hybridize with a particular location on an individual human chromosome. Moreover, there is a current need for identifying particular sites on the chromosome. Few chromosome marking reagents based on actual sequence data (repeat polymorphisms) are presently available for marking chromosomal location. The mapping of DNAs to chromosomes according to the present invention is an important first step in correlating those sequences with genes associated with disease.

In certain preferred embodiments in this regard, the cDNA and/or polynucleotides herein disclosed is used to clone genomic DNA of a Neutrokin- α and/or Neutrokin- α SV gene. This can be accomplished using a variety of well known techniques and libraries, which generally are available commercially. The genomic DNA then is used for in situ chromosome mapping using well known techniques for this purpose.

In addition, in some cases, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the cDNA. Computer analysis of the 3' untranslated region of the gene is used to rapidly select primers that do not span more than one exon in the genomic DNA, thus complicating the amplification process. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Fluorescence in situ hybridization ("FISH") of a cDNA clone to a metaphase chromosomal spread can be used to provide a precise chromosomal location in one step. This technique can be used with probes from the cDNA as short as 50 or 60 bp. For a review of this technique, see Verma et al., *Human Chromosomes: A Manual Of Basic Techniques*, Pergamon Press, New York (1988).

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data are found, for example, in V. McKusick, *Mendelian Inheritance In Man*, available on-line through Johns Hopkins University, Welch Medical Library. The relationship between genes and diseases that have been mapped to the same chromosomal region are then identified through linkage analysis (coinheritance of physically adjacent genes).

Next, it is necessary to determine the differences in the cDNA or genomic sequence between affected and unaffected individuals. If a mutation is observed in some or all of the affected individuals but not in any normal individuals, then the mutation is likely to be the causative agent of the disease.

With current resolution of physical mapping and genetic mapping techniques, a cDNA precisely localized to a chromosomal region associated with the disease could be one of between 50 and 500 potential causative genes. (This assumes 1 megabase mapping resolution and one gene per 20 kb).

Utilizing the techniques described above, the chromosomal location of Neutrokin- α and Neutrokin- α SV was determined with high confidence using a combination of somatic cell hybrids and radiation hybrids to chromosome position 13q34.

EXAMPLES

Having generally described the invention, the same will be more readily understood by reference to the following

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examples, which are provided by way of illustration and are not intended as limiting. Many of the following examples are set forth referring specifically to Neutrokin- α polynucleotides and polypeptides of the invention. Each example may also be practiced to generate and/or examine Neutrokin- α SV polynucleotides and/or polypeptides of the invention. One of ordinary skill in the art would easily be able to direct the following examples to Neutrokin- α SV.

Example 1a

Expression and Purification of "His-tagged" Neutrokin- α in *E. coli*

The bacterial expression vector pQE9 (p110) is used for bacterial expression in this example. (QIAGEN, Inc., supra). pQE9 encodes ampicillin antibiotic resistance ("Ampr") and contains a bacterial origin of replication ("ori"), an IPTG inducible promoter, a ribosome binding site ("RBS"), six codons encoding histidine residues that allow affinity purification using nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin sold by QIAGEN, Inc., supra, and suitable single restriction enzyme cleavage sites. These elements are arranged such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6xHis tag") covalently linked to the amino terminus of that polypeptide.

The DNA sequence encoding the desired portion of the Neutrokin- α protein comprising the extracellular domain sequence is amplified from the deposited cDNA clone using PCR oligonucleotide primers which anneal to the amino terminal sequences of the desired portion of the protein and to sequences in the deposited construct 3' to the cDNA coding sequence. Additional nucleotides containing restriction sites to facilitate cloning in the pQE9 vector are added to the 5' and 3' primer sequences, respectively.

For cloning the extracellular domain of the protein, the 5' primer has the sequence 5'-GTG GGA TCC AGC CTC CGG GCA GAG CTG-3' (SEQ ID NO:10) containing the underlined Bam HI restriction site followed by 18 nucleotides of the amino terminal coding sequence of the extracellular domain of the sequence in FIGS. 1A and 1B. One of ordinary skill in the art would appreciate, of course, that the point in the protein coding sequence where the 5' primer begins may be varied to amplify a DNA segment encoding any desired portion of the complete Neutrokin- α protein shorter or longer than the extracellular domain of the form. The 3' primer has the sequence 5'-GTG AAG CTT TTA TTA CAG CAG TTT CAA TGC ACC-3' (SEQ ID NO:11) containing the underlined Hind III restriction site followed by two stop codons and 18 nucleotides complementary to the 3' end of the coding sequence of the DNA sequence in FIGS. 1A and 1B.

The amplified DNA fragment and the vector pQE9 are digested with Bam HI and Hind III and the digested DNAs are then ligated together. Insertion of the DNA into the restricted pQE9 vector places the protein coding region downstream from the IPTG-inducible promoter and in-frame with an initiating AUG and the six histidine codons.

The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described in Sambrook et al., *Molecular Cloning: a Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989). *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kan^r"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for express-

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ing protein, is available commercially from QIAGEN, Inc., supra. Transformants are identified by their ability to grow on LB plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing. Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD₆₀₀") of between 0.4 and 0.6. Isopropyl-beta-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the lac repressor sensitive promoter, by inactivating the lacI repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

The cells are then stirred for 3-4 hours at 4° C. in 6M guanidine-HCl, pH 8. The cell debris is removed by centrifugation, and the supernatant containing the is loaded on to a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., supra). Proteins with a 6xHis tag bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist, 1995, QIAGEN, Inc., supra). Briefly the supernatant is loaded on to the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the Neutrokin- α and/or Neutrokin- α SV polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins can be eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4° C. or frozen at -80° C.

Example 1b

Expression and Purification of Neutrokin-Alpha in *E. coli*

The bacterial expression vector pQE60 is used for bacterial expression in this example. (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, Calif., 91311). pQE60 encodes ampicillin antibiotic resistance ("Amp^r") and contains a bacterial origin of replication ("ori"), an IPTG inducible promoter, a ribosome binding site ("RBS"), six codons encoding histidine residues that allow affinity purification using nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin sold by QIAGEN, Inc., supra, and suitable single restriction enzyme cleavage sites. These elements are arranged such that a DNA fragment encoding a polypeptide may be inserted in such as way as to produce that polypeptide with the six His residues (i.e., a "6xHis tag") covalently linked to the carboxyl terminus of that polypeptide. However, in this example, the polypeptide coding sequence is inserted such that translation of the six His codons is prevented and, therefore, the polypeptide is produced with no 6xHis tag.

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The DNA sequence encoding the desired portion of the protein comprising the extracellular domain sequence is amplified from the deposited cDNA clone using PCR oligonucleotide primers which anneal to the amino terminal sequences of the desired portion of the protein and to sequences in the deposited construct 3' to the cDNA coding sequence. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' sequences, respectively.

For cloning the extracellular domain of the protein, the 5' primer has the sequence 5'-GTG TCA TGA GCC TCC GCG CAG AGC TG-3' (SEQ ID NO:12) containing the underlined Bsp HI restriction site followed by 17 nucleotides of the amino terminal coding sequence of the extracellular domain of the sequence in FIGS. 1A and 1B. One of ordinary skill in the art would appreciate, of course, that the point in the protein coding sequence where the 5' primer begins may be varied to amplify a desired portion of the complete protein shorter or longer than the extracellular domain of the form. The 3' primer has the sequence 5'-GTG AAG CTT TTA TTA CAG CAG TTT CAA TGC ACC-3' (SEQ ID NO:13) containing the underlined Hind III restriction site followed by two stop codons and 18 nucleotides complementary to the 3' end of the coding sequence in the DNA sequence in FIGS. 1A and 1B.

The amplified DNA fragments and the vector pQE60 are digested with Bsp HI and Hind III and the digested DNAs are then ligated together. Insertion of the DNA into the restricted pQE60 vector places the protein coding region including its associated stop codon downstream from the IPTG-inducible promoter and in-frame with an initiating AUG. The associated stop codon prevents translation of the six histidine codons downstream of the insertion point.

The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described in Sambrook et al., *Molecular Cloning: a Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989). *E. coli* strain M15/rep4, containing multiple copies of the plasmid pRIIP4, which expresses the lac repressor and confers kanamycin resistance ("Kan^r"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for expressing protein, is available commercially from QIAGEN, Inc., supra. Transformants are identified by their ability to grow on LB plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

One of ordinary skill in the art recognizes that any of a number of bacterial expression vectors may be useful in place of pQE9 and pQE60 in the expression protocols presented in this example. For example, the novel pHE4 series of bacterial expression vectors, in particular, the pHE4-5 vector may be used for bacterial expression in this example (ATCC Accession No. 209311; and variations thereof). The plasmid DNA designated pHE4-5/MPHF023 in ATCC Deposit No. 209311 is vector plasmid DNA which contains an insert which encodes another ORF. The construct was deposited with the American Type Culture Collection, 10801 University Boulevard, Manassas, Va. 20110-2209, on Sep. 30, 1997. Using the Nde I and Asp 718 restriction sites flanking the irrelevant MPHF ORF insert, one of ordinary skill in the art could easily use current molecular biological techniques to replace the irrelevant ORF in the pHE4-5 vector with the Neutrokin- α ORF of the present invention.

The pHE4-5 bacterial expression vector includes a neomycin phosphotransferase gene for selection, an *E. coli* origin of

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replication, a T5 phage promoter sequence, two lac operator sequences, a Shine-Delgarno sequence, and the lactose operon repressor gene (*lacIq*). These elements are arranged such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6xHis tag") covalently linked to the amino terminus of that polypeptide. The promoter and operator sequences of the pHE4-5 vector were made synthetically. Synthetic production of nucleic acid sequences is well known in the art (CLONTECH 95/96 Catalog, pages 215-216, CLONTECH, 1020 East Meadow Circle, Palo Alto, Calif. 94303).

Clones containing the desired Neutrokin- α constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 μ g/ml) and kanamycin (25 μ g/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD₆₀₀") of between 0.4 and 0.6. Isopropyl-beta-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the lac repressor sensitive promoter, by inactivating the *lacI* repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

The cells are then stirred for 3-4 hours at 4° C. in 6M guanidine-HCl, pH 8. The cell debris is removed by centrifugation, and the supernatant containing the Neutrokin- α is dialyzed against 50 mM Na-acetate buffer pH 6, supplemented with 200 mM NaCl. Alternatively, the protein can be successfully refolded by dialyzing it against 500 mM NaCl, 20% glycerol, 25 mM Tris/HCl pH 7.4, containing protease inhibitors. After renaturation the protein can be purified by ion exchange, hydrophobic interaction and size exclusion chromatography. Alternatively, an affinity chromatography step such as an antibody column can be used to obtain pure protein. The purified protein is stored at 4° C. or frozen at -80° C.

In certain embodiments, it is preferred to generate expression constructs as detailed in this Example to mutate one or more of the three cysteine residues in the Neutrokin- α polypeptide sequence. The cysteine residues in the Neutrokin- α polypeptide sequence are located at positions 147, 232, and 245 as shown in SEQ ID NO:2 and at positions 213 and 226 of the Neutrokin- α polypeptide sequence as shown in SEQ ID NO:19 (there is no cysteine in the Neutrokin- α SV polypeptide sequence which corresponds to Cys-147 in the Neutrokin- α polypeptide sequence because amino acid residues 143-160 of the Neutrokin- α polypeptide sequence are not present in the Neutrokin- α SV polypeptide sequence).

Example 2

Cloning, Expression, and Purification of Neutrokin-Alpha Protein in a Baculovirus Expression System

In this illustrative example, the plasmid shuttle vector pA2GIP is used to insert the cloned DNA encoding the extracellular domain of the protein, lacking its naturally associated intracellular and transmembrane sequences, into a baculovirus to express the extracellular domain of the Neutrokin- α protein, using a baculovirus leader and standard methods as described in Summers et al., *A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures*, Texas Agricultural Experimental Station Bulletin No. 1555 (1987). This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis

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virus (AcMNPV) followed by the secretory signal peptide (leader) of the baculovirus gp67 protein and convenient restriction sites such as Bam HI, Xba I and Asp 718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak *Drosophila* promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate viable virus that expresses the cloned polynucleotide.

Many other baculovirus vectors could be used in place of the vector above, such as pAc373, pVL941 and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., *Virology* 170:31-39 (1989).

The cDNA sequence encoding an N-terminally deleted form of the extracellular domain of the Neutrokin- α protein in the deposited clone, lacking the AUG initiation codon, the naturally associated intracellular and transmembrane domain sequences, and amino acids Gln-73 through Leu-79 shown in FIGS. 1A and 1B (SEQ ID NO:2), is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the gene. The 5' primer has the sequence 5'-GTG GGAATC CCG GGC AGA GCT GCA GGG C-3' (SEQ ID NO:14) containing the underlined Bam HI restriction enzyme site followed by 18 nucleotides of the sequence of the extracellular domain of the Neutrokin- α protein shown in FIGS. 1A and 1B, beginning with the indicated N-terminus of the extracellular domain of the protein. The 3' primer has the sequence 5'-GTG GGAATC TTA TTA CAG CAG TTT CAA TGC ACC-3' (SEQ ID NO:15) containing the underlined Bam HI restriction site followed by two stop codons and 18 nucleotides complementary to the 3' coding sequence in FIGS. 1A and 1B.

In certain other embodiments, constructs designed to express the entire predicted extracellular domain of the Neutrokin- α (i.e., amino acid residues Gln-73 through Leu-285) are preferred. One of skill in the art would be able to use the polynucleotide and polypeptide sequences provided as SEQ ID NO:1 and SEQ ID NO:2, respectively, to design polynucleotide primers to generate such a clone.

In a further preferred embodiment, a pA2GIP expression construct encodes amino acid residues Leu-112 through Leu-285 of the Neutrokin- α polypeptide sequence shown as SEQ ID NO:2.

In another preferred embodiment, a pA2GIP expression construct encodes amino acid residues Ser-78 through Leu-285 of the Neutrokin- α polypeptide sequence shown as SEQ ID NO:2.

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Calif.). The fragment then is digested with Bam HI and again is purified on a 1% agarose gel. This fragment is designated herein F1.

The plasmid is digested with the restriction enzymes Bam HI and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("GeneClean" BIO 101 Inc., La Jolla, Calif.). This vector DNA is designated herein "V1".

Fragment F1 and the dephosphorylated plasmid V1 are ligated together with T4 DNA ligase, *E. coli* HB101 or other

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suitable *E. coli* hosts such as XL-1 Blue (Statagene Cloning Systems, La Jolla, Calif.) cells are transformed with the ligation mixture and spread on culture plates. Bacteria are identified that contain the plasmid with the human gene by digesting DNA from individual colonies using Bam III and then analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing. This plasmid is designated herein pA2GIP-Neutrokin- α .

Five micrograms of the plasmid pA2GIP-Neutrokin- α is co-transfected with 1.0 microgram of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, Calif.), using the lipofection method described by Felgner et al., *Proc. Natl. Acad. Sci. USA* 84: 7413-7417 (1987). One μ g of BaculoGold™ virus DNA and 5 micrograms of the plasmid pA2GIP Neutrokin- α are mixed in a sterile well of a microtiter plate containing 50 microliters of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, Md.). Afterwards, 10 microliters Lipofectin plus 90 microliters Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to S19 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C. for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc., Rockville, Md.) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Rockville, Md., page 9-10). After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 microliters of Grace's medium and the suspension containing the recombinant baculovirus is used to infect S19 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4° C. The recombinant virus is called V-Neutrokin- α .

To verify the expression of the Neutrokin- α gene S19 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus V-Neutrokin- α at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, Md.). After 42 hours, 5 microcuries of 35 S-methionine and 5 microcuries 35 S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the extracellular domain of the protein and thus the cleavage point and length of the secretory signal peptide.

In a specific experimental example, recombinant Neutrokin- α was purified from baculovirus infected S19 cell

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supernatants as follows. The insect cells were grown in EXCEL401 medium (JRH Scientific) with 1% (v/v) fetal bovine serum. At 92 hours post-infection, the harvested supernatant was clarified by centrifugation at 18,000xg followed by 0.45 μ m depth filtration. A de-lipid filtration step might be also used to remove the lipid contaminants and in turn to improve initial capturing of the Neutrokin- α protein.

The supernatant was loaded on to a set of Poros HS-50/HQ-50 in tandem mode. As alternatives, Toyopearl QAE, Toyopearl Super Q (Tosohass), Q-Sepharose (Pharmacia) and equivalent resins might be used. This step is used as a negative purification step to remove strong anion binding contaminants. The HS/HQ flow through material was adjusted to pH 7.5 with 1 M Tris-HCl pH 8, diluted with equal volume of 50 mM Tris-HCl pH 8, and loaded onto a poros PI-20 or PI-50 column. The PI column was washed first with 4 column volumes of 75 mM sodium chloride in 50 mM Tris-HCl at pH 7.5, then eluted using 3 to 5 column volumes of a stepwise gradient of 300 mM, 750 mM, 1500 mM sodium chloride in 50 mM Tris-HCl pH 7.5. Neutrokin- α protein appears as a 17 KD band on reduced SDS-PAGE and is present in the 0.75 M to 1.5M Sodium chloride fractions.

The PI fraction was further purified through a Sephacryl S100 IIR (Pharmacia) size exclusion column equilibrated with 0.15 M sodium chloride, 50 mM sodium acetate at pH 6. The S200 fractions were mixed with sodium chloride to a final concentration of 3 M and loaded onto a Toyopearl Hexyl 650C (Tosohass) column. The Hexyl column was eluted with a linear gradient from 3 M to 0.05 M sodium chloride in 50 mM Sodium acetate pH 6 in 5 to 15 column volumes. The sodium chloride gradient can also be replaced by ammonium sulfate gradient of 1M to 0 M in 50 mM sodium acetate pH 6 in the Hexyl chromatographic step. Fractions containing purified Neutrokin- α as analyzed through SDS-PAGE were combined and dialyzed against a buffer containing 150 mM Sodium chloride, 50 mM Sodium acetate, pH 6.

The final purified Neutrokin- α protein expressed in a baculovirus system as explained herein has an N-terminus sequence which begins with amino acid residue Ala-134 of SEQ ID NO:2. RP-HPLC analysis shows a single peak of greater than 95% purity. Endotoxin level was below the detection limit in LAL assay.

In another example, recombinant Neutrokin- α was purified from baculovirus infected S19 cell supernatants containing 0.25% bovine serum as follows.

The S19 supernatant was harvested by centrifugation at 18,000xg. The supernatant was then treated with 10 mM calcium chloride in slightly alkaline conditions for 10-15 minutes followed by centrifugation and then 0.22 micrometer depth filtration. The resulting SF-9 cell supernatant was then diluted 2-fold and loaded on to a Poros PI-50 column (available from PE Biosystems). The column was equilibrated with 50 mM Tris (pH 7.4). The PI-50 column was washed with 1 CV of 50 mM Tris (pH 7.4) and then eluted with 1.5 M NaCl in 50 mM NaOAc (pH 6) over 3 CV. The PI fraction was loaded on to a Sephacryl S200 column equilibrated with 50 mM NaOAc (pH 6), 125 mM NaCl. The S200 fraction was mixed with salts to final concentrations of 0.7 M ammonium sulfate and 0.6 M NaCl and loaded on to a Toyopearl Hexyl 650C column (available from Toso Haas) that had been equilibrated in a buffer containing 0.6 M NaCl, 0.7 M ammonium sulfate in 50 mM NaOAc (pH 6). The column was then washed with 2 CV of the same buffer. Recombinant Neutrokin- α was then eluted stepwise with 3 CV of 50 mM NaOAc (pH 6) followed by 2 CV of 20% ethanol wash. The recombinant Neutrokin- α protein was then eluted at the

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end of the ammonium sulfate (0.3 to 0 M salt) gradient. The appropriate fractions were pooled and dialyzed against a buffer containing 50 mM NaOAc (pH 6), and then passed through a Poros 50 HQ column. The HQ flow-through was diluted to 4 ms and loaded on to a Toyopearl DEAD 650M column and then eluted with 25 mM Na Citrate, 125 mM NaCl.

In another example, recombinant Neutrokin- α was expressed and purified using a baculoviral vector system in Sf+insect cells.

First, a polynucleotide encoding amino acid residues Ser-78 through Leu-285 of the Neutrokin- α polypeptide sequence shown in FIGS. 1A and 1B (which is exactly identical to amino acid residues Ser-78 through Leu-285 of the Neutrokin- α polypeptide sequence shown as SEQ ID NO:2) was subcloned into the baculovirus transfer construct PSC to generate a baculovirus expression plasmid. The pA2GP transfer vector, derived from pV1.941, contains the gp67 signal peptide, a modified multiple cloning site, and the lac Z gene cloned downstream of the *Drosophila* heat-shock promoter for selection of blue plaques. Using the sequence of Neutrokin- α (SEQ ID NO:2) and the sequence of the pA2GP vector, a cloning strategy was designed for seamlessly fusing the PSC signal peptide coding sequence to the Neutrokin- α coding sequence at Ala-134 (SEQ ID NO:2 and FIGS. 1A and 1B) and inserting it into a PSC baculovirus transfer plasmid. The strategy involved the use of a two-stage polymerase chain reaction (PCR) procedure. First, primers were designed for amplifying the Neutrokin- α sequences. The 5' primer consisted of the sequence encoding Ala-134 and following residues (5'-GGT CGC CGT TTC TAA CGC GGC CGT TCA GGG TCC AGA AG-3'; SEQ ID NO:31), preceded by the sequence encoding the PSC signal peptide C-terminus. The 3' primer (5'-CTG GTT CGG CCC AAG GTA CCA AGC TTG TAC CTT AGA TCT TTT CTA GAT C-3'; SEQ ID NO:32) consisted of the reverse complement of the pA2GP vector sequence immediately downstream from the Neutrokin- α coding sequence, preceded by a Kpn I restriction endonuclease site and a spacer sequence (for increased cutting efficiency by Kpn I). PCR was performed with the pA2GP containing Neutrokin- α plasmid template and primers O-1887 and O-1888, and the resulting PCR product was purified using standard techniques.

An additional PCR reaction was performed using the PSC baculovirus transfer plasmid pMGS12 as a template. The pMGS12 plasmid consists of the AcNPV EcoRI "I" fragment inserted into pUC8, with the polyhedrin coding sequences after the ATG start codon replaced with the PSC signal peptide and a polylinker site. The PCR reaction used pMGS12 as a template, a 5' primer (5'-CTG GTA GTT CTT CGG AGT GTG-3'; SEQ ID NO:33) which annealed in AcNPV ORF603 upstream of the unique NgoM IV and EcoRV sites, and a 3' primer (5'-CGC GTT AGA AAC GGC GAC C-3'; SEQ ID NO:34) which annealed to the 3' end of the sequence encoding the PSC signal peptide.

To generate a PCR product in which the PSC signal peptide was seamlessly fused to the Ala-134 of the Neutrokin- α coding sequence, the PCR product was combined with the PSC signal peptide-polyhedrin upstream region PCR product and subjected to an additional round of PCR. Because the 3' end of the PSC signal peptide PCR product (pMGS12/O-959/O-1044) overlapped the 5' end of the Neutrokin- α PCR product prepared with primers O-1887/O-1888, the two PCR products were combined and overlap-extended by PCR using primers O-959 and O-1888.

The resulting overlap-extended PCR product containing the PSC signal peptide fused to the Neutrokin- α

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sequence subsequently was inserted into baculovirus transfer plasmid pMGS12. The PCR product was digested with NgoM IV and Kpn I, and the fragment was purified and ligated into NgoM IV-Kpn I-cut pMGS12. After transformation of competent *E. coli* DH5 α cells with the ligation mix, colonies were picked and plasmid DNA mini-preps were prepared. Several positive clones from each ligation were identified by restriction digestion analysis of the plasmid DNA, and three clones (pAcC9669, pAcC9671, and pAcC9672) were selected for large scale plasmid purification. The resulting plasmid DNA was subjected to DNA sequence analysis to confirm and sequence the Neutrokin- α insert.

The following steps describe the recovery and purification process of recombinant Neutrokin- α from Sf+insect cells. Unless stated otherwise, the process is conducted at 2-8° C.

Recovery

Step 1. CaCl₂ Treatment

Sf+cell supernatant was harvested by centrifugation at 8,000 \times g. Recovery buffer-1 (1M CaCl₂) was added to the supernatant so that the final concentration of CaCl₂ was 10 mM. (In a further preferred embodiment, 1M ZnCl₂ is used in place of 1M CaCl₂.) The pH of the solution was adjusted to 7.7 \pm with Recovery buffer-2 (1M Tris pH 8 (\pm 0.2)). The solution was incubated for 15 minutes and then centrifuged at 8,000 \times g.

Purification

Step 1. Chromatography on Poros PI-50 Column

Sf+cell supernatant was loaded on to a Poros PI-50 column (PI Biosystem). The column was equilibrated in PI-1 buffer (50 mM Tris, 50 mM NaCl, pH 7.4 (\pm 0.2)). The PI-50 column was washed with 1-2 CV of PI-1 buffer and then eluted with PI-2 buffer (50 mM Na Citrate pH 6 (\pm 0.2)) over 3 CV linear gradient. The elution was monitored by ultraviolet (UV) absorbance at 280 nm. Fractions were collected across the eluate peak and analyzed by SDS page. Appropriate fractions were pooled.

Step 2. Chromatography on Toyopearl Hexyl 650C Column

The PI pool was mixed with salts to final concentrations of 0.7M (NH₄)₂SO₄ and loaded on to a Toyopearl Hexyl 650C (Toso Haas) column equilibrated in HIC-1 buffer (50 mM NaOAc, 0.6M NaCl, 0.7M (NH₄)₂SO₄ pH 6 (\pm 0.2)). The column was then washed with 2 CV of HIC-1 buffer. Subsequently, recombinant Neutrokin- α was then eluted stepwise with 3-5 CV of HIC-2 buffer (50 mM NaOAc pH 6.0 (\pm 0.2)) followed by a 2 CV 20% ethanol wash. The elution was monitored by UV absorbance at 280 nm and conductivity. Fractions were collected across the eluate peak and analyzed by SDS-PAGE. The appropriate fractions were then pooled.

Step 3. Chromatography on SP Sepharose FF

The Hexyl fraction was dialyzed and adjusted to pH 4.5 with SP-1 buffer (50 mM sodium acetate pH 4.5 (\pm 0.2)), diluted to 4 ms and loaded through a SP Sepharose (cation exchanger, Pharmacia) column equilibrated with SP-1 buffer (50 mM sodium acetate pH 4.5 (\pm 0.2)). Recombinant Neutrokin- α protein was then eluted from the SP column with SP-2 buffer (50 mM sodium acetate pH 5.5 (\pm 0.2)) at pH 5.5. The elution was then monitored by ultraviolet (UV) absorbance at 280 nm. Fractions were collected across the eluate peak and analyzed by SDS page. Appropriate fractions were pooled.

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Step 4. Dialysis of Recombinant Neurokinine-alpha

The SP fractions were placed into a 6-8 kd cutoff membrane device and then dialyzed or diafiltered into Dialysis Buffer (10 mM sodium citrate, 140 mM sodium chloride pH 6 (± 0.2)) overnight.

Step 5. Filtration and Fill

The protein concentration of the recombinant Neurokinine-alpha solution from Step 6 was determined by bicinchoninic acid (BCA) protein assay. Recombinant Neurokinine-alpha formulation was adjusted to the final protein concentration with the appropriate buffer and filtered under controlled conditions. The filtrate (bulk substance) was stored in suitable sterilized containers below -20°C .

In a specific embodiment, Neurokinine-alpha protein of the invention produced as described *infra* was adjusted to a final protein concentration of 1 to 5 mg/ml and buffered in 10 mM sodium citrate, 140 mM sodium chloride, pH $6.0 \pm (0.4)$ and stored at or below -20°C in Type I glass vials.

During chromatography runs, the processes are monitored by UV absorbance at 280 nm. When applicable, in-process chromatography intermediates are tested for conductivity, pH, and monitored by SDS and/or RP-HPLC.

Columns and purification equipment are cleaned and sanitized with 0.2 or 0.5 M NaOH followed by deionized water and then 0.1 or 0.5 M acetic acid. The column and purification equipment are rinsed with deionized water and, if necessary, stored in the appropriate storage solution. Prior to use, the equipment is equilibrated with appropriate buffers (as described herein or as is well known in the art).

In a further preferred embodiment, 1M ZnCl_2 is used in place of 1M CaCl_2 in Step 1 of the Recovery section described above. Also, in this embodiment, a combination of ZnCl_2 and CaCl_2 may be used. Many combinations of 0.1 M ZnCl_2 and 0.9 M CaCl_2 may be used in the Recovery process of recombinant Neurokinine-alpha protein such as, for example, but not limited to, a combination of 0.1 M ZnCl_2 and 0.9 M CaCl_2 , 0.2 M ZnCl_2 and 0.8 M CaCl_2 , 0.3 M ZnCl_2 and 0.7 M CaCl_2 , 0.4 M ZnCl_2 and 0.6 M CaCl_2 , 0.5 M ZnCl_2 and 0.5 M CaCl_2 , 0.6 M ZnCl_2 and 0.4 M CaCl_2 , 0.7 M ZnCl_2 and 0.3 M CaCl_2 , 0.8 M ZnCl_2 and 0.2 M CaCl_2 , 0.9 M ZnCl_2 and 0.1 M CaCl_2 , and others. However, the presence of EDTA will inhibit the recovery process. Moreover, the presence of ZnCl_2 and/or CaCl_2 in Recovery Buffer-1 will induce the formation of larger amounts of higher molecular weight (or molecular mass) Neurokinine-alpha multimers.

Example 3

Cloning and Expression of Neurokinine-Alpha in Mammalian Cells

A typical mammalian expression vector contains the promoter element, which mediates the initiation of transcription of mRNA, the protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription can be achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLV, HIV and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter). Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146) and pBC12MI (ATCC 67109). Mammalian host cells

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that could be used include, human HeLa, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells, Chinese hamster ovary (CHO) cells CHO-K1, NSO and HEK 293 cells.

Alternatively, the gene can be expressed in stable cell lines that contain the gene integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful to develop cell lines that carry several hundred or even several thousand copies of the gene of interest. Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., *Biochem J.* 227:277-279 (1991); Behbington et al., *BioTechnology* 10:169-175 (1992)). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

The expression vectors pC1 and pC4 contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., *Molecular and Cellular Biology*, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Bosch et al., *Cell* 41:521-530 (1985)). Multiple cloning sites, e.g., with the restriction enzyme cleavage sites Bam HI, Xba I and Asp 718, facilitate the cloning of the gene of interest. The vectors contain in addition the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene.

Example 3(a)

Cloning and Expression in COS Cells

The expression plasmid, pNeurokinine-alpha-HA, is made by cloning a portion of the deposited cDNA encoding the extracellular domain of the protein into the expression vector pcDNA1/Amp or pcDNAIII (which can be obtained from Invitrogen, Inc.). To produce a soluble, secreted form of the polypeptide, the extracellular domain is fused to the secretory leader sequence of the human II-6 gene.

The expression vector pcDNA1/amp contains: (1) an *E. coli* origin of replication effective for propagation in *E. coli* and other prokaryotic cells; (2) an ampicillin resistance gene for selection of plasmid-containing prokaryotic cells; (3) an SV40 origin of replication for propagation in eukaryotic cells; (4) a CMV promoter, a polylinker, an SV40 intron; (5) several codons encoding a hemagglutinin fragment (i.e., an "HA" tag to facilitate purification) followed by a termination codon and polyadenylation signal arranged so that a cDNA can be conveniently placed under expression control of the CMV promoter and operably linked to the SV40 intron and the polyadenylation signal by means of restriction sites in the polylinker. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein described by Wilson et al., *Cell* 37: 767 (1984). The fusion of the HA tag to the target protein allows easy detection and recovery of the recombinant protein with an antibody that recognizes the HA epitope. pcDNAIII contains, in addition, the selectable neomycin marker.

A DNA fragment encoding the extracellular domain of the Neurokinine-alpha polypeptide is cloned into the polylinker region of the vector so that recombinant protein expression is directed by the CMV promoter. The plasmid construction strategy is as follows. The Neurokinine-alpha cDNA of the deposited clone is amplified using primers that contain con-

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venient restriction sites, much as described above for construction of vectors for expression of Neutrokin- α in *E. coli*. Suitable primers include the following, which are used in this example. The 5' primer, containing the underlined Bam III site, a Kozak sequence, an AUG start codon, a sequence encoding the secretory leader peptide from the human IL-6 gene, and 18 nucleotides of the 5' coding region of the extracellular domain of Neutrokin- α protein, has the following sequence: 5'-GCG GGA TCC GCC ACC ATG AAC TCC TTC TCC ACA AGC GCC TTC GGT CCA GTT GCC TTC TCC CTG GGG CTG CTC CTG GTG TTG CTT GCT GCC TTC CCT GCC CCA GTT GTG AGA CAA GGG GAC CTG GCC AGC-3' (SEQ ID NO:16). The 3' primer, containing the underlined Bam III restriction site and 18 of nucleotides complementary to the 3' coding sequence immediately before the stop codon, has the following sequence: 5'-GTG GGATCC TTA CAG CAG TTT CAA TGC ACC-3' (SEQ ID NO:17).

The PCR amplified DNA fragment and the vector, pcDNA/Amp, are digested with Bam III and then ligated. The ligation mixture is transformed into *E. coli* strain SURF (available from Stratagene Cloning Systems, 11099 North Torrey Pines Road, La Jolla, Calif. 92037), and the transformed culture is plated on ampicillin media plates which then are incubated to allow growth of ampicillin resistant colonies. Plasmid DNA is isolated from resistant colonies and examined by restriction analysis or other means for the presence of the fragment encoding the Neutrokin- α extracellular domain.

For expression of recombinant Neutrokin- α , COS cells are transfected with an expression vector, as described above, using DEAE-DEXTRAN, as described, for instance, in Sambrook et al., *Molecular Cloning: a Laboratory Manual*, Cold Spring Laboratory Press, Cold Spring Harbor, N.Y. (1989). Cells are incubated under conditions for expression of Neutrokin- α by the vector.

Expression of the Neutrokin- α -HIA fusion protein is detected by radiolabeling and immunoprecipitation, using methods described in, for example Harlow et al., *Antibodies: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1988). To this end, two days after transfection, the cells are labeled by incubation in media containing 35 S-cysteine for 8 hours. The cells and the media are collected, and the cells are washed and the lysed with detergent-containing RIPA buffer: 150 mM NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% IXX, 50 mM TRIS, pH 7.5, as described by Wilson et al. cited above. Proteins are precipitated from the cell lysate and from the culture media using an HIA-specific monoclonal antibody. The precipitated proteins then are analyzed by SDS-PAGE and autoradiography. An expression product of the expected size is seen in the cell lysate, which is not seen in negative controls.

Example 3(b)

Cloning and Expression in CHO Cells

The vector pc4 is used for the expression of Neutrokin- α protein. Plasmid pc4 is a derivative of the plasmid pSV2-dhfr (ATCC Accession No. 37146). To produce a soluble, secreted form of the Neutrokin- α polypeptide, the portion of the deposited cDNA encoding the extracellular domain is fused to the secretory leader sequence of the human IL-6 gene. The vector plasmid contains the mouse DHFR gene under control of the SV40 early promoter. Chinese hamster ovary- or other cells lacking dihydrofolate activity that are transfected with these plasmids can be selected by

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growing the cells in a selective medium (alpha minus MEM, Life Technologies) supplemented with the chemotherapeutic agent methotrexate. The amplification of the DHFR genes in cells resistant to methotrexate (MTX) has been well documented (see, e.g., Alt, F. W., Kellems, R. M., Bertino, J. R., and Schimke, R. T., 1978, *J. Biol. Chem.* 253:1357-1370; Hamlin, J. L. and Ma, C., 1990, *Biochem. et Biophys. Acta*, 1097:107-143; Page, M. J. and Sydenham, M. A., 1991, *Biotechnology* 9:64-68). Cells grown in increasing concentrations of MTX develop resistance to the drug by overproducing the target enzyme, DHFR, as a result of amplification of the DHFR gene. If a second gene is linked to the DHFR gene, it is usually co-amplified and over-expressed. It is known in the art that this approach may be used to develop cell lines carrying more than 1,000 copies of the amplified gene(s). Subsequently, when the methotrexate is withdrawn, cell lines are obtained which contain the amplified gene integrated into one or more chromosome(s) of the host cell.

Plasmid pc4 contains for expressing the gene of interest the strong promoter of the long terminal repeat (LTR) of the Rous Sarcoma Virus (Cullen, et al., *Molecular and Cellular Biology*, March 1985:438-447) plus a fragment isolated from the enhancer of the immediate early gene of human cytomegalovirus (CMV) (Boshart et al., *Cell* 41:521-530 (1985)). Downstream of the promoter are the following single restriction enzyme cleavage sites that allow the integration of the genes: BamHI, Xba I, and Asp718. Behind these cloning sites the plasmid contains the 3' intron and polyadenylation site of the rat preproinsulin gene. Other high efficiency promoters can also be used for the expression, e.g., the human beta-actin promoter, the SV40 early or late promoters or the long terminal repeats from other retroviruses, e.g., HIV and HTLV. Montec's Tet-Off and Tet-On gene expression systems and similar systems can be used to express the Neutrokin- α in a regulated way in mammalian cells (Gossen, M., & Bujard, H., 1992, *Proc. Natl. Acad. Sci. USA* 89: 5547-5551). For the polyadenylation of the mRNA other signals, e.g., from the human growth hormone or globin genes can be used as well. Stable cell lines carrying a gene of interest integrated into the chromosomes can also be selected upon co-transfection with a selectable marker such as gpt, G418 or hygromycin. It is advantageous to use more than one selectable marker in the beginning, e.g., G418 plus methotrexate.

The plasmid pc4 is digested with the restriction enzymes Bam III and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

The DNA sequence encoding the extracellular domain of the Neutrokin- α protein is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the gene. The 5' primer, containing the underlined Bam III site, a Kozak sequence, an AUG start codon, a sequence encoding the secretory leader peptide from the human IL-6 gene, and 18 nucleotides of the 5' coding region of the extracellular domain of Neutrokin- α protein, has the following sequence: 5'-GCG GGA TCC GCC ACC ATG AAC TCC TTC TCC ACA AGC GCC TTC GGT CCA GTT GCC TTC TCC CTG GGG CTG CTC CTG GTG TTG CTT GCT GCC TTC CCT GCC CCA GTT GTG AGA CAA GGG GAC CTG GCC AGC-3' (SEQ ID NO:16). The 3' primer, containing the underlined Bam III and 18 of nucleotides complementary to the 3' coding sequence immediately before the stop codon, has the following sequence: 5'-GTG GGATCC TTA CAG CAG TTT CAA TGC ACC-3' (SEQ ID NO:17).

The amplified fragment is digested with the endonuclease Bam III and then purified again on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then

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ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC4 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene are used for transfection. Five μ g of the expression plasmid pC4 is cotransfected with 0.5 μ g of the plasmid pSV-neo using lipofectin (Felgner et al., supra). The plasmid pSV2-neo contains a dominant selectable marker, the neo gene from *Trf5* encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μ M, 2 μ M, 5 μ M, 10 μ M, 20 μ M). The same procedure is repeated until clones are obtained which grow at a concentration of 100-200 μ M. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

At least six Neurokinine-alpha expression constructs have been generated by the inventors herein to facilitate the production of Neurokinine-alpha and/or Neurokinine-alphaSV polypeptides of several sizes and in several systems. The expression constructs are as follows: (1) pNa.A71-I.285 (expresses amino acid residues Ala-71 through Leu-285), (2) pNa.A81-I.285 (expresses amino acid residues Ala-81 through Leu-285), (3) pNa.I.112-I.285 (expresses amino acid residues Leu-112 through Leu-285), (4) pNa.A134-I.285 (expresses amino acid residues Ala-134 through Leu-285), (5) pNa.I.147-I.285 (expresses amino acid residues Leu-147 through Leu-285), and (6) pNa.G161-I.285 (expresses amino acid residues Gly-161 through Leu-285).

In preferred embodiments, the expression constructs are used to express various Neurokinine-alpha mutants from bacterial, baculoviral, and mammalian systems.

In certain additional preferred embodiments, the constructs express a Neurokinine-alpha polypeptide fragment fused at the N- and/or C-terminus to a heterologous polypeptide, e.g., the signal peptide from human IL-6, the signal peptide from CK-beta8 (amino acids -21 to -1 of the CK-beta8 sequence disclosed in published PCT application PCT/US95/09058), or the human IgG Fc region. Other sequences could be used which are known to those of skill in the art.

Example 4

Tissue Distribution of Neurokinine-Alpha mRNA Expression

Northern blot analysis is carried out to examine Neurokinine-alpha gene expression in human tissues, using methods described by, among others, Sambrook et al., cited above. A cDNA probe containing the entire nucleotide sequence of the Neurokinine-alpha protein (SEQ ID NO:1) is labeled with 32 P using the RediprimeTM DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using a C18ROMA S10-100 column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled

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probe is then used to examine various human tissues for Neurokinine-alpha and/or Neurokinine-alpha mRNA.

Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) are obtained from Clontech and are examined with the labeled probe using ExpressHybTM hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are mounted and exposed to film at -70° C. overnight, and films developed according to standard procedures.

To determine the pattern of Neurokinine-alpha and/or Neurokinine-alpha expression a panel of multiple tissue Northern blots were probed. This revealed predominant expression of single 2.6 kb mRNA in peripheral blood leukocytes, spleen, lymph node and bone marrow, and detectable expression in placenta, heart, lung, fetal liver, thymus and pancreas. Analysis of a panel of cell lines demonstrated high expression of Neurokinine-alpha and/or Neurokinine-alpha in HL60 cells, detectable expression in K562, but no expression in Raji, HeLa, or MOLT-4 cells. Overall it appears that Neurokinine-alpha and/or Neurokinine-alpha mRNA expression is enriched in the immune system.

Example 5

Gene Therapy Using Endogenous Neurokinine-Alpha Gene

Another method of gene therapy according to the present invention involves operably associating the endogenous Neurokinine-alpha sequence with a promoter via homologous recombination as described, for example, in U.S. Pat. No. 5,641,670, issued Jun. 24, 1997; International Publication No. WO 96/29411, published Sep. 26, 1996; International Publication No. WO 94/12650, published Aug. 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); and Zijlstra et al., Nature 342:435-438 (1989). This method involves the activation of a gene which is present in the target cells, but which is not expressed in the cells, or is expressed at a lower level than desired. Polynucleotide constructs are made which contain a promoter and targeting sequences, which are homologous to the 5' non-coding sequence of endogenous Neurokinine-alpha, flanking the promoter. The targeting sequence will be sufficiently near the 5' end of Neurokinine-alpha so the promoter will be operably linked to the endogenous sequence upon homologous recombination. The promoter and the targeting sequences can be amplified using PCR. Preferably, the amplified promoter contains distinct restriction enzyme sites on the 5' and 3' ends. Preferably, the 3' end of the first targeting sequence contains the same restriction enzyme site as the 5' end of the amplified promoter and the 5' end of the second targeting sequence contains the same restriction site as the 3' end of the amplified promoter.

The amplified promoter and the amplified targeting sequences are digested with the appropriate restriction enzymes and subsequently treated with calf intestinal phosphatase. The digested promoter and digested targeting sequences are added together in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The construct is size fractionated on an agarose gel then purified by phenol extraction and ethanol precipitation.

In this Example, the polynucleotide constructs are administered as naked polynucleotides via electroporation. However, the polynucleotide constructs may also be administered with transfection-facilitating agents, such as liposomes, viral

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sequences, viral particles, precipitating agents, etc. Such methods of delivery are known in the art.

Once the cells are transfected, homologous recombination will take place which results in the promoter being operably linked to the endogenous Neutrokin- α sequence. This results in the expression of Neutrokin- α in the cell. Expression may be detected by immunological staining, or any other method known in the art.

Fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in DMEM+10% fetal calf serum. Exponentially growing or early stationary phase fibroblasts are trypsinized and rinsed from the plastic surface with nutrient medium. An aliquot of the cell suspension is removed for counting, and the remaining cells are subjected to centrifugation. The supernatant is aspirated and the pellet is resuspended in 5 ml of electroporation buffer (20 mM HEPES pH 7.3, 137 mM NaCl, 5 mM KCl, 0.7 mM Na₂HPO₄, 6 mM dextrose). The cells are recentrifuged, the supernatant aspirated, and the cells resuspended in electroporation buffer containing 1 mg/ml acetylated bovine serum albumin. The final cell suspension contains approximately 3×10^6 cells/ml. Electroporation should be performed immediately following resuspension.

Plasmid DNA is prepared according to standard techniques. For example, to construct a plasmid for targeting to the Neutrokin- α locus, plasmid pUC18 (MBI Fermentas, Amherst, N.Y.) is digested with HindIII. The CMV promoter is amplified by PCR with an XbaI site on the 5' end and a BamHI site on the 3' end. Two Neutrokin- α non-coding sequences are amplified via PCR: one Neutrokin- α non-coding sequence (Neutrokin- α fragment 1) is amplified with a HindIII site at the 5' end and an XbaI site at the 3' end; the other Neutrokin- α non-coding sequence (Neutrokin- α fragment 2) is amplified with a BamHI site at the 5' end and a HindIII site at the 3' end. The CMV promoter and Neutrokin- α fragments are digested with the appropriate enzymes (CMV promoter: XbaI and BamHI; Neutrokin- α fragment 1: HindIII and XbaI; Neutrokin- α fragment 2: BamHI and HindIII) and ligated together. The resulting ligation product is digested with HindIII, and ligated with the HindIII-digested pUC18 plasmid.

Plasmid DNA is added to a sterile cuvette with a 0.4 cm electrode gap (Bio-Rad). The final DNA concentration is generally at least 120 μ g/ml. 0.5 ml of the cell suspension (containing approximately 1.5×10^6 cells) is then added to the cuvette, and the cell suspension and DNA solutions are gently mixed. Electroporation is performed with a Gene-Pulser apparatus (Bio-Rad). Capacitance and voltage are set at 960 μ F and 250-300 V, respectively. As voltage increases, cell survival decreases, but the percentage of surviving cells that stably incorporate the introduced DNA into their genome increases dramatically. Given these parameters, a pulse time of approximately 14-20 mSec should be observed.

Electroporated cells are maintained at room temperature for approximately 5 min, and the contents of the cuvette are then gently removed with a sterile transfer pipette. The cells are added directly to 10 ml of prewarmed nutrient media (DMEM with 15% calf serum) in a 10 cm dish and incubated at 37° C. The following day, the media is aspirated and replaced with 10 ml of fresh media and incubated for a further 16-24 hours.

The engineered fibroblasts are then injected into the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads. The fibroblasts now produce

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the protein product. The fibroblasts can then be introduced into a patient as described above.

Example 6

Neutrokin- α , a Novel Member of the Tumor Necrosis Factor Ligand Family that Functions as a B Lymphocyte Stimulator

A 285 amino acid protein was identified in a human neutrophil/monocyte-derived cDNA library that shared significant homology within its predicted extracellular receptor-ligand binding domain to APRIL (28.7%) (Hahne, M., et al., *J. Exp. Med.* 188, 1185-90 (1998)), TNF- α (16.2%) (Penttilä, D., et al., *Nature* 312, 724-729 (1984)) and LT- α (14.1%) (Gray, *Nature* 312, 721-724 (1984)) (FIGS. 7A-1 and 7A-2). We have designated this cytokine Neutrokin- α (we have also designated this molecule as B Lymphocyte Stimulator (BLyS) based on its biological activity). Hydrophobicity analyses of the Neutrokin- α protein sequence have revealed a potential transmembrane spanning domain between amino acid residues 47 and 73 which is preceded by non-hydrophobic amino acids suggesting that Neutrokin- α , like other members of the TNF ligand family, is a type II membrane bound protein (Cosman, D., *Stem. Cells*, 12:440-55 (1994)). Expression of this cDNA in mammalian cells (HEK 293 and Chinese Hamster Ovary) and Sf9 insect cells identified a 152 amino acid soluble form with an N-terminal sequence beginning with the alanine residue at amino acid 134 (arrow in FIGS. 7A-1 and 7A-2). Reconstruction of the mass to charge ratio defined a mass for Neutrokin- α of 17,038 Daltons, a value in consistent with that predicted for this 152 amino acid protein with a single disulfide bond (17037.5 Daltons).

Using human/hamster somatic cell hybrids and a radiation-hybrid mapping panel, the gene encoding Neutrokin- α was found linked to marker SHG136171 which maps to human chromosome 13q34, a region not previously associated with any other member of the TNF superfamily of genes (Cosman, D., *Stem. Cells*, 12:440-55 (1994)).

The expression profile of Neutrokin- α was assessed by Northern blot (FIG. 7B) and flow cytometric analyses (Table V and FIGS. 8A, 8B and 8C). Neutrokin- α is encoded by a single 2.6 kb mRNA found at high levels in peripheral blood leukocytes, spleen, lymph node and bone marrow. Lower expression levels were detected in placenta, heart, lung, fetal liver, thymus and pancreas. Among a panel of cell lines, Neutrokin- α mRNA was detected in HL-60 and K562, but not in Raji, HeLa, or MOLT-4 cells. These results were confirmed by flow cytometric analyses using the Neutrokin- α -specific mAb 2E5. As shown in Table V, Neutrokin- α expression is not detected on T or B lineage cells but rather restricted to cells within the myeloid origin. Further analyses of normal blood cell types demonstrated significant expression on resting monocytes that was upregulated approximately 4-fold following exposure of cells to IFN- γ (100 U/ml.) for three days (FIGS. 8A and 8B). A concomitant increase in Neutrokin- α -specific mRNA was also detected (FIG. 8C). By contrast, Neutrokin- α was not expressed on freshly isolated peripheral blood granulocytes, T cells, B cells, or NK cells.

Purified recombinant Neutrokin- α ("rNeutrokin- α ") was assessed for its ability to induce activation, proliferation, differentiation or death in numerous cell based assays involving B cells, T cells, monocytes, NK cells, hematopoietic progenitors, and a variety of cell types of endothelial and epithelial origin. Among these assays, Neutrokin- α was

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specifically found to increase B cell proliferation in a standard co-stimulatory assay in which purified tonsillar B cells are cultured in the presence of either formalin-fixed *Staphylococcus aureus* Cowan I (SAC) or immobilized anti-human IgM as priming agents (Sieckmann, D. G., et al., *J. Exp. Med.* 147:814-29 (1978); Ringden, O., et al., *Scand. J. Immunol.* 6:1159-69 (1977)). As shown in FIG. 9A, recombinant Neutrokin-alpha induced a dose-dependent proliferation of tonsillar B cells. This response was similar to that of rIL-2 over the dose range from 0.1 to 10,000 ng/ml. Neutrokin-alpha also induces B cell proliferation when cultured with cells co-stimulated with immobilized anti-IgM (FIG. 9B). A dose-dependent response is readily observed as the amount of crosslinking agent increases in the presence of a fixed concentration of either IL-2 or rNeutrokin-alpha.

In an attempt to correlate the specific biological activity on B cells with receptor expression, purified Neutrokin-alpha was biotinylated. The resultant biotin-Neutrokin-alpha protein retained biological function in the standard B cell proliferation assays. Lineage-specific analyses of whole human peripheral blood cells indicated that binding of biotinylated Neutrokin-alpha was undetectable on T cells, monocytes, NK cells and granulocytes as assessed by CD3, CD14, CD56, and CD66b respectively (FIGS. 10A, 10B, 10C, 10D and 10E). In contrast, biotinylated Neutrokin-alpha bound peripheral CD20⁺ B cells. Receptor expression was also detected on the B cell tumor lines R1H, ARH-77, Raji, Namahwa, RPMI8226, and IM-9 but not any of the myeloid-derived lines tested including THP-1, HL-60, K-562, and U-937. Representative flow cytometric profiles for the myeloma cell line IM-9 and the histiocytic line U-937 are shown in FIGS. 10F and 10G. Similar results were also obtained using a biologically active FLAG-tagged Neutrokin-alpha protein instead of the chemically modified biotin-Neutrokin-alpha. Taken together, these results confirm that Neutrokin-alpha displays a clear B cell tropism in both its receptor distribution and biological activity. It remains to be shown whether cellular activation may induce expression of Neutrokin-alpha receptors on peripheral blood cells, other normal cell types or established cell lines.

To examine the species specificity of Neutrokin-alpha, mouse splenic B cells were cultured in the presence of human Neutrokin-alpha and SAC. Results demonstrate that rNeutrokin-alpha induced in vitro proliferation of murine splenic B cells and bound to a cell surface receptor on these cells. Interestingly, immature surface Ig negative B cell precursors isolated from mouse bone marrow did not proliferate in response to Neutrokin-alpha nor did they bind the ligand.

To assess the in vivo activity of rNeutrokin-alpha, BALB/c mice (3/group) were injected (i.p.) twice per day with buffer only, or 0.08 mg/kg, 0.8 mg/kg, 2 mg/kg or 8 mg/kg of rNeutrokin-alpha. Mice received this treatment for 4 consecutive days at which time they were sacrificed and various tissues and serum collected for analyses. In an alternative embodiment, BALB/c mice may be injected (i.p.) twice per day with any amount of rNeutrokin-alpha in a range of 0.01 to 10 mg/kg. In a preferred embodiment, BALB/c mice are injected (i.p.) twice per day with any amount of rNeutrokin-alpha in a range of 0.01 to 3 mg/kg (specific preferred exemplary dosages in this embodiment include, but are not limited to, 0.01 mg/kg, 0.02 mg/kg, 0.03 mg/kg, 0.04 mg/kg, 0.05 mg/kg, 0.06 mg/kg, 0.07 mg/kg, 0.08 mg/kg, 0.09 mg/kg, 0.1 mg/kg, 0.2 mg/kg, 0.3 mg/kg, 0.4 mg/kg, 0.5 mg/kg, 0.6 mg/kg, 0.7 mg/kg, 0.8 mg/kg, 0.9 mg/kg, 1.0 mg/kg, 1.1 mg/kg, 1.2 mg/kg, 1.3 mg/kg, 1.4 mg/kg, 1.5 mg/kg, 1.6 mg/kg, 1.6 mg/kg, 1.7 mg/kg, 1.8 mg/kg, 1.9 mg/kg, 2.0 mg/kg, 2.1 mg/kg, 2.2 mg/kg, 2.3

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mg/kg, 2.4 mg/kg, 2.5 mg/kg, 2.6 mg/kg, 2.7 mg/kg, 2.8 mg/kg, 2.9 mg/kg, and 3.0 mg/kg). In an additional preferred embodiment, BALB/c mice are injected (i.p.) twice per day with any amount of rNeutrokin-alpha in a range of 0.02 to 2 mg/kg (specific preferred exemplary dosages in this embodiment include, but are not limited to, 0.02 mg/kg, 0.03 mg/kg, 0.04 mg/kg, 0.05 mg/kg, 0.06 mg/kg, 0.07 mg/kg, 0.08 mg/kg, 0.09 mg/kg, 0.1 mg/kg, 0.2 mg/kg, 0.3 mg/kg, 0.4 mg/kg, 0.5 mg/kg, 0.6 mg/kg, 0.7 mg/kg, 0.8 mg/kg, 0.9 mg/kg, 1.0 mg/kg, 1.1 mg/kg, 1.2 mg/kg, 1.3 mg/kg, 1.4 mg/kg, 1.5 mg/kg, 1.6 mg/kg, 1.6 mg/kg, 1.7 mg/kg, 1.8 mg/kg, 1.9 mg/kg, and 2.0 mg/kg).

Microscopically, the effects of Neutrokin-alpha administration were clearly evident in sections of spleen stained with routine hematoxylin and eosin (H&E) and immunohistochemically with a mAb specific for CD45R(B220) (FIG. 11A). Normal splenic architecture was altered by a dramatic expansion of the white pulp marginal zone and a distinct increase in cellularity of the red pulp (FIG. 11A). Marginal zone expansion appeared to be the result of increased numbers of lymphocytes expressing the B cell marker CD45R(B220). In addition, the T cell dense periarteriolar lymphoid sheath (PALS) areas were also infiltrated by moderate numbers of CD45R(B220) positive cells. This suggests the white pulp changes were due to increased numbers of B cells. The densely packed cell population that frequently filled red pulp spaces did not stain with CD45R(B220). Additional experiments will be required to characterize all the cell types involved and further define the mechanism by which Neutrokin-alpha alters splenic architecture.

Flow cytometric analyses of the spleens from mice treated with 2 mg/kg Neutrokin-alpha-treated indicated that Neutrokin-alpha increased the proportion of mature (CD45R(B220)^{high}, Th13^{high}) B cells approximately 10-fold over that observed in control mice (FIGS. 11B and 11C). Further analyses performed in which mice were treated with buffer, 0.08 mg/kg, 0.8 mg/kg, 2 mg/kg, or 8 mg/kg Neutrokin-alpha indicated that 0.08 mg/kg, 0.8 mg/kg, and 2 mg/kg each increased the proportion of mature (CD45R(B220)^{high}, Th13^{high}) B cells approximately 10-fold over that observed in control mice, whereas buffer and 8 mg/kg produced approximately equal proportions of mature B cells. See, Table IV.

TABLE IV

FACS Analysis of Mouse Spleen B Cell Population.

Neutrokin-alpha (mg/kg)	% Mature B Cells (R2)	% CD45R-positive (R1)
Control (buffer)	1.26	52.17
0.08 mg/kg	16.15	56.53
0.8 mg/kg	18.54	57.56
2 mg/kg	16.54	57.55
8 mg/kg	1.24	61.42

A potential consequence of increased mature B cell representation in vivo is a relative increase in serum Ig titers. Accordingly, serum IgA, IgG and IgM levels were compared between buffer and Neutrokin-alpha-treated mice (FIGS. 11D, 11E, and 11F). Neutrokin-alpha administration resulted in a 2- and 5-fold increase in IgA and IgM serum levels respectively. Interestingly, circulating levels of IgG did not increase.

Moreover, a dose-dependent response was observed in serum IgA titers in mice treated with various amounts of Neutrokin-alpha over a period of four days, whereas no apparent dose-dependency was observed by administration

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of the same amounts of Neurokinine-alpha over a period of two days. In the case of administration over four days, administration of 8, 2, 0.8, 0.08, and 0 mg/kg Neurokinine-alpha resulted in serum IgA titers of approximately 800 micrograms/ml, 700 micrograms/ml, 400 micrograms/ml, 200 micrograms/ml and 200 micrograms/ml. That is, administration of 8, 2, 0.8, and 0.08 mg/kg Neurokinine-alpha over four days resulted in approximately 4-fold, 3.75-fold, 2-fold, and minimal-fold, respectively, increases in IgA serum levels over background or basal levels observed by administration of buffer only. In an alternative embodiment, these experiments may be performed with any amount of rNeurokinine-alpha in a range of 0.01 to 10 mg/kg. In a preferred embodiment, Neurokinine-alpha is administered in a range of 0.01 to 3 mg/kg (specific preferred exemplary dosages in this embodiment include, but are not limited to, 0.01 mg/kg, 0.02 mg/kg, 0.03 mg/kg, 0.04 mg/kg, 0.05 mg/kg, 0.06 mg/kg, 0.07 mg/kg, 0.08 mg/kg, 0.09 mg/kg, 0.1 mg/kg, 0.2 mg/kg, 0.3 mg/kg, 0.4 mg/kg, 0.5 mg/kg, 0.6 mg/kg, 0.7 mg/kg, 0.8 mg/kg, 0.9 mg/kg, 1.0 mg/kg, 1.1 mg/kg, 1.2 mg/kg, 1.3 mg/kg, 1.4 mg/kg, 1.5 mg/kg, 1.6 mg/kg, 1.7 mg/kg, 1.8 mg/kg, 1.9 mg/kg, 2.0 mg/kg, 2.1 mg/kg, 2.2 mg/kg, 2.3 mg/kg, 2.4 mg/kg, 2.5 mg/kg, 2.6 mg/kg, 2.7 mg/kg, 2.8 mg/kg, 2.9 mg/kg, and 3.0 mg/kg). In an additional preferred embodiment, Neurokinine-alpha is administered in a range of 0.02 to 2 mg/kg (specific preferred exemplary dosages in this embodiment include, but are not limited to, 0.02 mg/kg, 0.03 mg/kg, 0.04 mg/kg, 0.05 mg/kg, 0.06 mg/kg, 0.07 mg/kg, 0.08 mg/kg, 0.09 mg/kg, 0.1 mg/kg, 0.2 mg/kg, 0.3 mg/kg, 0.4 mg/kg, 0.5 mg/kg, 0.6 mg/kg, 0.7 mg/kg, 0.8 mg/kg, 0.9 mg/kg, 1.0 mg/kg, 1.1 mg/kg, 1.2 mg/kg, 1.3 mg/kg, 1.4 mg/kg, 1.5 mg/kg, 1.6 mg/kg, 1.7 mg/kg, 1.8 mg/kg, 1.9 mg/kg, and 2.0 mg/kg).

The data presented herein define Neurokinine-alpha, as a novel member of the TNF-ligand superfamily that induces both in vivo and in vitro B cell proliferation and differentiation. Neurokinine-alpha is distinguished from other B cell growth and differentiation factors such as IL2 (Metzger, D. W., et al., *Res. Immunol.* 146:499-505 (1995)), IL4 (Armitage, R. J., et al., *Adv. Exp. Med. Biol.* 292:121-30 (1991); Yokota, T., et al., *Proc. Natl. Acad. Sci. U.S.A.* 83:5894-98 (1986)), IL5 (Takatsu, K., et al., *Proc. Natl. Acad. Sci. U.S.A.* 84:4234-38 (1987); Bertolini, J. N., et al., *Eur. J. Immunol.* 23:398-402 (1993)), IL6 (Poupart, P., et al., *EMBO J.* 6:1219-24 (1987); Hirano, T., et al., *Nature* 324:73-76 (1986)) IL7 (Goodwin, R. G., et al., *Proc. Natl. Acad. Sci. U.S.A.* 86:302-06 (1989); Namen, A. E., et al., *Nature* 333:571-73 (1988)), IL13 (Punnonen, J., et al., *Allergy* 49:576-86 (1994)), IL15 (Armitage, R. J., et al., *J. Immunol.* 154:483-90 (1995)), CD40L (Armitage, R. J., et al., *Nature* 357:80-82 (1992); Van Kooten, C. and Banchereau, J., *Int. Arch. Allergy Immunol.* 113:393-99 (1997)) or CD27L (CD27) (Oshima, H., et al., *Int. Immunol.* 10:517-26 (1998); Lens, S. M., et al., *Semin. Immunol.* 10:491-99 (1998)) by its monocyte-specific gene/protein expression pattern and its specific receptor distribution and biological activity on B lymphocytes. Taken together these data suggest that Neurokinine-alpha is likely involved in the exchange of signals between B cells and monocytes or their differentiated progeny. Although all B cells may utilize this mode of signaling, the restricted expression patterns and Ig secretion suggest a role for Neurokinine-alpha in the activation of CD5⁺ or "unconventional" B cell responses. These B cells provide a critical component to the innate immune system and provide protection from environmental pathogens through their secretion of polyreactive IgM and IgA antibodies (Pennell, C. A., et al., *Eur. J. Immunol.* 19:1289-95 (1989); Hayakawa, K., et al., *Proc. Natl. Acad. Sci. U.S.A.* 81:2494-

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98(1984)). Alternatively, Neurokinine-alpha may function as a regulator of T cell independent responses in a manner analogous to that of CD40 and CD40L in T cell dependent antigen activation (van den Hertwegh, A. J., et al., *J. Exp. Med.* 178: 1555-65 (1993); Grabstein, K. H., et al., *J. Immunol.* 150: 3141-47 (1993)). As such, Neurokinine-alpha, its receptor or related antagonists have utility in the treatment of B cell disorders associated with autoimmunity, neoplasia and/or immunodeficient syndromes.

Methods

Mice, BALB/cAnNCr (6-8 weeks) were purchased from Charles River Laboratories, Inc. and maintained according to recommended standards (National Research Council, Guide for the care and use of laboratory animals (1999)) in microisolator cages with recycled paper bedding (Harlan Sprague Dawley, Inc., Indianapolis, Ind.) and provided with pelleted rodent diet (Harlan Sprague Dawley, Inc.) and bottled drinking water on an ad libitum basis. The animal protocols used in this study were reviewed and approved by the HGS Institutional Animal Care and Use Committee.

Isolation of full length Neurokinine-alpha cDNA. The BLAST algorithm was used to search the Human Genome Sciences Inc. expressed sequence tag (EST) database for sequences with homology to the receptor-binding domain of the TNF family. A full length Neurokinine-alpha clone was identified, sequenced and submitted to GenBank (Accession number AF132600). The Neurokinine-alpha open reading frame was PCR amplified utilizing a 5' primer (5'-CAG ACT GGA TCC GCC ACC ATG GAT GAC TCC ACA GAA AG-3') (SEQ ID NO:39) annealing at the predicted start codon and a 3' primer (5'-CAG ACT GGT ACC GTC CTG CTT GCA CTA CAT GGC-3') (SEQ ID NO:40) designed to anneal at the predicted downstream stop codon. The resulting amplicon was tailed with Bam HI and Asp 718 restriction sites and subcloned into a mammalian expression vector. Neurokinine-alpha was also expressed in p-CMV-1 (Sigma Chemicals).

Purification of recombinant human Neurokinine-alpha. The full length cDNA encoding Neurokinine-alpha was subcloned into the baculovirus expression vector pA2 and transfected into Sf9 insect cells (Patel, V. P., et al., *J. Exp. Med.* 185:1163-72 (1997)). Recombinant Neurokinine-alpha was purified from cell supernatants at 92 h post-infection using a combination of anion-exchange, size exclusion, and hydrophobic interaction columns. The purified protein was formulated in a buffer containing 0.15 M NaCl, 50 mM NaOAc at pH 6, sterile filtered and stored at 4° C. until needed. Both SDS-PAGE and RP-HPLC analyses indicate that rNeurokinine-alpha is greater than 95% pure. Endotoxin levels were below the detection limit in the LAL assay (Associates of Cape Cod, Falmouth, Mass.). The final purified Neurokinine-alpha protein has an N-terminus sequence of Ala-Val-Gln-Gly-Pro. This corresponds identically to the sequence of soluble Neurokinine-alpha derived from CHO cell lines stably transfected with the full length Neurokinine-alpha gene.

Monoclonal antibody generation. BALB/cAnNCr mice were immunized with 50 micrograms of HisTag-Neurokinine-alpha suspended in complete Freund's adjuvant followed by 2 challenges in incomplete Freund's adjuvant. Hybridomas and monoclonal antibodies were prepared as described (Geffler, M. L., et al., *Somatic Cell Genet.* 3:231-36 (1977); Akerstrom, B., et al., *J. Immunol.* 135:2589-92 (1985)).

Cell lines. All human cell lines were purchased from ATCC (American Type Culture Collection, Manassas, Va.).

FACS analysis. Neurokinine-alpha expression was assessed on human cell lines, freshly isolated normal peripheral blood nucleated cells, and in vitro cultured monocytes, a mouse

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anti-human Neutrokin- α mAb 2E5 (IgG1) followed by PE-conjugated F(ab')₂ goat antibody to mouse IgG (CAL-TAG Laboratories, Burlingame, Calif.). Cells were analyzed using a FACScan (Becton Dickinson Immunocytometry Systems, San Jose, Calif.) with propidium iodide to exclude dead cells. Neutrokin- α binding was assessed using rNeutrokin- α biotinylated with a N-hydroxysuccinimidobiotin reagent (Pierce, Rockford, Ill.) followed by PE-conjugated streptavidin (Dako Corp, Glostrup, Denmark).

Chromosomal mapping. To determine the chromosomal location of the Neutrokin- α gene, a panel of monoclonal somatic cell hybrids (Quantum Biotechnology, Canada) retaining individual chromosomes was screened by PCR using Neutrokin- α specific primers (5' primer: 5'-TGG TGT CTT TCT ACC AGG TGG-3' (SEQ ID NO:41) and 3' primer: 5'-TTT CTT CTG GAC CTT GAA CGG-3' (SEQ ID NO:42)). The predicted 233 bp PCR product was only detected in human chromosome 13 hybrids. Using a panel of 83 radiation hybrids (Research Genetics, St. Louis, Mo.) and the Stanford Human Genome Center Database (<http://www.shgc.stanford.edu/RI/rlserver>), Neutrokin- α was found linked to the SHGC-36171 marker on chromosome 13. Superposition of this map with the cytogenetic map of human chromosome 13 allowed the assignment of human Neutrokin- α to chromosomal band 13q34.

B lymphocyte proliferation assay. Human tonsillar B cells were purified by magnetic bead (MACS) depletion of CD3-positive cells. The resulting cell population was routinely greater than 95% B cells as assessed by expression of CD19 and CD20. Various dilutions of human rNeutrokin- α or the control protein recombinant human IL-2 were placed into individual wells of a 96-well plate to which was added 10^5 B cells suspended in culture medium (RPMI 1640 containing 10% FBS, 5×10^{-5} M 2ME, 100 U/ml penicillin, 100 microgram/ml streptomycin, and 10^{-5} dilution of Pansorbin (SAC) or anti-IgM) in a total volume of 150 microliters. Proliferation was quantitated by a 20 h pulse (1 microCi/well) of ³H-thymidine (6.7 Ci/mM) beginning 72 h post factor addition.

Histological analyses. Spleens were fixed in 10% neutral buffered formalin, embedded in paraffin, sectioned at 5 micrometers, mounted on glass slides and stained with hematoxylin and eosin or by enzyme-labeled indirect method immunohistochemistry for CD45R(B220) (Hilbert, D. M., et al., *Eur. J. Immunol.* 23:2412-18 (1993)).

TABLE V

Neutrokin- α cell surface expression		
Cell line	Cellular Morphology	Neutrokin- α cell surface expression
<u>Monocytic lineage</u>		
U-937	Lymphoma, histiocytic macrophage	+
BL-60	Leukemia, acute promyelocytic	+
K-562	Leukemia, chronic myelogenous	+
TMP-1	Leukemia, acute monocytic	+
<u>T-lineage</u>		
Jurkat	Leukemia, T lymphocytic	-
SUP-T13	Leukemia, T lymphoblastic	-
MOLT-4	Leukemia, T lymphoblastic	-
<u>B-lineage</u>		
Daudi	Burkitt's, lymphoblastic	-
Namaha	Burkitt's, lymphocyte	-
Raji	Burkitt's, lymphocyte	-

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TABLE V-continued

Neutrokin- α cell surface expression		
Cell line	Cellular Morphology	Neutrokin- α cell surface expression
Reh	Leukemia, lymphocytic	-
ARH-77	Leukemia, plasma cell	-
IM9	Myeloma	-
RPMI 8226	Myeloma	-

Example 7

Assays to Detect Stimulation or Inhibition of B Cell Proliferation and Differentiation

Generation of functional humoral immune responses requires both soluble and cognate signaling between B-lineage cells and their microenvironment. Signals may impart a positive stimulus that allows a B-lineage cell to continue its programmed development, or a negative stimulus that instructs the cell to arrest its current developmental pathway. To date, numerous stimulatory and inhibitory signals have been found to influence B cell responsiveness including IL-2, IL-4, IL-5, IL-6, IL-7, IL-10, IL-13, IL-14 and IL-15. Interestingly, these signals are by themselves weak effectors but can, in combination with various co-stimulatory proteins, induce activation, proliferation, differentiation, homing, tolerance and death among B cell populations. One of the best studied classes of B-cell co-stimulatory proteins is the TNF-superfamily. Within this family CD40, CD27, and CD30 along with their respective ligands CD154, CD70, and CD153 have been found to regulate a variety of immune responses. Assays which allow for the detection and/or observation of the proliferation and differentiation of these B-cell populations and their precursors are valuable tools in determining the effects various proteins may have on these B-cell populations in terms of proliferation and differentiation. Listed below are two assays designed to allow for the detection of the differentiation, proliferation, or inhibition of B-cell populations and their precursors.

In Vitro assay-Purified Neutrokin- α and/or Neutrokin- α SV protein, or truncated forms thereof, is assessed for its ability to induce activation, proliferation, differentiation or inhibition and/or death in B-cell populations and their precursors. The activity of Neutrokin- α and/or Neutrokin- α SV protein on purified human tonsillar B cells, measured qualitatively over the dose range from 0.1 to 10,000 ng/mL, is assessed in a standard B-lymphocyte co-stimulation assay in which purified tonsillar B cells are cultured in the presence of either formalin-fixed *Staphylococcus aureus* Cowan 1 (SAC) or immobilized anti-human IgM antibody as the priming agent. Second signals such as IL-2 and IL-15 synergize with SAC and IgM crosslinking to elicit B cell proliferation as measured by tritiated-thymidine incorporation. Novel synergizing agents can be readily identified using this assay. The assay involves isolating human tonsillar B cells by magnetic bead (MACS) depletion of CD3-positive cells. The resulting cell population is greater than 95% B cells as assessed by expression of CD45R(B220). Various dilutions of each sample are placed into individual wells of a 96-well plate to which are added 10^5 B-cells suspended in culture medium (RPMI 1640 containing 10% FBS, 5×10^{-5} M 2ME, 100 U/ml penicillin, 10 ug/ml streptomycin, and 10^{-5} dilution of SAC) in a total volume of 150 μ l. Proliferation or inhibition is quantitated by a 20 h pulse (1 μ Ci/well) with

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³H-thymidine (6.7 Ci/mM) beginning 72 h post factor addition. The positive and negative controls are IL-2 and medium respectively.

Agonists (including Neurokinine-alpha and/or Neurokinine-alphaSV polypeptide fragments) demonstrate an increased B cell proliferation when compared to that observed when the same number of B cells is contacted with the same concentration of priming agent. Antagonists according to the invention exhibit a decreased B cell proliferation when compared to controls containing the same number of B cells, the same concentration of priming agent, and the same concentration of a soluble form of Neurokinine-alpha that elicits an increase in B cell proliferative activity (e.g., 71-285, 81-285, 112-285 or 134-285 of the Neurokinine-alpha polypeptide shown in SEQ ID NO:2) in the absence the antagonist.

In Vivo assay-BALB/c mice are injected (i.p.) twice per day with buffer only, or 2 mg/Kg of Neurokinine-alpha and/or Neurokinine-alphaSV protein, or truncated forms thereof. Mice receive this treatment for 4 consecutive days, at which time they are sacrificed and various tissues and serum collected for analyses. Comparison of H&E sections from normal and Neurokinine-alpha and/or Neurokinine-alphaSV protein-treated spleens identify the results of the activity of Neurokinine-alpha and/or Neurokinine-alphaSV protein on spleen cells, such as the diffusion of peri-arterial lymphatic sheaths, and/or significant increases in the nucleated cellularity of the red pulp regions, which may indicate the activation of the differentiation and proliferation of B-cell populations. Immunohistochemical studies using a B cell marker, anti-CD45R(B220), are used to determine whether any physiological changes to splenic cells, such as splenic disorganization, are due to increased B-cell representation within loosely defined B-cell zones that infiltrate established T-cell regions.

Flow cytometric analyses of the spleens from Neurokinine-alpha and/or Neurokinine-alphaSV protein-treated mice is used to indicate whether Neurokinine-alpha and/or Neurokinine-alphaSV protein specifically increases the proportion of ThB+, CD45R(B220)dull B cells over that which is observed in control mice.

Likewise, a predicted consequence of increased mature B-cell representation in vivo is a relative increase in serum Ig titers. Accordingly, serum IgM and IgA levels are compared between buffer and Neurokinine-alpha and/or Neurokinine-alphaSV protein-treated mice.

Example 8

Effect of Neurokinine-Alpha and its Agonists in Treating Graft-Versus-Host Disease Associated Lymphoid Atrophy and Hypoplasia in Mice

An analysis of the use of Neurokinine-alpha to treat, prevent, and/or diagnose graft-versus-host disease (GVHD)-associated lymphoid hypoplasia/atrophy is performed through the use of a C57BL/6 parent into (BALB/c X C57BL/6) F1 (CBF1) mouse model. This parent into F1 mouse model is a well-characterized and reproducible animal model of GVHD in bone marrow transplant patients, which is well known to one of ordinary skill in the art (see, Gleichmann, et al., *Immunol. Today* 5:324, 1984). Soluble Neurokinine-alpha is expected to induce the proliferation and differentiation of B lymphocyte, and correct the lymphoid hypoplasia and atrophy observed in this animal model of GVHD (Piguet, et al., *J. Exp. Med.* 166:1280 (1987); Hattori, et al., *Blood* 90:542 (1997)).

Initiation of the GVHD condition is induced by the intravenous injection of approximately $1-5 \times 10^8$ spleen cells from

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C57BL/6 mice into (BALB/c X C57BL/6) F1 mice (both are available from Jackson Lab, Bar Harbor, Me.). Groups of 6 to 8 mice receive daily either 0.1 to 5.0 mg/kg of Neurokinine-alpha or buffer control intraperitoneally, intramuscularly or intradermally starting from the days when lymphoid hypoplasia and atrophy are mild (~day 5), moderate (~day 12) or severe (~day 20) following the parental cell injection. The effect of Neurokinine-alpha on lymphoid hypoplasia and atrophy of spleen is analyzed by FACS and histopathology at multiple time points (3-4) between day 10-30. Briefly, splenocytes are prepared from normal (CBF1, GVHD) or Neurokinine-alpha-treated mice, and stained with fluorescein phycoerythrin-conjugated anti-IL-2 Kb, biotin-conjugated anti-IL-2 Kd, and FITC-conjugated anti-CD4, anti-CD8, or anti-B220, followed by a CyChrome-conjugated avidin. All of these conjugated antibodies can be purchased from Pharmingen (San Diego, Calif.). Cells are then analysis on a FAC-Scan (Becton Dickinson, San Jose, Calif.). Recipient and donor lymphocytes are identified as IL-2 Kb+Kd+ and IL-2 Kb+Kd-cells, respectively. Cell numbers of CD4+T, CD8+T and B220+B cells of recipient or donor origin are calculated from the total numbers of splenocytes recovered and the percentages of each subpopulation are determined by the three color analysis. Histological evaluation of the relative degree of tissue damage in other GVHD-associated organs (liver, skin and intestine) may be conducted after sacrificing the animals.

Finally, Neurokinine-alpha and buffer-treated animals undergo a clinical evaluation every other day to assess cachexia, body weight and lethality.

Neurokinine-alpha agonists and antagonists may also be examined in this acute GVHD murine model.

Example 9

Isolation of Antibody Fragments Directed Against Neurokinine-Alpha Polypeptides from a Library of scFvs

Naturally occurring V-genes isolated from human PBLs are constructed into a large library of antibody fragments which contain reactivities against Neurokinine-alpha and/or Neurokinine-alphaSV to which the donor may or may not have been exposed (see e.g., U.S. Pat. No. 5,885,793 incorporated herein in its entirety by reference).

Rescue of the Library:

A library of scFvs is constructed from the RNA of human PBLs as described in WO92/01047 (which is hereby incorporated by reference in its entirety). To rescue phage displaying antibody fragments, approximately 10^9 *E. coli* harboring the phagemid are used to inoculate 50 ml of 2xTY containing 1% glucose and 100 micrograms/ml of ampicillin (2xTY-AMP-GLU) and grown to an O.D. of 0.8 with shaking. Five ml of this culture is used to inoculate 50 ml of 2xTY-AMP-GLU, 2×10^8 TU of delta gene 3 helper (M13 delta gene III, see WO92/01047) are added and the culture incubated at 37° C. for 45 minutes without shaking and then at 37° C. for 45 minutes with shaking. The culture is centrifuged at 4000 r.p.m. for 10 min. and the pellet resuspended in 2 liters of 2xTY containing 100 micrograms/ml ampicillin and 50 micrograms/ml kanamycin and grown overnight. Phage are prepared as described in WO92/01047.

M13 delta gene III is prepared as follows: M13 delta gene III helper phage does not encode gene III protein, hence the phage(mid) displaying antibody fragments have a greater avidity of binding to antigen. Infectious M13 delta gene III particles are made by growing the helper phage in cells har-

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boring a pUC19 derivative supplying the wild type gene III protein during phage morphogenesis. The culture is incubated for 1 hour at 37° C. without shaking and then for a further hour at 37° C. with shaking. Cells were spun down (HCC-Centra 8, 4000 revs/min for 10 min), resuspended in 300 ml 2xTY broth containing 100 micrograms ampicillin/ml and 25 micrograms kanamycin/ml (2xTY-AMP-KAN) and grown overnight, shaking at 37° C. Phage particles are purified and concentrated from the culture medium by two PEG-precipitations (Sambrook et al., 1990), resuspended in 2 ml PBS and passed through a 0.45 micrometer filter (Minisart NML; Sartorius) to give a final concentration of approximately 10¹³ transducing units/ml (ampicillin-resistant clones).

Panning the Library.

Immunotubes (Nunc) are coated overnight in PBS with 4 ml of either 100 micrograms/ml or 10 micrograms/ml of a polypeptide of the present invention. Tubes are blocked with 2% Marvel-PBS for 2 hours at 37° C. and then washed 3 times in PBS. Approximately 10¹³ TU of phage is applied to the tube and incubated for 30 minutes at room temperature tumbling on an over and under turntable and then left to stand for another 1.5 hours. Tubes are washed 10 times with PBS 0.1% Tween-20 and 10 times with PBS. Phage are eluted by adding 1 ml of 100 mM triethylamine and rotating 15 minutes on an under and over turntable after which the solution is immediately neutralized with 0.5 ml of 1.0M Tris-HCl, pH 7.4. Phage are then used to infect 10 ml of mid-log *E. coli* TGI by incubating eluted phage with bacteria for 30 minutes at 37° C. The *E. coli* are then plated on TYE plates containing 1% glucose and 100 micrograms/ml ampicillin. The resulting bacterial library is then rescued with delta gene 3 helper phage as described above to prepare phage for a subsequent round of selection. This process is then repeated for a total of 4 rounds of affinity purification with tube-washing increased to 20 times with PBS, 0.1% Tween-20 and 20 times with PBS for rounds 3 and 4.

Characterization of Binders.

Eluted phage from the third and fourth rounds of selection are used to infect *E. coli* HB 2151 and soluble self is produced (Marks, et al., 1991) from single colonies for assay. ELISAs are performed with microtiter plates coated with either 10 picograms/ml of the polypeptide of the present invention in 50 mM bicarbonate pH 9.6. Clones positive in ELISA are further characterized by PCR fingerprinting (see e.g., WO92/01047) and then by sequencing.

Example 10

Neutralization of Neutrokinine-Alpha/Neutrokinine-Alpha Receptor Interaction with an Anti-Neutrokinine-Alpha Monoclonal Antibody

Monoclonal antibodies were generated against Neutrokinine-alpha protein according to the following method. Briefly, mice were given a subcutaneous injection (front part of the dorsum) of 50 micrograms of His-tagged Neutrokinine-alpha protein produced by the method of Example 2 in 100 microliters of PBS emulsified in 100 microliters of complete Freund's adjuvant. Three additional subcutaneous injections of 25 micrograms of Neutrokinine-alpha in incomplete Freund's adjuvant were given at 2-week intervals. The animals were rested for a month before they received the final intraperitoneal boost of 25 micrograms of Neutrokinine-alpha in PBS. Four days later mice were sacrificed and splenocytes taken for fusion.

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The process of "Fusion" was accomplished by fusing splenocytes from one spleen were with 2x10¹⁷ P3X63Ag8.653 plasmacytoma cells using PEG 1500 (Boehringer Mannheim), according to the manufacturer's modifications of an earlier described method. (See, Gelfer, M. L., et al. *Somatic Cell Genet.* 3:231-36 (1977); Boehringer Mannheim. PEG 1500 (Cat. No. 783641), product description.)

After fusion, the cells were resuspended in 400 ml of HAT medium supplemented with 20% FBS and 4% Hybridoma Supplement (Boehringer Mannheim) and distributed to 96 well plates at a density of 200 microliters per well. At day 7 post-fusion, 100 microliters of medium was aspirated and replaced with 100 microliters of fresh medium. At day 14 post-fusion, the hybridomas were screened for antibody production.

Hybridoma supernatants were screened by ELISA for binding to Neutrokinine-alpha protein immobilized on plates. Plates were coated with Neutrokinine-alpha by overnight incubation of 100 microliters per well of Neutrokinine-alpha in PBS at a concentration of 2 micrograms per ml. Hybridoma supernatants were diluted 1:10 with PBS were placed in individual wells of Neutrokinine-alpha-coated plates and incubated overnight at 4° C. On the following day, the plates were washed 3 times with PBS containing 0.1% Tween-20 and developed using the anti-mouse IgG ABC system (Vector Laboratories). The color development reaction was stopped with the addition of 25 ml/well of 2M H₂SO₄. The plates were then read at 450 nm.

Hybridoma supernatants were checked for Ig isotype using Isostrips. Cloning was done by the method of limiting dilutions on HT medium. About 3x10⁶ cells in 0.9 ml of HBSS were injected in pristane-primed mice. After 7-9 days, ascitic fluid was collected using a 19 g needle. All antibodies were purified by protein G affinity chromatography using the Acta PLC system (Pharmacia).

After primary and two consecutive subcutaneous injections, all three mice developed a strong immune response; the serum titer was 10¹⁷ as assessed by ELISA on Neutrokinine-alpha-coated plates.

In one experiment, using the splenocytes from the positive mouse more than 1000 primary hybridomas were generated. 917 of them were screened for producing anti-Neutrokinine-alpha antibody. Screening was performed using 1:1 diluted supernatants in order to detect all positive clones. Of 917 hybridomas screened, 76 were found to be positive and 17 of those were found to be IgG producers. After affinity testing and cloning, 9 of them were chosen for further expansion and purification.

All purified monoclonal antibodies were able to bind different forms of Neutrokinine-alpha (including His-tagged and protein produced from a baculoviral system (see Example 2)) in both Western blot analysis and ELISA. Six of nine clones were also able to bind Neutrokinine-alpha on the surface of THP-1 cells. However, none of the antibodies tested were able to capture Neutrokinine-alpha from solution.

High affinity anti-Neutrokinine-alpha monoclonal antibodies were generated that recognize Neutrokinine-alpha expressed on the cell surface but not in solution can be used for neutralization studies in vivo and in monocyte and B cell assays in vitro. These antibodies are also useful for sensitive detection of Neutrokinine-alpha on Western blots.

In an independent experiment, using the splenocytes from the positive mouse, more than 1000 primary hybridomas were generated. 729 of the primary hybridomas were then screened for the production of an anti-Neutrokinine-alpha antibody. Screening was performed under stringent conditions using 1:10 diluted supernatants in order to pick up only clones

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of higher affinity. Of 729 hybridomas screened, 23 were positive, including 16 IgM and 7 IgG producers (among the latter, 4 gave a strong IgM background). In this experiment, the isotype distribution of IgG antibodies was biased towards the IgG2 subclasses. Three of seven IgG hybridomas produced antibodies of IgG2a subclass and two produced an antibody of IgG2b subclass, while the remaining two were IgG1 producers.

Supernatants from all positive hybridomas generated in the second experiment were tested for the ability to inhibit Neurotrophin- α -mediated proliferation of B cells. In the first screening experiment, two hybridomas producing IgG-neutralizing antibodies were detected (these are antibodies 16C9 and 12C5). In additional experiments, the IgG-neutralizing activity of the hybridomas (i.e., 16C9 and 12C5) were confirmed and two additional strongly neutralizing supernatants from hybridomas 15C10 and 4A6 were identified.

Three clones were subsequently expanded *in vivo* (a single clone, i.e., 15C10, was also expanded in a hollow fiber system), and the antibody purified by affinity chromatography. All three of the clones were able to bind Neurotrophin- α on the surface of THP-1 cells and were also able to bind (i.e., "capture") Neurotrophin- α from solution.

Specifically, experiments were performed using the anti-Neurotrophin- α monoclonal antibodies described in the second experiment above to determine whether the antibodies neutralize Neurotrophin- α /Neurotrophin- α Receptor binding. Briefly, Neurotrophin- α protein was biotinylated using the EZ-link T NHS-biotin reagent (Pierce, Rockford, Ill.). Biotinylated Neurotrophin- α was then used to identify

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cell surface proteins that bind Neurotrophin- α . Preliminary experiments demonstrated that Neurotrophin- α binds to a receptor on B lymphoid cells.

The inclusion of anti-Neurotrophin- α antibodies generated in the second experiment described above neutralized binding of Neurotrophin- α to a Neurotrophin- α receptor. In a specific embodiment, anti-Neurotrophin- α antibody 15C10 neutralizes binding of Neurotrophin- α to a Neurotrophin- α Receptor.

Thus, the anti-Neurotrophin- α monoclonal antibodies generated in the second experiment described above (in particular, antibody 15C10) recognize and bind to both membrane-bound and soluble Neurotrophin- α protein and neutralize Neurotrophin- α /Neurotrophin- α Receptor binding *in vitro*.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

The entire disclosure of all publications (including patents, patent applications, journal articles, laboratory manuals, books, or other documents) cited herein are hereby incorporated by reference.

Further, the Sequence Listing submitted herewith, and the Sequence Listings submitted in copending application Ser. Nos. 09/005,874, filed Jan. 12, 1998, US60/036,100, filed Jan. 14, 1997, and PCT/US96/17957, filed Oct. 25, 1996, in both computer and paper forms in each case, are hereby incorporated by reference in their entireties.

SEQUENCE LISTING

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<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (212)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (255)
<223> OTHER INFORMATION: n equals a, t, g or c
<221> NAME/KEY: misc feature
<222> LOCATION: (297)
<223> OTHER INFORMATION: n equals a, t, g or c
<221> NAME/KEY: misc feature
<222> LOCATION: (300)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (320)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (335)
<223> OTHER INFORMATION: n equals a, t, g, or c

<400> SEQUENCE: 7
ggntaactct cctgaggggt gagccaagcc ctgccatgta gtgcacgcag gacatcanca      60
aacacannnn ncaggaaata atccattccc tgtggtcact tattctaaag gccccaacct      120
tcaaagttca agtagtgata tggatgactc cacagaaagg gacagctcac gccttacttc      180
ttgccttlaag aaaagagaag aaatgaaact gnaagqagtg tgttccalc ctcccacgga      240
aggaaagccc ctctntccga tctccaaaag acggaagact gctggctgca accttgnn      300
tggcattgtg ttcttgctgn ctcaaggtgg tgttntt      337

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<210> SEQ ID NO 8
<211> LENGTH: 509
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: n
      equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (10)
<223> OTHER INFORMATION: n equals a, t, g, or c

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<221> NAME/KEY: misc feature
<222> LOCATION: (13)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (209)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (315)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (322)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (325)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (334)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (343)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (347)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (351)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (356)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (409) (410)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (416)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (422)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (424)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (426) .. (427)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (429)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (431)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (433)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (438) .. (439)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (443) .. (444)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (446) .. (447)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (449) .. (450)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (452) .. (453)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (458)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (461) .. (462)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (466)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc feature
<222> LOCATION: (469)

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<22> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (471)..(472)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (474)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (472)..(481)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (496)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (498)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (504)
<223> OTHER INFORMATION: n equals a, t, g, or c

<400> SEQUENCE: 8

aattcggcan agnaaactgg ttactttttt atatatgggc aggttttata tactgataag      60
acctacgcc a tgggacatct agtccagagg aagaaggccc atgtcttttg ggaatgaattg      120
agtcctgtga ctttgttttg atgtattcaa aatatgcctg aaacactacc caataattcc      180
tgcattccag ctggcattgc aaaactggna ggaaggagat gaaactcaac ttgcaatacc      240
aggggaaaat gcacaattat cactgggatg gagatgttca ctttttttgg gtgccattga      300
aactctctgt acctctttac aacangtctt gttngctatt ttneetnctt ntctctgtgt      360
aacctcttla gaaaggaagg a tcttaactg gyaataacc caaaaaaann ttaaaagggt      420
angrynnana ngnggggngg tnnnnngnn gnnrtttngg nntatntnt nntngggrrn      480
ngtaaaaatg gggccnangg gggnttttt      509

<210> SEQ ID NO 9
<211> LENGTH: 497
<212> TYPR: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (168)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (213)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (286)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (325)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (346)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (406)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (415)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (419)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (437)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (442)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (467)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature

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<222> LOCATION: (473)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (476)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (481)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (483)...(484)
<223> OTHER INFORMATION: n equals a, t, g, or c
<221> NAME/KEY: misc_feature
<222> LOCATION: (494)
<223> OTHER INFORMATION: n equals a, t, g, or c

<400> SEQUENCE: 9

aattcggcac gagcaaggcc ggccctggagg aagctccagc tgtcaccgcg ggactgaaaa 60
tcttrgaacc accagctcca ggagaaggca actccagtcg gaacagcaga aataagcgtg 120
ccgttcaggg tccagaagaa acagtcacac aagactgctt gcaactgntt gcagacagtg 180
aaacaccaac tatacaaaaa ggctcccttc tgnctccaca ttggggccaa ggaatggaga 240
gattctcttg tctggaaaca ttctgccaaa ctcttcagat actctttnct ctctgggaat 300
caaaagaaaa tctctactta gattnacaca ttctgtccca tgggtntctt aagttttaaa 360
aggggagtgc ccttagggag aanaagggat aaatattggc caaggnactg gttantttnt 420
aaatatggc aggtttntat anctggtagg cctcgccatg ggcattnatt cangngagg 480
ncttctttt qnyntga 497

<210> SEQ ID NO 10
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: primer bind
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 10

gtggatcca gctccgggc agagctg 27

<210> SEQ ID NO 11
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: primer bind
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 11

gtgaagcttt tattacagca gtttcaatgc acc 33

<210> SEQ ID NO 12
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: primer bind
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 12

gtgtcatgag cctccgggca gagctg 26

<210> SEQ ID NO 13
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<221> NAME/KEY: primer bind
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 13

gtgaagcttt tattacagca gtttcaatgc acc 33

<210> SEQ ID NO 14
 <211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: primer bind
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 14

gtgggatccc cgggcagagc tgcagggc 28

<210> SEQ ID NO 15
 <211> LENGTH: 33
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: primer bind
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 15

gtgggatcct tattacagca gtttcaatgc acc 33

<210> SEQ ID NO 16
 <211> LENGTH: 129
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: primer bind
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 16

gctgggatccg caccatgaa ctctctctcc acaagcgcct tgggtccagt tgcctctctcc 60

ctggggctgc tctgtgtgtt gctgtctgct ttctctgccc cagttytgag acaaggggac 120

ctggccagc 129

<210> SEQ ID NO 17
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: primer bind
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 17

gtgggatccc tacagcagtt tcaatgcacc 30

<210> SEQ ID NO 18
 <211> LENGTH: 903
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(798)

<400> SEQUENCE: 18

atg gat gac tcc aca gaa agg gag cag tca cgc ctt act tct tgc ctt 48
 Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
 1 5 10 15

aag aaa aga gaa gaa atg aaa ctg aag gag tgt gtt tcc atc ctc cca 96
 Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro

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20	25	30	
cgg aag gaa agc ccc tct gtc cga tcc tcc aaa qac gga aag ctg ctg			144
Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu			
35	40	45	
gct gca acc ttg ctg ctg gca ctg ctg tct tgc tgc ctc acg gtg gtg			192
Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val			
50	55	60	
tct ttc tac cag gtg gcc gcc ctg caa ggg gac ctg gcc agc ctc cgg			240
Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg			
65	70	75	80
gca gag ctg cag ggc cac cac gcg gag aag ctg cca gca gga gca gga			288
Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly			
85	90	95	
gcc ccc aag gcc ggc ctg gag gaa gcc cca gct gtc acc gcg gga ctg			336
Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu			
100	105	110	
aaa atc ttt gaa cca cca gct cca gga gaa ggc aac tcc agt cag aac			384
Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn			
115	120	125	
agc aga aat aag cgt gcc gtt cag ggt cca gaa gaa aca gga tct tac			432
Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Gly Ser Tyr			
130	135	140	
aca ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt gcc cta gaa			480
Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu			
145	150	155	160
gaa aaa gag aat aaa ata ttg gtc aaa gaa act ggt tac ttt ttt ata			528
Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile			
165	170	175	
tat ggt cag gtt tta tat act gat aag acc tac gcc atg gga car cta			576
Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu			
180	185	190	
att cag agg aag aag gtc cat gtc ttt ggg gat gaa ttg agt ctg gtc			624
Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val			
195	200	205	
act ttg ttt cga tgt att caa aat atg cct gaa aca cta ccc aat aat			672
Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn			
210	215	220	
tcc tgc tat tca gct ggc att gca aaa ctg gaa gaa gga gat gaa ctc			720
Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu			
225	230	235	240
caa ctt gca ata cca aga gaa aat gca caa ata tca ctg ggt gga gat			768
Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp			
245	250	255	
gtc aca ttt ttt ggt gca ttg aaa ctg ctg tgacctatc acaccatgtc			816
Val Thr Phe Phe Gly Ala Leu Lys Leu Leu			
260	265		
tgtagctatt tctctccctt tctctgtacc tctaagaaga aagaatctaa ctgaaaatac			878
caaaaaaaaaa aaaaaaaaaa aaaaa			903
<p><210> SEQ ID NO 19 <211> LENGTH: 266 <212> TYPE: PRT <213> ORGANISM: Homo sapiens</p>			
<p><400> SEQUENCE: 19</p>			
Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu			
1	5	10	15
Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro			
20	25	30	

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Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
 35 40 45
 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
 50 55 60
 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
 65 70 75 80
 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
 85 90 95
 Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
 100 105 110
 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
 115 120 125
 Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Gly Ser Tyr
 130 135 140
 Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu
 145 150 155 160
 Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile
 165 170 175
 Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu
 180 185 190
 Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val
 195 200 205
 Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn
 210 215 220
 Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Gln Gly Asp Glu Leu
 225 230 235 240
 Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp
 245 250 255
 Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
 260 265

<210> SEQ ID NO 20

<211> LENGTH: 136

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp Asp
 1 5 10 15
 Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly Arg
 20 25 30
 Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly Val
 35 40 45
 Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr Met
 50 55 60
 Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu Phe
 65 70 75 80
 Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn Ser
 85 90 95
 Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu Ser
 100 105 110
 Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His Gly
 115 120 125
 Thr Phe Leu Gly Phe Val Lys Leu
 130 135

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<210> SEQ ID NO 21
<211> LENGTH: 462
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE 21
atggtgttcc agggctccga agaaacggtt actcaggact gccttcagct galegcagac   60
cttgaaactc cgaccatcca gaaagggtct tacacctttg ttcttggct gctttctttc   120
aaacgtgggt ctgccttggg agagaagaa aacaaaatcc tggtaaga aactgggtac   180
ttctttatct acggtcaggc tctttacact gataagacct acgccatggg tcacctgatt   240
cagcgtaaga aagttcacgt ttctgggtgac gagctgcttc tggttactct gtttcgctgc   300
attcagaaca tgcgggaacc tcttctcaac aactcctgct actctgctgg catcgcaaaa   360
ctggaaagag gtctatgaact gcagctggca attcctcctg aaaaacgaca aatttctctg   420
gacgggtgatg taacctctct tgggtgactg aaacttctgt aa                     462

<210> SEQ ID NO 22
<211> LENGTH: 1540
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1) (1468)

<400> SEQUENCE: 22
cgc gtg gta gac ctg tca gct cct cct gca cca tgc ctg cct gga tgc   48
Arg Val Val Asp Leu Ser Ala Pro Pro Ala Pro Cys Leu Pro Gly Cys
1 5 10 15

cgc cat tct cca cat gat gat aat gga atg aac ctg aga aac aga act   96
Arg His Ser Gln His Asp Asp Asn Gly Met Asn Leu Arg Asn Arg Thr
20 25 30

tac aca ttt gtt cca tgg ctt ctg agc ttt aaa aga gga aat gcc ttg   144
Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu
35 40 45

gag gag aag gag aac aaa ata gtg gtg agg caa aca ggc tat ttc ttc   192
Glu Glu Lys Glu Asn Lys Ile Val Val Arg Gln Thr Gly Tyr Phe Phe
50 55 60

atc tac agc caq gtt cta tac acg gac ccc atc ttt gct atg ggt cat   240
Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro Ile Phe Ala Met Gly His
65 70 75 80

gtc atc cag agg aag aaa gta cac gtc ttt ggg gac gag ctg agc ctg   288
Val Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
85 90 95

gtg acc ctg ttc cga tgt att cag aat atg ccc aaa aca ctg ccc aac   336
Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Lys Thr Leu Pro Asn
100 105 110

aat tcc tgc tac tgg gcl ggc atc gcy agg ctg gaa gaa gga gat gag   384
Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu
115 120 125

att cag ctt gca att cct cgg gag aat gca cag att tca cgc aac gga   432
Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly
130 135 140

gac gac acc ttc ttt ggt gcc cta aaa ctg ctg taa ctcccttgcct   478
Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu
145 150 155

ggagtgcgtg atcccccttc ctgcttttct ctgtacctcc gagggagaaa cagacgactg   538

gaaaaactaa aagatgggga aagccgtcag cgaaggtttt ctctgacccc gttgaatctg   598

atccaaacca ggaaatataa cagacagcca caaccgaagt gtgccatgtg agttatgaga   658

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aacggagccc gcgctcagaa agaccggatg aggaagaccg tttctccag tcttttgcca 718
aacgcaccg caaccttgc ttttgccttg ggtgacacat gttcagaatg caggagagatt 778
tctttgtttt gcgatttgc atgagaagag ggcccacaac tgcaggtcac tgaagcattc 838
acgctaagtc tcaggattta cctccccttc tcatgctaag tacacacacg cttttttcca 898
ggtaatacta tgggatacta tggaaagggt gtttggtttt aaatcagaa gcttgaact 958
ggcaatagac aaaaatcctt ataaattcaa gtgtaataa aacttaarta aaagggttta 1018
agtgtgaaaa aaaaaaaaaa aa 1040

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<210> SEQ ID NO 23
<211> LENGTH: 155
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 23

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Arg Val Val Asp Leu Ser Ala Pro Pro Ala Pro Cys Leu Pro Gly Cys
 1          5          10          15
Arg His Ser Gln His Asp Asp Asn Gly Met Asn Leu Arg Asn Arg Thr
          20          25          30
Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu
          35          40          45
Glu Glu Lys Glu Asn Lys Ile Val Val Arg Gln Thr Gly Tyr Phe Phe
 50          55          60
Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro Ile Phe Ala Met Gly His
 65          70          75          80
Val Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
          85          90          95
Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Lys Thr Leu Pro Asn
          100          105          110
Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu
          115          120          125
Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly
          130          135          140
Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu
          145          150          155

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<210> SEQ ID NO 24
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: primer bind
<223> OTHER INFORMATION: primer

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<400> SEQUENCE: 24

ccaccagctc caggagaagg caactc

26

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<210> SEQ ID NO 25
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: primer bind
<223> OTHER INFORMATION: primer

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<400> SEQUENCE: 25

accgcgggac tgaaaatct

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-continued

<210> SEQ ID NO 26
 <211> LENGTH: 23
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 26

cacgcttatt tctgctgttc tga

23

<210> SEQ ID NO 27
 <211> LENGTH: 657
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 27

taccaggctgg cyggcgtgca aggggacctg gccagcctcc gggcagagct gcaaggccac 60
 cacgcggaga agctgccagc aagagcaaga gcccccagg ccggctctggg gguagctcca 120
 gctgtcaccg caggactgaa aatctttgaa ccacagctc caggagaagg caactccagt 180
 cagagcagca gaaataagcg tgctattcag ggtycagaag aaacagtcac tcaagactgc 240
 ttgcaactga ttgcagacag tgaacacca actatacaaa aaggatctta cacatttctt 300
 ccatggcttc tcagctttaa aaggggaggt gccctagaag aaaaagagaa taagatattg 360
 gtcaaaagaa ctggttactt ttttatatat ggtcagggtt tatacactga taagacctat 420
 gccatgggac atctaatcca gaggaagaaa gtccatgctt ttggggatga attgagctct 480
 gtgactttgt ttgcagatct tcaaaatarg cctgaacac taccacaata tccctgctat 540
 tcagctggca ttgcataact ggaayaagga gatgaacttc aacttgcatt acccagagaa 600
 aatgcacaaa tatcactgga tggagatgtc acattttttg gtgcctctaa actgctg 657

<210> SEQ ID NO 28
 <211> LENGTH: 219
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 28

Tyr Gln Val Ala Val Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu
 1 5 10 15
 Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Arg Ala Arg Ala Pro
 20 25 30
 Lys Ala Gly Leu Gly Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile
 35 40 45
 Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Ser Ser Arg
 50 55 60
 Asn Lys Arg Ala Ile Gln Gly Ala Glu Glu Thr Val Ile Gln Asp Cys
 65 70 75 80
 Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser
 85 90 95
 Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu
 100 105 110
 Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe
 115 120 125
 Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His
 130 135 140
 Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
 145 150 155 160

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-continued

Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn
165 170 175

Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu
180 185 190

Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly
195 200 205

Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
210 215

<210> SEQ ID NO 29

<211> LENGTH: 657

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 29

taccaggtgg cggccgtgca aggggacctg gccagctcc gggcagagct gcagagccac 60
cacgaggaga agctgccagc aagagcaaga gcccceaaagg cccgtctggg ggaagctcca 120
gctgtaccg cgggactgaa aatctttgaa ccaccagctc caggagaagg caactccagt 180
cagagcagca gaaataagcg tgctattcag ggtgcagaag aaacagtcac tcaagactgc 240
ttgcaactga ttgcagacag tgaaacacca actatacaaa aaggacttta cacatttgc 300
ccatggcttc tcagctttaa aaggggaagt gccctagaag aaaaagagaa taatatattg 360
gtcaaaagaa ctggttaact ttttatatat ggctcaggttt tatacactga taagacctat 420
gccatgggac atctaattca gaggaaaaaa gtccatgtct ttggggatga attgagtctg 480
gtgacrrtgt ttgatgtat tcaaaatag cctgaacac taccacaataa ttcctgctat 540
tcagctggca ttgcaaaact ggaagaaggg gatgaacttc aacttgcac accacagaaa 600
aatgcacaaa tatcactgga tggagatgtc acattttttg gtgcctctaa actgctg 657

<210> SEQ ID NO 30

<211> LENGTH: 219

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 30

Tyr Gln Val Ala Val Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu
1 5 10 15

Leu Gln Ser His His Ala Glu Lys Leu Pro Ala Arg Ala Arg Ala Pro
20 25 30

Lys Ala Gly Leu Gly Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile
35 40 45

Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Ser Ser Arg
50 55 60

Asn Lys Arg Ala Ile Gln Gly Ala Glu Glu Thr Val Ile Gln Asp Cys
65 70 75 80

Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser
85 90 95

Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu
100 105 110

Glu Glu Lys Gly Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe
115 120 125

Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His
130 135 140

Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
145 150 155 160

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-continued

Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn
 165 170 175
 Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu
 180 185 190
 Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly
 195 200 205
 Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
 210 215

<210> SEQ ID NO 31
 <211> LENGTH: 38
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: primer bind
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 31

ggtagccggtt tctaacgcgg cggttcaggg tccagaag

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<210> SEQ ID NO 32
 <211> LENGTH: 49
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: primer bind
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 32

ctgggtcggg ccagggacc aagcttgtag cttagatctt ttctagatc

49

<210> SEQ ID NO 33
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: primer bind
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 33

ctggtagtct ttcggagtgt g

21

<210> SEQ ID NO 34
 <211> LENGTH: 19
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: primer bind
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 34

cgcgttagaa acgycgacc

19

<210> SEQ ID NO 35
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: primer bind
 <223> OTHER INFORMATION: primer
 <221> NAME/KEY: misc feature
 <222> LOCATION: (7)
 <223> OTHER INFORMATION: n equals deoxyinosine
 <221> NAME/KEY: misc feature
 <222> LOCATION: (12)
 <223> OTHER INFORMATION: n equals deoxyinosine
 <221> NAME/KEY: misc feature
 <222> LOCATION: (16)

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<223> OTHER INFORMATION: n equals deoxyinosine

<400> SEQUENCE: 35

taccagntgg cngccntgca ag

22

<210> SEQ ID NO 36

<211> LENGTH: 22

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<221> NAME/KEY: primer bind

<223> OTHER INFORMATION: primer

<221> NAME/KEY: misc feature

<222> LOCATION: {3}

<223> OTHER INFORMATION: n equals deoxyinosine

<221> NAME/KEY: misc feature

<222> LOCATION: {14}

<223> OTHER INFORMATION: n equals deoxyinosine

<221> NAME/KEY: misc feature

<222> LOCATION: {16}..{17}

<223> OTHER INFORMATION: n equals deoxyinosine

<400> SEQUENCE: 36

gtacacgcag tttnanrkjca cc

22

<210> SEQ ID NO 37

<211> LENGTH: 566

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 37

atggatgagr ctgcaaaagac cctgccacca ccgctgctct gtttttctc cgagaagga 60

gaagatatga aagctgggaa tgatcccatc actctgaga agggaggagg tjcctgggtt 120

gggatctgca gggatggaa gctgctggct gctacctcc tctgggccc gttgtccagc 180

agtttccag cgtatgctct gtaccagttg gctgctctc aagcagacct gatgaacctg 240

cgcatggagg tgcagagcta ccgaggttca gcaacaccag ccgcgcgggg tctccagag 300

ttgacccctg gacgcaaat cctgacaccy gaagctctc gacccacaa ctccagccgc 360

ggccacagga acagacgcgc ctccagggca ccagaggaaa cagaacaaga tctagacctc 420

tcagctctc ctgcaccatg cctgcttggg tgcgcgctt ctcaacatga tgataatgga 480

atgaacctca gaaacatcat tcaagactgt ctgcagctga ttgcagacag cgacacgcgc 540

gccttggagg agaaagagaa caaatagtg gtgaggcaaa caggctattt ctccatctac 600

agccaggttc tatcacagga ccccatcttc gctatgggtc atgtcatcca gaggaagaaa 660

gtacacgtct ttggggacga gctyagcttg gtgacctgt tccgatglat tcagaatatg 720

ccccaaacac tgcacaacaa ttcctgctac tgggtggca tgcgagggct ggaagaagga 780

gatgagatcc agcttgcaat tctcggggag aatgcacaga ttccacgaa cggagacgac 840

accttttttg gtgcctataa actgct 866

<210> SEQ ID NO 38

<211> LENGTH: 289

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 38

Met Asp Glu Ser Ala Lys Thr Leu Pro Pro Pro Cys Leu Cys Phe Cys
1 5 10 15Ser Glu Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro
20 25 30

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-continued

Gln Lys Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu
 35 40 45
 Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala
 50 55 60
 Met Ser Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu
 65 70 75 80
 Arg Met Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala
 85 90 95
 Gly Ala Pro Glu Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala
 100 105 110
 Pro Arg Pro His Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe
 115 120 125
 Gln Gly Pro Glu Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro
 130 135 140
 Ala Pro Cys Leu Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly
 145 150 155 160
 Met Asn Leu Arg Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp
 165 170 175
 Ser Asp Thr Pro Ala Leu Glu Glu Lys Glu Asn Lys Ile Val Val Arg
 180 185 190
 Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro
 195 200 205
 Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys Val His Val Phe
 210 215 220
 Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met
 225 230 235 240
 Pro Lys Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg
 245 250 255
 Leu Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala
 260 265 270
 Gln Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu
 275 280 285
 Leu

<210> SEQ ID NO 39
 <211> LENGTH: 38
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: primer bind
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 39

cagactggat ccgccacct ggaatgactcc acagaaag

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<210> SEQ ID NO 40
 <211> LENGTH: 33
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: primer bind
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 40

cagactggta ccgtctcg tgcaactacat ggc

33

<210> SEQ ID NO 41
 <211> LENGTH: 21
 <212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: primer, bind
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 41

tggtgtcttt ctaccagggtg g

21

<210> SEQ ID NO 42
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: primer, bind
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 42

ttttctctgg accctgaacy g

21

What is claimed is:

1. A method of inhibiting B lymphocytes comprising administering an effective amount of an antibody that binds a protein whose amino acid sequence is
 MDISTIEREQS RLTSCLKKRE EMKIKECVSI
 LPRKESPSVR SSKIXKILAA TLLALLSCU LTVVS-
 FYQVAALQGHILASLR AELQGHILAEKLPAGAGAPKA
 GLEAPAVTA GLKIFEPAP GEGNSSQNSR
 NKRAVQGPFE TVTQDCLQL ADSEIPTIQK GSYT-
 FVPWLL SFKRGSALKE KENKILVKET GYFFIYGQVL
 YTDKTYAMGILLQRRKKVHYF GDEI SILTLE RCION-
 MPETL PNNSCYSAGI AKLEEGDEIQ LAIPRENAQI
 SLDGDVTFFGALKIL (SEQ ID NO:2)

wherein B lymphocytes are inhibited.

2. A method of inhibiting B lymphocyte proliferation comprising administering an effective amount of an antibody that binds Neutrokin- α (SEQ ID NO:2), wherein B lymphocyte proliferation is inhibited.

3. A method of inhibiting B lymphocyte differentiation comprising administering an effective amount of an antibody that binds Neutrokin- α (SEQ ID NO:2), wherein B lymphocyte differentiation is inhibited.

4. The method of any one of claims 1-3, wherein the antibody is a monoclonal antibody.

5. The method of any one of claims 1-3, wherein the antibody is recombinantly produced.

6. The method of any one of claims 1-3, wherein the antibody is a chimeric antibody.

7. The method of any one of claims 1-3, wherein the antibody is a humanized antibody.

8. The method of any one of claims 1-3, wherein the antibody comprises human constant domains.

9. The method of any one of claims 1-3, wherein the antibody is a F(ab')₂ fragment.

10. The method of any one of claims 1-3, wherein the antibody is a polyclonal antibody.

11. The method of any one of claims 1-3, wherein the antibody is a Fab fragment.

12. The method of any one of claims 1-3, wherein the antibody is administered to an individual.

13. The method of any one of claims 1-3, wherein the antibody is administered to a cell culture.

14. A method of treating an autoimmune disease or disorder comprising administering to an individual, an effective amount of an antagonistic antibody or portion thereof that

specifically binds a protein consisting of the amino acid sequence of amino acid residues 134-285 of SEQ ID NO:2.

15. The method of claim 14 wherein the antibody or portion thereof is a monoclonal antibody.

16. The method of claim 14 wherein the antibody or portion thereof is a polyclonal antibody.

17. The method of claim 14 wherein the antibody or portion thereof is a Fab fragment.

18. The method of claim 14 wherein the antibody or portion thereof is labeled.

19. The method of claim 18 wherein the label is selected from the group consisting of:

- (a) an enzyme label;
- (b) a radioisotope;
- (c) a fluorescent label; and
- (d) biotin.

20. The method of claim 19 wherein the label is a radioisotope selected from the group consisting of:

- (a) ¹²⁵I;
- (b) ¹³¹I;
- (c) ¹³¹I;
- (d) ¹¹²In; and
- (e) ^{99m}Tc.

21. The method of claim 14 wherein the autoimmune disease or disorder is systemic lupus erythematosus.

22. The method of claim 14 wherein said antibody or portion thereof is administered intravenously.

23. The method of claim 14 which comprises administering between 0.1 and 20 mg/kg of the patient's body weight of said antibody or portion thereof.

24. The method of claim 14, wherein the autoimmune disease or disorder is selected from the group consisting of systemic lupus erythematosus, idiopathic thrombocytopenic purpura (ITP), Sjogren's syndrome, Waldenstrom's macroglobulinaemia, multiple sclerosis, cancer, asthma, nephritis, diabetes, scleroderma, vasculitis, cryoglobulinaemia, graft-versus-host disease (GVHD), renal transplantation, and antiphospholipid syndrome.

25. The method of claim 24, wherein the antibody or portion thereof is a monoclonal antibody.

26. The method of claim 24, wherein the antibody or portion thereof is a polyclonal antibody.

27. The method of claim 24, wherein the antibody or portion thereof is a Fab fragment.

28. The method of claim 24, wherein the antibody or portion thereof is labeled.

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29. The method of claim 28, wherein the label is selected from the group consisting of:

- (a) an enzyme label;
- (b) a radioisotope;
- (c) a fluorescent label; and
- (d) biotin.

30. The method of claim 29, wherein the label is a radioisotope selected from the group consisting of:

- (a) ^{125}I ;
- (b) ^{121}I ;
- (c) ^{131}I ;
- (d) ^{112}In ; and
- (e) $^{99\text{m}}\text{Tc}$.

31. The method of claim 24, wherein the antibody or portion thereof is administered intravenously.

32. The method of claim 24, wherein the method comprises administering between 0.1 and 20 mg/kg of the patient's body weight of the antibody or portion thereof.

33. The method of claim 24, wherein the autoimmune disease or disorder is idiopathic thrombocytopenic purpura (ITP).

34. The method of claim 24, wherein the autoimmune disease or disorder is Sjogren's syndrome.

35. The method of claim 24, wherein the autoimmune disease or disorder is multiple sclerosis.

36. The method of claim 24, wherein the autoimmune disease or disorder is renal transplantation.

37. A method of treating rheumatoid arthritis comprising administering to an individual, an effective amount of an antagonistic antibody or portion thereof that specifically binds a protein consisting of the amino acid sequence of amino acid residues 134-285 of SEQ ID NO:2.

38. The method of claim 37 wherein the antibody or portion thereof is a monoclonal antibody.

39. The method of claim 37 wherein the antibody or portion thereof is a polyclonal antibody.

40. The method of claim 37 wherein the antibody or portion thereof is a Fab fragment.

41. The method of claim 37 wherein the antibody or portion thereof is labeled.

42. The method of claim 41 wherein the label is selected from the group consisting of:

- (a) an enzyme label;
- (b) a radioisotope;
- (c) a fluorescent label; and
- (d) biotin.

43. The method of claim 42 wherein the label is a radioisotope selected from the group consisting of:

- (a) ^{125}I ;
- (b) ^{121}I ;
- (c) ^{131}I ;
- (d) ^{112}In ; and
- (e) $^{99\text{m}}\text{Tc}$.

44. The method of claim 37 wherein said antibody or portion thereof is administered intravenously.

45. The method of claim 37 which comprises administering between 0.1 and 20 mg/kg of the patient's body weight of said antibody or portion thereof.

46. A method of inhibiting B lymphocyte proliferation, differentiation or survival comprising administering to an individual or a cell culture containing B lymphocytes, an effective amount of an antagonistic antibody or portion thereof that specifically binds a protein consisting of an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of amino acid residues n to 285 of SEQ ID NO:2, where n is an integer in the range of 2-190;

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(b) the amino acid sequence of amino acid residues 1 to m of SEQ ID NO:2, where m is an integer in the range of 274 to 284; and

(c) the amino acid sequence of amino acid residues n to m of SEQ ID NO:2, where n is an integer in the range of 2-190 and m is an integer in the range of 274-284.

47. The method of claim 46 wherein the protein consists of amino acid sequence (a).

48. The method of claim 46 wherein the protein consists of amino acid sequence (b).

49. The method of claim 46 wherein the protein consists of amino acid sequence (c).

50. The method of claim 46 wherein the antibody or portion thereof is a monoclonal antibody.

51. The method of claim 46 wherein the antibody or portion thereof is a polyclonal antibody.

52. The method of claim 46 wherein the antibody or portion thereof is a Fab fragment.

53. The method of claim 46 wherein the antibody or portion thereof is labeled.

54. The method of claim 53 wherein the label is selected from the group consisting of:

- (a) an enzyme label;
- (b) a radioisotope;
- (c) a fluorescent label; and
- (d) biotin.

55. The method of claim 54 wherein the label is a radioisotope selected from the group consisting of:

- (a) ^{125}I ;
- (b) ^{121}I ;
- (c) ^{131}I ;
- (d) ^{112}In ; and
- (e) $^{99\text{m}}\text{Tc}$.

56. The method of claim 46 which comprises administering to an individual an effective amount of said antagonistic antibody or portion thereof.

57. The method of claim 46 which comprises administering to a cell culture containing B lymphocytes an effective amount of said antagonistic antibody or portion thereof.

58. A method of inhibiting B lymphocyte proliferation, differentiation, or survival comprising administering to an individual or a cell culture containing B lymphocytes, an effective amount of an antagonistic antibody or portion thereof that specifically binds a protein consisting of the amino acid sequence of amino acid residues 134-285 of SEQ ID NO:2.

59. The method of claim 58 wherein the antibody or portion thereof is a monoclonal antibody.

60. The method of claim 58 wherein the antibody or portion thereof is a polyclonal antibody.

61. The method of claim 58 wherein the antibody or portion thereof is a Fab fragment.

62. The method of claim 58 wherein the antibody or portion thereof is labeled.

63. The method of claim 62 wherein the label is selected from the group consisting of:

- (a) an enzyme label;
- (b) a radioisotope;
- (c) a fluorescent label; and
- (d) biotin.

64. The method of claim 63 wherein the label is a radioisotope selected from the group consisting of:

- (a) ^{125}I ;
- (b) ^{121}I ;
- (c) ^{131}I ;
- (d) ^{112}In ; and
- (e) $^{99\text{m}}\text{Tc}$.

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65. The method of claim 58 which comprises administering to an individual an effective amount of said antagonistic antibody or portion thereof.

66. The method of claim 58 which comprises administering to a cell culture containing B lymphocytes an effective amount of said antagonistic antibody or portion thereof.

67. A method of treating an autoimmune disease or disorder comprising administering to an individual, an effective amount of an antagonistic antibody or portion thereof that specifically binds to an isolated recombinant Neutrokin- α protein purified from a cell culture wherein the cells in said cell culture comprise a polynucleotide encoding amino acids 1-285 of SEQ ID NO:2 operably associated with a regulatory sequence that controls gene expression.

68. The method of claim 67 wherein the antibody or portion thereof is a monoclonal antibody.

69. The method of claim 67 wherein the antibody or portion thereof is a polyclonal antibody.

70. The method of claim 67 wherein the antibody or portion thereof is a Fab fragment.

71. The method of claim 67 wherein the antibody or portion thereof is labeled.

72. The method of claim 71 wherein the label is selected from the group consisting of:

- (a) an enzyme label;
- (b) a radioisotope;
- (c) a fluorescent label; and
- (d) biotin.

73. The method of claim 72 wherein the label is a radioisotope selected from the group consisting of:

- (a) ^{125}I ;
- (b) ^{121}I ;
- (c) ^{111}I ;
- (d) ^{112}In ; and
- (e) $^{99\text{m}}\text{Tc}$.

74. The method of claim 67 wherein the autoimmune disease or disorder is systemic lupus erythematosus.

75. The method of claim 67 wherein said antibody or portion thereof is administered intravenously.

76. The method of claim 67 which comprises administering between 0.1 and 20 mg/kg of the patient's body weight of said antibody or portion thereof.

77. The method of claim 67, wherein the autoimmune disease or disorder is selected from the group consisting of systemic lupus erythematosus, idiopathic thrombocytopenic purpura (ITP), Sjogren's syndrome, Waldenstrom's macroglobulinaemia, multiple sclerosis, cancer, asthma, nephritis, diabetes, scleroderma, vasculitis, cryoglobulinaemia, graft-versus-host disease (GVHD), renal transplantation, and antiphospholipid syndrome.

78. The method of claim 77, wherein the autoimmune disease or disorder is systemic lupus erythematosus.

79. The method of claim 77, wherein the autoimmune disease or disorder is idiopathic thrombocytopenic purpura (ITP).

80. The method of claim 77, wherein the autoimmune disease or disorder is Sjogren's syndrome.

81. The method of claim 77, wherein the autoimmune disease or disorder is multiple sclerosis.

82. The method of claim 77, wherein the autoimmune disease or disorder is renal transplantation.

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83. A method of treating rheumatoid arthritis comprising administering to an individual, an effective amount of an antagonistic antibody or portion thereof that specifically binds to an isolated recombinant Neutrokin- α protein purified from a cell culture wherein the cells in said cell culture comprise a polynucleotide encoding amino acids 1-285 of SEQ ID NO:2 operably associated with a regulatory sequence that controls gene expression.

84. The method of claim 83 wherein the antibody or portion thereof is a monoclonal antibody.

85. The method of claim 83 wherein the antibody or portion thereof is a polyclonal antibody.

86. The method of claim 83 wherein the antibody or portion thereof is a Fab fragment.

87. The method of claim 83 wherein the antibody or portion thereof is labeled.

88. The method of claim 87 wherein the label is selected from the group consisting of:

- (a) an enzyme label;
- (b) a radioisotope;
- (c) a fluorescent label; and
- (d) biotin.

89. The method of claim 88 wherein the label is a radioisotope selected from the group consisting of:

- (a) ^{125}I ;
- (b) ^{121}I ;
- (c) ^{131}I ;
- (d) ^{112}In ; and
- (e) $^{99\text{m}}\text{Tc}$.

90. The method of claim 83 wherein said antibody or portion thereof is administered intravenously.

91. The method of claim 83 which comprises administering between 0.1 and 20 mg/kg of the patient's body weight of said antibody or portion thereof.

92. A method of treating an autoimmune disease in an animal comprising administering a therapeutically effective amount of an anti-Neutrokin- α antibody that binds to human Neutrokin α polypeptide having the amino acid sequence of SEQ ID NO:2.

93. The method of claim 92, wherein the antibody is a monoclonal antibody.

94. The method of claim 92, wherein the antibody is recombinantly produced.

95. The method of claim 92, wherein the antibody is a chimeric antibody.

96. The method of claim 92, wherein the antibody is a humanized antibody.

97. The method of claim 92, wherein the antibody comprises human constant domains.

98. The method of claim 92, wherein the antibody is a F(ab')₂ fragment.

99. The method of claim 92, wherein the animal is human.

100. The method of claim 92, further comprising detecting the levels of B cell growth and immunoglobulin production in the animal.

101. The method of claim 92, further comprising detecting the level of B cell growth in the animal.

102. The method of claim 92, further comprising detecting the level of immunoglobulin production in the animal.

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